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(FILE 'HCAPLUS' ENTERED AT 09:08:19 ON 07 APR 1998)

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      DEL HIS Y
L1      100 S MAGE 1
L2      0 S 11540
L3      5 S 11540/AB
L4      0 S L3 AND (ANTIBOD? OR MONOCLONAL OR ANTIBOD?/AB OR MONOCL
L5      122515 S PROTEIN# (L) SEQUENCE#
L6      204326 S SEQUENCE#
L7      13 S L1 (L) L6
L8      16383 S TUMOR (L) (PROTEIN# OR ANTIGEN#)
L9      8675 S MELANOMA#
L10     76803 S MOLECULAR WEIGHT OR KD OR KILODALTON? OR KILO DALTON# O
L11     368491 S (MOLECULAR WEIGHT OR KD OR KILODALTON? OR KILO DALTON#
L12     666 S L8 AND L9
L13     64 S L12 AND L11
L14     77 S L12 AND (L10 OR L11)
L15     735 S (46 OR 34) (L) (L10 OR L11)
L16     1 S L14 AND L15
L17     17 S (46 OR 46/AB OR 34/AB OR 34) (L) (KDS OR KDS/AB)
L18     0 S L17 AND L14

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=> d .ca 17 1-13; all 116

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L7      ANSWER 1 OF 13 HCAPLUS COPYRIGHT 1998 ACS
AN      1997:625618 HCAPLUS
DN      127:304120
TI      Recombinant tumor-specific antigen-encoding adenoviral vectors for
human tumor gene therapy
IN      Boon, Falleur; Duffour, Marie-therese; Haddada, Hedi; Lurquin,
Christophe; Perricaudet, Michel; Uyttenhoveghesquiere, Catherine;
Warnier, Guy
PA      Rhone-Poulenc Rorer S.A., Fr.; Ludwig Institute for Cancer Research;
Boon, Falleur; Duffour, Marie-Therese; Haddada, Hedi; Lurquin,
Christophe; Perricaudet, Michel; Uyttenhoveghesquiere, Catherine;
Warnier, Guy
SO      PCT Int. Appl., 41 pp.
CODEN: PIXXD2
PI      WO 9734009 A1 970918
DS      W: AL, AU, BA, BB, BG, BR, CA, CN, CU, CZ, EE, GE, GH, HU, IL, IS,
JP, KP, KR, LC, LK, LR, LT, LV, MG, MK, MN, MX, NO, NZ, PL, RO,
SG, SI, SK, TR, TT, UA, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD,
RU, TJ, TM
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FI, FR, GA, GB,
GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG
AI      WO 97-FR435 970312
PRAI    FR 96-3207 960314
DT      Patent
LA      French
AB      A method for treating human tumors by gene therapy is disclosed. In
particular, defective recombinant viruses with a sequence coding for
a human tumor-specific antigen, and the use thereof for treating or
preventing human tumors, as well as producing specific cytotoxic
T-cells (CTLs) in vitro or ex vivo, are disclosed. Preferred

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tumor-specific antigens are Mage-1, Mage-3, Bage, Rage and Gage. Pharmaceutical compns. comprising said viruses, particularly in injectable form, are also disclosed.

IC ICM C12N015-86
ICS C07K014-705; A61K048-00; C12N005-10; A61K039-00; C12N015-12

CC 3-5 (Biochemical Genetics)
Section cross-reference(s): 1

IT DNA **sequences**
(of tumor antigen **Mage-1**, Mage-3 and P1A
peptide-encoding DNA of mammal)

IT 197253-12-6
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(**Mage-1** peptide-encoding **sequence**;
recombinant tumor-specific antigen-encoding adenoviral vectors
for human tumor gene therapy)

L7 ANSWER 2 OF 13 HCAPLUS COPYRIGHT 1998 ACS
AN 1996:610305 HCAPLUS
DN 125:273611
TI Peptides derived from tumor rejection antigen precursor molecule
MAGE-1 that bind MHC molecule HLA-C clone 10, and their uses
IN Van der Bruggen, Pierre; Boon-Falleur, Thierry
PA Ludwig Institute for Cancer Research, USA
SO U.S., 6 pp. Cont.-in-part of U.S. Ser. 8,446, abandoned.
CODEN: USXXAM

PI US 5558995 A 960924
AI US 94-195186 940214
PRAI US 93-8446 930122
DT Patent
LA English

AB The invention relates to the identification of complexes of
HLA-C-clone 10 and MAGE-1 derived peptides on the surfaces of
abnormal cells. These peptides presented by HLA-C-clone 10 are
identical to those presented by HLA-A1. These peptides can
therefore be used in the diagnosis of melanoma and in treatment by
selection of pools of cytotoxic T-lymphocytes.

IC ICM C12N005-08
ICS C07K007-06; C07K007-08; G01N033-68

NCL 435007240
CC 15-2 (Immunochemistry)

IT 168836-14-4 170140-66-6 170173-06-5
RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological
study); USES (Uses)
(amino acid **sequence**; peptides derived from tumor
rejection antigen precursor mol. **MAGE-1** that
bind MHC mol. HLA-C clone 10, and their uses)

L7 ANSWER 3 OF 13 HCAPLUS COPYRIGHT 1998 ACS
AN 1996:494712 HCAPLUS
DN 125:165697
TI Monoclonal antibodies which bind to tumor rejection antigen
precursor MAGE-1 and recombinant MAGE-1 oligopeptides
IN Chen, Yao-tseng; Stockert, Elisabeth; Chen, Yachi; Garin-chesa,
Pilar; Rettig, Wolfgang J.; Van, Der Bruggen Pierre; Boon-falleur,
Thierry; Old, Lloyd J.
PA Ludwig Institute for Cancer Research, USA; Cornell Research

Foundation, Inc.

SO U.S., 14 pp. Cont.-in-part of U.S. Ser. No. 37,280.
CODEN: USXXAM

PI US 5541104 A 960730

AI US 94-190411 940201

PRAI US 91-705702 910523
US 91-728838 910709
US 91-764365 910923
US 91-807043 911212
US 93-37230 930326

DT Patent

LA English

AB The invention relates to monoclonal antibodies which specifically bind to the tumor rejection antigen precursor mol. MAGE-1, hybridomas which produce these monoclonal antibodies, and their use. Also described is a recombinant form of MAGE-1, peptides which are useful as immunogens, and immunogenic compns. contg. the peptides and an adjuvant. In example, demonstrated were mol. cloning of recombinant MAGE-1 gene from human melanoma cell line MZ2-MEL 3.1, prepn. of peptides for raising monoclonal antibodies, binding of the monoclonal antibody 454 to testis lysate and MAGE-1-pos. melanomas, etc.

IC ICM C12P021-04
ICS C12P021-08; C12N005-00; C07K016-00

NCL 435240270

CC 15-3 (Immunochemistry)
Section cross-reference(s): 3

IT Deoxyribonucleic acid **sequences**
Protein **sequences**
Testis
(prepn. of monoclonal antibodies and recombinant peptides of tumor rejection antigen precursor **MAGE-1** as immunogen)

IT 180473-66-9
RL: PRP (Properties)
(nucleotide **sequence**; prepn. of monoclonal antibodies and recombinant peptides of tumor rejection antigen precursor **MAGE-1** as immunogen)

L7 ANSWER 4 OF 13 HCAPLUS COPYRIGHT 1998 ACS

AN 1996:22405 HCAPLUS

DN 124:53579

TI MAGE-1-specific precursor cytotoxic T-lymphocytes present among tumor-infiltrating lymphocytes from a patient with breast cancer: characterization and antigen-specific activation

AU Toso, John F.; Oei, Coreen; Oshidari, Farshid; Tartaglia, James; Paoletti, Enzo; Lyster, H. Kim; Talib, Sohel; Weinhold, Kent J.

CS Departments of Pathology and Surgery, Duke University Medical Center, Durham, NC, 27710, USA

SO Cancer Res. (1996), 56(1), 16-20
CODEN: CNREA8; ISSN: 0008-5472

DT Journal

LA English

AB A potential target for development of tumor-specific immunotherapeutic strategies is the MAGE-1 gene. The authors have utilized a recently developed recombinant canarypox (ALVAC) virus vector contg. the MAGE-1 gene (vCP235) to activate CTLs from a

breast cancer patient bearing a MAGE-1+ tumor. Tumor-infiltrating lymphocytes (TILs) obtained from the tumor of a patient were stimulated in vitro with irradiated autologous peripheral blood mononuclear cells acutely infected with the vCP235 construct. These TILs preferentially expanded approx. 6-fold over a 16-day culture period and specifically recognized an allogeneic transformed B-cell line acutely infected with a vaccinia-MAGE-1 recombinant targeting vector (vP1188) in the context of HLA-A2 and/or B7. TCR V.beta. anal. of in vitro expanded T cells by a quant. multiprobe RNase protection assay revealed preferential expansion of TCR V.beta.6.3 and V.beta.6.4. In addn., homologous T-cell receptor .beta. CDR3 joining sequences were found in the in vitro stimulated cultures. These results suggest that tumor antigen-specific, MHC-restricted CTLs may be derived from precursor CTLs present in TILs obtained from patients with MAGE-1+ tumors by in vitro stimulation with recombinant avipox MAGE-1 virus-infected autologous cells. Collectively, these findings provide a rationale for tumor-assocd. antigen-based immunization as a means of activating precursor CTLs residing in patients with tumors expressing defined tumor-assocd. antigens such as MAGE-1.

- CC 15-8 (Immunohistochemistry)
Section cross-reference(s): 3, 14
- IT Protein **sequences**
(TCR .beta.-subunit VDJ CDR3 junction **sequences** in **MAGE-1**-specific precursor cytotoxic T-lymphocytes present among tumor-infiltrating lymphocytes from human with breast cancer)
- IT Gene, animal
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(TCR .beta.-subunit VDJ CDR3 junction **sequences** in **MAGE-1**-specific precursor cytotoxic T-lymphocytes present among tumor-infiltrating lymphocytes from human with breast cancer)
- IT Antigen receptors
Receptors
RL: BOC (Biological occurrence); BIOL (Biological study); OCCU (Occurrence)
(TCR .alpha..beta. (T-cell antigen receptor .alpha..beta.), .beta.-subunit, genes for; TCR .beta.-subunit VDJ CDR3 junction **sequences** in **MAGE-1**-specific precursor cytotoxic T-lymphocytes present among tumor-infiltrating lymphocytes from human with breast cancer)
- L7 ANSWER 5 OF 13 HCAPLUS COPYRIGHT 1998 ACS
AN 1995:874800 HCAPLUS
DN 123:283637
TI Monoclonal antibodies which bind to tumor rejection antigen precursor MAGE-1, recombinant MAGE-1, and MAGE-1-derived immunogenic peptides
IN Chen, Yao-Tseng; Stockert, Elisabeth; Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.; Van Der Bruggen, Pierre; Boon-Falleur, Thierry; Old, Lloyd J.
PA Ludwig Institute for Cancer Research, USA; Memorial Sloan-Kettering Cancer Center
SO PCT Int. Appl., 33 pp.
CODEN: PIXXD2

PI WO 9520974 A1 950810
 DS W: AU, CA, CN, FI, JP, NO, NZ
 RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
 AI WO 95-US95 950105
 PRAI US 94-190411 940201
 DT Patent
 LA English
 AB Monoclonal antibodies are provided which specifically bind to the tumor rejection antigen precursor mol. MAGE-1, as well as hybridomas which produce these monoclonal antibodies, and their use. Also described is a recombinant form of MAGE-1, peptides which are useful as immunogens, and immunogenic compns. contg. the peptides and an adjuvant.
 IC ICM A61K038-04
 ICS A61K038-10; A61K038-16; A61K039-395; A61K045-00; C07K014-46; C07K014-435; C07K016-30; C12N005-20; G01N033-53; G01N033-536
 CC 15-3 (Immunochemistry)
 Section cross-reference(s): 3
 IT Protein **sequences**
 (of tumor rejection antigen precursor **MAGE-1** from human)
 IT Deoxyribonucleic acid **sequences**
 (complementary, for tumor rejection antigen precursor **MAGE-1** from human)
 IT 169440-60-2P
 RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
 (nucleotide **sequence**; monoclonal antibodies which bind to tumor rejection antigen precursor **MAGE-1**, recombinant **MAGE-1**, and **MAGE-1**-derived immunogenic peptides)
 L7 ANSWER 6 OF 13 HCAPLUS COPYRIGHT 1998 ACS
 AN 1995:826118 HCAPLUS
 DN 123:225742
 TI Multiple specificities in the repertoire of a melanoma patient's cytolytic T lymphocytes directed against tumor antigen MAGE-1.A1
 AU Romero, Pedro; Pannetier, Christophe; Herman, Jean; Jongeneel, C. Victor; Cerottini, Jean-Charles; Coulie, Pierre G.
 CS Ludwig Inst. for Cancer Res., Univ. of Lausanne, Epalinges, CH-1066, Switz.
 SO J. Exp. Med. (1995), 182(4), 1019-28
 CODEN: JEMEAV; ISSN: 0022-1007
 DT Journal
 LA English
 AB Peptide MAGE-1.A1 is a nonamer derived from protein MAGE-1 that can assoc. with the HLA-A1 mol. It was shown previously to be recognized by an antitumor cytolytic T lymphocyte (CTL) clone derived from the blood of melanoma patient MZ2. We derived two other anti-MAGE-1.A1 CTL clones from different blood samples of the same patient and compared the fine specificity of recognition of the three CTL by testing them on variant MAGE-1.A1 peptides incorporating different amino acid substitutions. The epitopes recognized by the CTL proved to be different. While modifications of residues at positions 5, 6, or 7 in the antigenic peptide affected recognition by the three CTL, each of the modifications of residues at positions 1, 4, or 8 affected recognition by one CTL

only. The sequences of both the .alpha. and .beta. chains of the T cell antigen receptor of the three CTL were completely different. The results indicate a long-lasting diversity in terms of fine specificity and of T cell antigen receptor structure in the repertoire of antitumor CTL derived from the blood of a melanoma patient and directed against a defined tumor antigen.

CC 15-8 (Immunocytochemistry)

IT Protein **sequences**

(TCR receptor; multiple specificities in the repertoire of a melanoma human's cytolytic T lymphocytes directed against tumor antigen **MAGE-1.A1**)

L7 ANSWER 7 OF 13 HCAPLUS COPYRIGHT 1998 ACS

AN 1995:764993 HCAPLUS

DN 123:331445

TI Sequence analysis of the MAGE gene family encoding human tumor-rejection antigens

AU Imai, Yasuhisa; Shichijo, Shigeki; Yamada, Akira; Katayama, Takafumi; Yano, Hirohisa; Itoh, Kyogo

CS Department of Immunology, Kurume University School of Medicine, Kurume, 830, Japan

SO Gene (1995), 160(2), 287-90
CODEN: GENED6; ISSN: 0378-1119

DT Journal

LA English

AB The MAGE multigene family, which includes the MAGE-1 and -3 genes that encode tumor-rejection antigens on HLA-A1 recognized by cytotoxic T-lymphocytes (CTL), is preferentially expressed at the mRNA level on human malignant cells, but not on normal cells. However, little is known about the MAGE-4, MAGE-41, and MAGE-6 genes. In this study, 1040 bp (MAGE-1), 1061 bp (MAGE-3 and MAGE-6), and 1064 bp (MAGE-4 and MAGE-41) cDNA fragments, including the entire coding sequences (927-951 bp), were amplified using the reverse transcription-polymerase chain reaction (RT-PCR) method followed by nucleotide (nt) sequencing. One member had >80 or 66% homol. with the other members at the nt or deduced amino acid (aa) levels, resp. Higher homol. was found between MAGE-3 and -6 (98% at the nt level) and also between MAGE-4 and -41 (98%). The results of this investigation demonstrated high homol., as well as the clear differences between the members of the MAGE family at the coding sequence level.

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 6, 13

IT Gene, animal

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(**MAGE-1**; **sequence** anal. of the MAGE gene family encoding human tumor-rejection antigens)

L7 ANSWER 8 OF 13 HCAPLUS COPYRIGHT 1998 ACS

AN 1995:634555 HCAPLUS

DN 123:31227

TI Cloning and characterization of the complete MAGE-1 antigen gene and immunogenicity of its peptide fragments

IN Fikes, John D.; Livingston, Brian D.; Sette, Alessandro D.; Sidney, John C.

PA Cytel Corp., USA

SO PCT Int. Appl., 57 pp.
 CODEN: PIXXD2
 PI WO 9504542 A1 950216
 DS W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB,
 GE, HU, JP, KE, KG, KP, KR, KZ, LK, LT, LU, LV, MD, MG, MN, MW,
 NL, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, US, UZ,
 VN
 RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR,
 IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG
 AI WO 94-US8721 940802
 PRAI US 93-103623 930806
 DT Patent
 LA English
 AB The complete nucleotide and amino acid sequences of the human MAGE-1
 antigen are provided. Peptides from residues of the C-terminal are
 used to define epitopes that stimulate HLA-restricted cytotoxic T
 lymphocyte activity against MAGE-1 antigens. The peptides are
 particularly useful in methods for stimulating the immune response
 of individuals against MAGE-1 antigens assocd. with melanomas.
 IC ICM A61K038-00
 ICS A61K039-00; C07H021-04; C12N001-19; C12N001-21; C12N005-10;
 C12N015-00; C12N015-70; C12N015-79; C12P021-06
 CC 15-2 (Immunochemistry)
 Section cross-reference(s): 1, 3
 IT Deoxyribonucleic acid **sequences**
 Genetic vectors
 Immunostimulants
 Melanoma
 Molecular cloning
 Protein **sequences**
 (cloning and characterization of human **MAGE-1**
 antigen gene and immunogenicity of its peptide fragments)
 IT 157298-43-6P 164251-72-3P
 RL: BAC (Biological activity or effector, except adverse); BPN
 (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use);
 BIOL (Biological study); PREP (Preparation); USES (Uses)
 (amino acid **sequence**; cloning and characterization of
 human **MAGE-1** antigen gene and immunogenicity
 of its peptide fragments)
 IT 164108-94-5
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (nucleotide **sequence**; cloning and characterization of
 human **MAGE-1** antigen gene and immunogenicity
 of its peptide fragments)
 L7 ANSWER 9 OF 13 HCAPLUS COPYRIGHT 1998 ACS
 AN 1994:678846 HCAPLUS
 DN 121:278846
 TI Genes for tumor rejection antigens and the precursor MAGE-1 and
 their diagnostic and therapeutic uses
 IN Boon, Thierry; van der Bruggen, Pierre; van den Eynde, Benoit; van
 Pel, Aline; de Plaen, Etienne; Lurquin, Christophe; Chomez, Patrick;
 Traversari, Catia
 PA Ludwig Institute for Cancer Research, USA
 SO U.S., 65 pp. Cont.-in-part of U.S. Ser. No. 764,364, abandoned.
 CODEN: USXXAM

PI US 5342774 A 940830
 AI US 91-807043 911212
 PRAI US 91-705702 910523
 US 91-728838 910709
 US 91-764364 910923
 DT Patent
 LA English
 AB Mouse genes for a group of tumor cell antigens that are recognized by cytotoxic T cells, leading to lysis of the tumor is cloned and expressed in animal cells for use in diagnostics and therapeutics. The genes were cloned by expression from a partial digest bank of tumor cell line DNA in cosmids using cytotoxic T-lymphocyte assays to detect expression. Presentation of the antigens was H-2 phenotype-dependent. Northern blots of tumors and normal tissue showed that the genes were expressed in a large array of tumors, but not in the normal tissues tested. CDNAs for several human mage precursor isoforms were cloned.
 IC ICM C12P021-02
 ICS C12P019-34; C12N015-00; C12N007-00; C12N005-00; C12N001-21; C12N001-16; C12N001-18; C07K003-00; C07H015-12
 NCL 435240200
 CC 15-2 (Immunochemistry)
 Section cross-reference(s): 1, 9
 IT 136361-96-1, Antigen (mouse clone C1A.3.1 gene PlA reduced)
 RL: BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (amino acid **sequence**; genes for tumor rejection antigens and the precursor **MAGE-1** and their diagnostic and therapeutic uses)
 IT 140297-32-1, GenBank M36387 140767-62-0, GenBank M36386
 146313-12-4, Deoxyribonucleic acid (human clone B3 gene **MAGE-1**)
 146707-11-1, Deoxyribonucleic acid (mouse clone p815A gene p1A plus 5'- and 3'-flanking region fragment)
 146707-15-5, Deoxyribonucleic acid (human melanoma gene **MAGE-21** antigen fragment-specifying) 146707-16-6 146707-18-8, Deoxyribonucleic acid (human melanoma 1-121-gene **MAGE-31** antigen-specifying plus 5'-flanking region fragment) 146707-29-1, Deoxyribonucleic acid (human melanoma gene **MAGE-6** antigen fragment-specifying) 158968-97-9 158968-98-0 158968-99-1 158969-00-7 158969-01-8 158969-02-9
 RL: BOC (Biological occurrence); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (nucleotide **sequence**; genes for tumor rejection antigens and the precursor **MAGE-1** and their diagnostic and therapeutic uses)
 L7 ANSWER 10 OF 13 HCAPLUS COPYRIGHT 1998 ACS
 AN 1994:555075 HCAPLUS
 DN 121:155075
 TI Cloning and analysis of **MAGE-1**-related genes
 AU Ding, Min; Beck, Raymond J.; Keller, Christopher J.; Fenton, Robert G.
 CS Clinical Research Branch, NCI, Frederick, MD, 21702, USA
 SO Biochem. Biophys. Res. Commun. (1994), 202(1), 549-55
 CODEN: BBRCA9; ISSN: 0006-291X
 DT Journal
 LA English

AB The spectrum of MAGE gene expression in the human melanoma cell line DM150 was examd. using reverse transcription polymerase chain reaction and cDNA cloning. Five full-length cDNAs were isolated from DM150 which were identified as MAGE-1, MAGE-3, MAGE-12, and 2 previously undescribed MAGE genes, MAGE-3b and MAGE-X2. DNA sequence anal. of the coding regions of the MAGE-3b and MAGE-X2 genes revealed 83 and 88% identity with MAGE-1, whereas MAGE-3b was 98% homologous with the full-length MAGE-3 clone. The predicted amino acid sequences of MAGE-X2 and MAGE-3b contain consensus HLA-A1 peptide binding motifs, suggesting that, like MAGE-1, they may code for tumor-assocd. antigens. In addn., a nonamer peptide encoded by both the MAGE-3 and MAGE-12 genes was shown by direct binding studies to contain an aggretope for HLA-A2.

CC 15-2 (Immunochemistry)
Section cross-reference(s): 3

IT Melanoma
(**MAGE-1**-related antigens of human, **sequence** and aggretope moieties of)

IT Gene, animal
RL: BIOL (Biological study)
(for melanoma-assocd. **MAGE-1**-related antigens, of human cell line DM150, **sequence** of)

IT Antigens
RL: BIOL (Biological study)
(melanoma-assocd. **MAGE-1**, amino acid **sequence** and aggretope moieties of, of human cell line DM150)

IT Protein **sequences**
(of melanoma-assocd. **MAGE-1**-related antigens, of human cell line DM150)

IT Deoxyribonucleic acid **sequences**
(complementary, for melanoma-assocd. **MAGE-1**-related antigens, of human cell line DM150)

IT 157298-41-4, Melanoma-assocd. antigen MAGE-X2 (human cell line DM150) 157298-42-5, Melanoma-assocd. antigen MAGE-3b (human cell line DM150) 157298-43-6, Melanoma-assocd. antigen **MAGE-1** (human cell line DM150) 157298-44-7, Melanoma-assocd. antigen MAGE-12f (human cell line DM150)
RL: BIOL (Biological study)
(amino acid **sequence** and aggretope moieties of)

L7 ANSWER 11 OF 13 HCAPLUS COPYRIGHT 1998 ACS
AN 1993:167452 HCAPLUS
DN 118:167452
TI Cloning of genes for tumor rejection antigen precursors and their uses
IN Boon, Thierry; Van der Bruggen, Pierre; Van den Eynde, Benoit; Van Pel, Aline; De Plaen, Etienne; Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
PA Ludwig Institute for Cancer Research, USA
SO PCT Int. Appl., 143 pp.
CODEN: PIXXD2
PI WO 9220356 A1 921126
DS W: AU, BB, BG, BR, CA, CS, FI, HU, JP, KP, KR, LK, MG, MW, NO, PL, RO, RU, SD, US
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR, IT, LU, MC, ML, MR, NL, SE, SN, TD, TG

AI WO 92-US4354 920522
 PRAI US 91-705702 910523
 US 91-728838 910709
 US 91-764364 910923
 US 91-807043 911212
 DT Patent
 LA English
 AB The genes or cDNA for tumor rejection antigen (TRA) precursors, e.g. the precursors for MAGE melanoma antigen, the P1A mastocytoma antigen, and the antigen F of human, and the murine counterpart of MAGE, smage, are cloned. The coding sequences of these TRA can be used for prepn. of vaccines by expression of the sequences alone or together with the gene for a cytokine, e.g., interleukin (IL)-2 or IL-4. They can also be expressed with a gene for an MHC or HLA antigen which presents the tumor rejection antigen derived from the precursor to the cytotoxic T cells. Expression of the TRA by tumor cells can lead to cell lysis mediated by the cytotoxic T cells that recognize the antigens. The TRA may be used for prepn. of pharmaceuticals, antibodies, and diagnostics for clin. applications.
 IC A61K035-14; A61K039-00; A61K037-22; C07K003-00; C07K015-00; C07K017-00; C12Q001-68; C12Q001-00; C12Q015-00
 CC 15-2 (Immunochemistry)
 IT Section cross-reference(s): 1, 3, 9
 140101-03-7, Deoxyribonucleic acid (human clone B3 gene **MAGE** -1 plus 5'- and 3'-flanking region fragment) 146707-11-1
 146707-12-2 146707-13-3 146707-15-5 146707-16-6 146707-18-8
 146707-20-2 146707-22-4 146707-24-6 146707-25-7 146707-27-9
 146707-29-1 146707-30-4 146707-32-6 146707-34-8 146707-36-0
 146707-38-2 146707-40-6 146707-42-8
 RL: BIOL (Biological study); PRP (Properties)
 (nucleotide **sequence** and cloning of)
 IT 136362-51-1, Deoxyribonucleic acid (mouse clone C1A.3.1 gene P1A coding region) 146313-12-4, Deoxyribonucleic acid (human clone B3 gene **MAGE-1**) 146707-14-4 146707-17-7
 146707-19-9 146707-21-3 146707-23-5 146707-26-8 146707-28-0
 146707-31-5 146707-33-7 146707-35-9 146707-37-1 146707-39-3
 146707-41-7
 RL: BIOL (Biological study); PRP (Properties)
 (nucleotide **sequence** and cloning of, complete)
 L7 ANSWER 12 OF 13 HCAPLUS COPYRIGHT 1998 ACS
 AN 1993:121916 HCAPLUS
 DN 118:121916
 TI A gene encoding an antigen recognized by cytolytic T lymphocytes on a human melanoma
 AU Van der Bruggen, P.; Traversari, C.; Chomez, P.; Lurquin, C.; De Plaen, E.; Van den Eynde, B.; Knuth, A.; Boon, T.
 CS Ludwig Inst. Cancer Res., Brussels, B-1200, Belg.
 SO Science (Washington, D. C., 1883-) (1991), 254(5038), 1643-7
 CODEN: SCIEAS; ISSN: 0036-8075
 DT Journal
 LA English
 AB Many human melanoma tumors express antigens that are recognized in vitro by cytolytic T lymphocytes (CTLs) derived from the tumor-bearing patient. A gene was identified that directed the expression of antigen MZ2-E on a human melanoma cell line. This gene shows no similarity to known sequences and belongs to a family

of at least three genes. It is expressed by the original melanoma cells, other melanoma cell lines, and by some tumor cells of other histol. types. No expression was obsd. in a panel of normal tissues. Antigen MZ2-E appears to be presented by HLA-A1; anti-MZ2-E CTLs of the original patient recognized two melanoma cell lines of other HLA-A1 patients that expressed the gene. Thus, precisely targeted immunotherapy directed against antigen MZ2-E could be provided to individuals identified by HLA typing and anal. of the RNA of a small tumor sample.

- CC 14-1 (Mammalian Pathological Biochemistry)
 Section cross-reference(s): 3, 15
- IT 146313-13-5, Antigen (human clone B3 gene **MAGE-1**
 reduced)
 RL: PRP (Properties)
 (amino acid **sequence** of, complete)
- IT 140101-03-7, Deoxyribonucleic acid (human clone B3 gene **MAGE**
 -1 plus 5'- and 3'-flanking region fragment)
 RL: PRP (Properties)
 (nucleotide **sequence** of)
- IT 146313-12-4, Deoxyribonucleic acid (human clone B3 gene **MAGE**
 -1)
 RL: PRP (Properties)
 (nucleotide **sequence** of, complete)
- L7 ANSWER 13 OF 13 HCAPLUS COPYRIGHT 1998 ACS
 AN 1992:631775 HCAPLUS
 DN 117:231775
 TI A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1
 by cytolytic T lymphocytes directed against tumor antigen MZ2-E
 AU Traversari, Catia; Van der Bruggen, Pierre; Luescher, Immanuel F.;
 Lurquin, Christophe; Chomez, Patrick; Van Pel, Aline; De Plaen,
 Etienne; Amar-Costesec, Alain; Boon, Thierry
 CS Brussels Branch, Ludwig Inst. Cancer Res., Brussels, B-1200, Belg.
 SO J. Exp. Med. (1992), 176(5), 1453-7
 CODEN: JEMEAV; ISSN: 0022-1007
 DT Journal
 LA English
 AB The authors reported the identification of human gene MAGE-1, which
 directs the expression of an antigen recognized on a melanoma by
 autologous cytolytic T lymphocytes (CTL). CTL directed against this
 antigen, which was named MZ2-E, recognize a nonapeptide encoded by
 the third exon of gene MAGE-1. The CTL also recognize this peptide
 when it is presented by mouse cells transfected with an HLA-A1 gene,
 confirming the assocn. of antigen MZ2-E with the HLA-A1 mol. Other
 members of the MAGE gene family do not code for the same peptide,
 suggesting that only MAGE-1 produces the antigen recognized by the
 anti-MZ2-E CTL. The results open the possibility of immunizing
 HLA-A1 patients whose tumor expresses MAGE-1 either with the
 antigenic peptide or with autologous antigen-presenting cells pulsed
 with the peptide.
- CC 15-2 (Immunocytochemistry)
 IT Protein **sequences**
 (of gene **MAGE-1**-encoded antigen, of humans)

ALL IS NOT A RECOGNIZED COMMAND

=> d all 116

L16 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 1998 ACS
 AN 1990:53087 HCAPLUS
 DN 112:53087
 TI Synthesis of vitamin K-dependent **proteins** by cultured human **tumor** cells
 AU Al-Mondhiry, Hamid; Wallin, Reidar
 CS Coll. Med., Pennsylvania State Univ., Hershey, PA, 17033, USA
 SO Thromb. Haemostasis (1989), 62(2), 661-6
 CODEN: THHADQ; ISSN: 0340-6245
 DT Journal
 LA English
 CC 14-1 (Mammalian Pathological Biochemistry)
 Section cross-reference(s): 13
 AB The observation that warfarin inhibits the growth and metastasis of certain types of clin. and exptl. tumors suggests a role for vitamin K in tumor biol. The synthesis of vitamin K-dependent proteins was investigated in four malignant (lung epidermoid carcinoma, melanoma, colon adenocarcinoma, and breast adenocarcinoma) and three normal (colon epithelium, breast epithelium, and fibroblasts) cell lines of human origin grown in tissue cultures. The results show the following: 1) vitamin K-dependent carboxylase activity is present in all of the malignant and normal cell lines studied; 2) the malignant, as well as normal, cell lines synthesize a family of vitamin K-dependent proteins, and microsomal precursors of these proteins with apparent mol. masses of 74, 62, and 34 kDa are common to all malignant and normal cell lines, whereas precursors of higher and lower mol. mass seem to be synthesized by some but not all tumor cell lines; and 3) the 74-kDa precursor synthesized by colon carcinoma and breast carcinoma was pos. identified as a precursor of protein S.
 ST vitamin K **protein** formation **tumor** cell
 IT **Melanoma**
 Neoplasm, metabolism
 (vitamin K-dependent **protein** formation by, of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)
 IT Fibroblast
 (vitamin K-dependent protein formation by, of humans)
 IT Protein formation
 (vitamin K-dependent, by neoplastic and normal cells of humans)
 IT Carcinoma
 (adeno-, vitamin K-dependent protein formation by, of intestine and mammary gland of humans)
 IT Intestine, neoplasm
 (colon, adenocarcinoma, vitamin K-dependent **protein** formation by, of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)
 IT Intestine, metabolism
 (colon, epithelium, vitamin K-dependent protein formation by, of humans)
 IT Blood coagulation
 (disorder, hypercoagulability, vitamin K-dependent protein formation by human neoplastic cells in relation to)

- IT Carcinoma
(epidermoid, vitamin K-dependent protein formation by, of lung of human)
- IT Lung, neoplasm
(epidermoid carcinoma, vitamin K-dependent **protein** formation by, of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)
- IT Mammary gland
(epithelium, vitamin K-dependent protein formation by, of humans)
- IT Mammary gland
(neoplasm, adenocarcinoma, vitamin K-dependent **protein** formation by, of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)
- IT Blood-coagulation factors
RL: BIOL (Biological study)
(protein S, precursor of, formation of, by colon carcinoma and breast carcinoma cells, of humans)
- IT Proteins, specific or class
RL: BIOL (Biological study)
(.gamma.-carboxyglutamic acid-contg., 23,000-mol.-wt., formation of vitamin K-dependent, by neoplastic cells of humans)
- IT Proteins, specific or class
RL: BIOL (Biological study)
(.gamma.-carboxyglutamic acid-contg., 30,000-mol.-wt., formation of vitamin K-dependent, by neoplastic cells of humans)
- IT **Proteins**, specific or class
RL: BIOL (Biological study)
(.gamma.-carboxyglutamic acid-contg., 34,000-mol.-wt., formation of vitamin K-dependent, by neoplastic and normal cells of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)
- IT **Proteins**, specific or class
RL: BIOL (Biological study)
(.gamma.-carboxyglutamic acid-contg., 62,000-mol.-wt., formation of vitamin K-dependent, by neoplastic and normal cells of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)
- IT **Proteins**, specific or class
RL: BIOL (Biological study)
(.gamma.-carboxyglutamic acid-contg., 74,000-mol.-wt., formation of vitamin K-dependent, by neoplastic and normal cells of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)
- IT Proteins, specific or class
RL: BIOL (Biological study)
(.gamma.-carboxyglutamic acid-contg., 89,000-mol.-wt., formation of vitamin K-dependent, by neoplastic cells of humans)
- IT 12001-79-5, Vitamin K
RL: BIOL (Biological study)
(protein formation dependent on, of normal and neoplastic human cells)

<-----User Break----->

=> fil wpids

FILE 'WPIDS' ENTERED AT 09:22:01 ON 07 APR 1998
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FILE LAST UPDATED: 06 APR 1998 <19980406/UP>
>>>UPDATE WEEKS:
MOST RECENT DERWENT WEEK 199814 <199814/DW>
DERWENT WEEK FOR CHEMICAL CODING: 199809
DERWENT WEEK FOR POLYMER INDEXING: 199811
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE
>>> D COST AND SET NOTICE DO NOT REFLECT SUBSCRIBER DISCOUNTS -
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>>> MEXICO NOW COVERED - SEE NEWS <<<

=> d his

(FILE 'WPIDS' ENTERED AT 09:17:35 ON 07 APR 1998)
DEL HIS Y
L1 9 S MAGE 1
L2 2 S 11540
L3 0 S L2 AND (ANTIBOD? OR MONOCLONAL?)
L4 1459 S (TUMOR# OR TUMOUR#) (6A) (PROTEIN# OR ANTIGEN#)
L5 1403 S MELANOMA
L6 96 S L4 AND L5
L7 0 S L6 AND (46 OR 34)
L8 8 S L6 AND (KD OR KDS OR KILODALTON# OR KILO DALTON#)

FILE 'WPIDS' ENTERED AT 09:21:18 ON 07 APR 1998

FILE 'WPIDS' ENTERED AT 09:22:01 ON 07 APR 1998

=> d .wp 11 1-9; d .wp 18 1-8

L1 ANSWER 1 OF 9 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
AN 98-086733 [08] WPIDS
DNC C98-029335
TI Inducing anti-tumour cytotoxic T lymphocytes - by cross-priming
with artificial antigen, then immunisation with tumour cells
modified in vitro to express the same antigen, does not require
characterisation of tumour-specific antigens.
DC B04 D16
IN FALO, L D; ROCK, K L
PA (DAND) DANA FARBER CANCER INST INC; (UYPI-N) UNIV PITTSBURGH
CYC 77
PI WO 9800163 A1 980108 (9808)* EN 44 pp
RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL
OA PT SD SE SZ UG ZW
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI
GB GE GH HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD
MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR
TT UA UG UZ VN YU ZW

ADT WO 9800163 A1 WO 97-US10195 970618
 PRAI US 96-675332 960628
 AB WO 9800163 A UPAB: 980223

Anti-tumour immunisation in a mammal comprises: (a) immunising the host with an artificial target antigen (A) to produce a cytotoxic T lymphocyte (CTL) response; (b) resecting tumour from the host; (c) culturing tumour cells in vitro; (d) engineering these cells to include (A) so that presentation of (A) on the cell surface is promoted, and (e) inactivating the cultured cells and returning them to the host. In a modification, step (a) is omitted and the engineered cells are returned to the host simultaneously with immunisation by (A).

In step (a), (A) is administered as a particulate complex, e.g. by injection or particle bombardment. In step (d), cells are transfected with nucleic acid expressing (A), or (A) is introduced by peptide pulsing. Specified (A) are (i) tumour antigens such as Melan-A, p53, carcinoembryonal antigen, gp100, **MAGE-1** or -2; (ii) a viral antigen such as HIV gp120 or gp100, influenza virus nucleoprotein or hepatitis B surface antigen or (iii) chicken ovalbumin (OVA, especially preferred) or keyhole limpet haemocyanin.

USE - The method is used for treatment or prevention of tumours, specifically in humans. A similar method is used (not claimed) for treatment of viral infections, e.g. with human immunodeficiency virus (HIV).

ADVANTAGE - The method of cross-priming results in a CTL response to many, undefined, MHC Class I-restricted tumour antigens expressed on the surface of unmodified tumour cells. It can be applied to a wide range of tumours and does not require isolation and characterisation of particular tumour (or viral) antigens.
 Dwg.5/8

L1 ANSWER 2 OF 9 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
 AN 97-212603 [19] WPIDS
 DNC C97-068627

TI Use of DNA coated particles - for therapeutic or prophylactic immunisation of mammals, partic. for neoplastic cells or virus infected cells.

DC B04 D16
 IN FALO, L D; ROCK, K L
 PA (DAND) DANA FARBER CANCER INST INC; (UYPI-N) UNIV PITTSBURGH
 CYC 69

PI WO 9711605 A1 970403 (9719)* EN 46 pp
 RW: AT BE CH DE DK EA ES FI FR GB GR IE IT KE LS LU MC MW NL OA
 PT SD SE SZ UG
 W: AL AM AT AU AZ BB BG BR BY CA CH CN CZ DE DK EE ES FI GB GE
 HU IS JP KE KG KP KR KZ LK LR LS LT LU LV MD MG MK MN MW MX
 NO NZ PL PT RO RU SD SE SG SI SK TJ TM TR TT UA UG UZ VN

AU 9672515 A 970417 (9732)

ADT WO 9711605 A1 WO 96-US15728 960927; AU 9672515 A AU 96-72515 960927
 FDT AU 9672515 A Based on WO 9711605
 PRAI US 95-535556 950928
 AB WO 9711605 A UPAB: 970512

In vivo method (A) of therapeutic or prophylactic genetic immunisation of a mammalian host comprises:

(a) generating a DNA fragment which expresses an antigenic protein or fragment,

(b) distributing the DNA fragment on a particle surface, resulting in a particulate polynucleotide (PP),
(c) inoculating the mammalian host with the PP and
(d) delivering the PP to the cytoplasm of a target cell within the mammalian host, such that the expressed antigenic protein or fragment is presented to the membrane surface of the target cell through the major histocompatibility complex (MHC) class I pathway.

Also claimed are:

(1) an ex vivo method (B) of therapeutic or prophylactic genetic immunisation of a mammalian host, comprising:

(a) generating a DNA fragment which expresses an antigenic protein or fragment,

(b) distributing the DNA fragment on a particle surface, resulting in a PP,

(c) delivering the PP to the cytoplasm of a target cell of a mammalian host in vitro, such that the expressed antigenic protein or fragment is presented on the membrane surface of the target cell through the MHC class I pathway and

(d) inoculating the mammalian host with the target cell by direct injection, and

(3) an ex vivo method (C) of therapeutic or prophylactic genetic immunisation of a mammalian host, comprising:

(a) generating a DNA fragment which expresses a molecule which enhances the antigen presentation function of an antigen presenting cell (APC),

(b) distributing the DNA fragment on a particle surface, resulting in a PP,

(c) delivering the PP to the cytoplasm of a target cell of a mammalian host in vitro, such that the expressed antigen presentation enhancing protein is expressed in a biologically significant form and at biologically significant levels and

(d) inoculating the mammalian host with the target cell by direct injection.

USE - The methods are used for producing antigen-specific immune responses to antigens such as tumour rejection antigens, e.g. **MAGE-1**, **MAGE-3**, **MelanA**, **gp100**, **p53**, **CEA** or **HER2/neu** or viral antigens, eg. **HIV gp120**, **HIV gp160**, influenza virus nucleoprotein or hepatitis B surface antigen. They can be used for therapeutic or prophylactic treatment (all claimed).

ADVANTAGE - The PP can target delivery of antigens to APCs to increase the efficiency of genetic immunisation while reducing unwanted deleterious effects. Proper presentation of the antigenic peptides through the MHC class I pathway stimulates cytotoxic T lymphocyte (CTL) production and in turns promotes destruction of cells such as neoplastic cells or virally infected cells.
Dwg.0/6

L1 ANSWER 3 OF 9 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
AN 97-108910 [10] WPIDS
DNN N97-090092 DNC C97-034778
TI Prepn. of photo-reactive peptide derivs. - by substitution. with photoreactive amino acid then radio-iodination, giving prods. used to assess ability of peptide to bind to specific major histocompatibility complex mols..
DC B04 D16 K08 S03
IN ANJUERE, F; CERROTINI, J; LAYERE, A; LEUSCHER, I; ROMERO, P
PA (LUDW-N) LUDWIG INST CANCER RES

CYC 23
 PI WO 9702282 A1 970123 (9710)* EN 36 pp
 RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE
 W: AU CA CN FI JP NO NZ
 AU 9665418 A 970205 (9721)
 ADT WO 9702282 A1 WO 96-US10869 960625; AU 9665418 A AU 96-65418 960625
 FDT AU 9665418 A Based on WO 9702282
 PRAI US 95-498461 950705
 AB WO 9702282 A UPAB: 970326

Prepn. of synthetic photoreactive peptide derivs. (I) comprises:
 (a) linear synthesis of a peptide;
 (b) substitution. of an amino acid (aa) in the peptide with a photoreactive aa at a position that does not alter its binding ability, and
 (c) specific radio-iodination of the photoreactive aa.
 Also new are peptides of formula (Ia) Q-X-A-Tyr (Ia)
 Q = photoreactive gp., specifically iodinated
 2,3-(4-azido-salicyloyl)-diaminopropionic acid (AzDAP);
 X = Ala or Val;
 A = any 6 aa.

USE - The method is esp. applied to the melanoma-derived MAGE peptides, esp. **MAGE-1**, -3, -4a, -6 or -12, to give cpds. used to assess ability of a peptide to bind to specific MHC mols. Peptides which bind specifically, are used to screen either MHC mols. for cross-reactivity or peptides for their ability to inhibit the photoaffinity labelling reaction. A partic. application is identification of MHC able to present a given cytotoxic T cell epitope.

ADVANTAGE - The method provides a radio-iodination yield of over 90% without significant formation of di-iodinated prod., so that HPLC purificn. of the prod. is not required and reverse-phase purificn. provides complete sepn. of the prod. from non-iodinated precursors. Photoaffinity labelling is very specific, so does require isolation of MHC from cells, making possible rapid testing of panels of peptides or cell lines expressing different MHC.
 Dwg.0/0

L1 ANSWER 4 OF 9 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
 AN 95-320586 [41] WPIDS
 CR 92-415460 [50]; 94-100844 [12]; 94-333192 [41]; 95-283606 [37]
 DNC C95-142446
 TI Determn. of cancerous condition(s) - using a nucleic acid as a primer to determine expression of a MAGE tumour rejection antigen precursor.
 DC B04 D16
 IN BOON-FALLEUR, T; BRASSEUR, F; CHOMEZ, P; DE PLAEN, E; DE SMET, C; GAUGLER, B; LETHE, B; MARCHAND, M; PATARD, J; SZIKORA, J; VAN DEN EYNDE, B; VAN DER BRUGGEN, P; WEYNANTS, P; BASSEUR, F; DEPLAEN, E
 PA (LUDW-N) LUDWIG INST CANCER RES
 CYC 24
 PI WO 9523874 A1 950908 (9541)* EN 122 pp
 RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
 W: AU CA FI JP KR NO NZ
 AU 9519682 A 950918 (9551)
 US 5512437 A 960430 (9623) 5 pp
 US 5512444 A 960430 (9623) 10 pp
 FI 9603393 A 960830 (9646)

NO 9603589 A 961031 (9702)
 US 5612201 A 970318 (9717) 72 pp
 JP 09509832 W 971007 (9750) 132 pp
 ADT WO 9523874 A1 WO 95-US2203 950223; AU 9519682 A AU 95-19682 950223;
 US 5512437 A US 94-204727 940301; US 5512444 A CIP of US 94-204727
 940301, US 94-346774 941130; FI 9603393 A WO 95-US2203 950223, FI
 96-3393 960830; NO 9603589 A WO 95-US2203 950223, NO 96-3589 960828;
 US 5612201 A CIP of US 91-705702 910523, CIP of US 91-728838 910709,
 CIP of US 91-764364 910923, CIP of US 91-807043 911212, CIP of WO
 92-US4354 920522, CIP of US 93-37230 930326, US 94-299849 940901; JP
 09509832 W JP 95-522934 950223, WO 95-US2203 950223
 FDT AU 9519682 A Based on WO 9523874; US 5612201 A CIP of US 5327252,
 CIP of US 5342774; JP 09509832 W Based on WO 9523874
 PRAI US 94-346774 941130; US 94-204727 940301; US 94-209172 940310;
 US 94-299849 940901; US 91-705702 910523; US 91-728838 910709;
 US 91-764364 910923; US 91-807043 911212; WO 92-US4354 920522;
 US 93-37230 930326
 AB WO 9523874 A UPAB: 980126
 Isolated nucleic acid (NA) useful as a primer in determining the
 expression of a member of the melanoma antigen (MAGE) group of
 tumour rejection antigen precursors selected from one of 20 given
 sequences. Also claimed is a kit for determining the expression of a
 MAGE tumour rejection antigen precursor comprising at least 1
 specific pair of the above NA sequences.
 USE - The NA is useful in cancer determination assays, esp.
 melanoma, bead (sic) or neck squamous cell carcinoma, prostate
 carcinoma or bladder tumour (claimed).
 Dwg.0/20

L1 ANSWER 5 OF 9 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
 AN 95-292948 [38] WPIDS
 CR 94-263764 [32]; 95-051741 [07]
 DNC C95-131893
 TI Identification of cells presenting HLA-C-clone 10 or **MAGE-**
1 derived peptide - allows diagnosis and treatment of
 individuals with cellular abnormalities, e.g. melanoma, also HLA-Cw
 1601 derived peptide(s).
 DC B04 D16
 IN BOEL, P; BOON-FALLEUR, T; COULIE, P; SZIKORA, J; VAN, DER BRUGGEN P;
 WILDMANN, C; WILDMANN, C
 PA (LUDW-N) LUDWIG INST CANCER RES
 CYC 26
 PI WO 9521630 A1 950817 (9538)* EN 26 pp
 RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
 W: AU CA CN FI JP NO NZ
 AU 9520899 A 950829 (9548)
 ZA 9501177 A 960424 (9622) 30 pp
 FI 9603170 A 960813 (9644)
 NO 9603347 A 960814 (9644)
 US 5558995 A 960924 (9644) 6 pp
 EP 789591 A1 970820 (9738) EN
 R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE
 ADT WO 9521630 A1 WO 95-US1446 950126; AU 9520899 A AU 95-20899 950126;
 ZA 9501177 A ZA 95-1177 950214; FI 9603170 A WO 95-US1446 950126, FI
 96-3170 960813; NO 9603347 A WO 95-US1446 950126, NO 96-3347 960812;
 US 5558995 A CIP of US 93-8446 930122, US 94-195186 940214; EP
 789591 A1 EP 95-913476 950126, WO 95-US1446 950126

FDT AU 9520899 A Based on WO 9521630; EP 789591 A1 Based on WO 9521630
 PRAI US 94-292492 940818; US 94-195186 940214; US 94-196630 940215;
 US 93-8446 930122
 AB WO 9521630 A UPAB: 961111

A novel method for identifying a candidate for treatment with a therapeutic agent specific for complexes of HLA-C-clone 10 and the peptide (I): Ser-Ala-Tyr-Gly-Glu-Pro-Arg-Lys-Leu (I) comprises: (i) contacting an abnormal cell sample from a subject with a cytolytic T cell specific for the complexes; and (ii) determining lysis of at least part of the abnormal cell sample as an indication of a candidate for the treatment.

USE - The method can be used to treat a subject with a cellular abnormality eg melanoma or to identify an abnormal cell which presents a complex of HLA-C-clone 10 and (I) on its surface. The isolated peptides are useful in diagnosing cancer. The isolated nucleic acid mols are useful as probes for the determination of expression of HLA-Cw*1601. HLA typing is important in tissue typing for transplantation.

Dwg.0/2

L1 ANSWER 6 OF 9 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
 AN 95-283606 [37] WPIDS
 CR 92-415460 [50]; 94-100844 [12]; 94-333192 [41]; 95-320586 [41]
 DNN N95-215847 DNC C95-127959
 TI New monoclonal antibody binding specifically to **MAGE-1** - useful for diagnosis and monitoring of cancer, also new hybridomas, recombinant **MAGE-1** and immunogenic peptide(s).
 DC B04 D16 S03
 IN BOON-FALLEUR, T; CHEN, Y; GARIN-CHESA, P; OLD, L J; RETTIG, W J; STOCKERT, E; VAN DER BRUGGEN, P; OLD, L
 PA (LUDW-N) LUDWIG INST CANCER RES; (SLOK) SLOAN KETTERING INST CANCER RES; (CORR) CORNELL RES FOUND INC; (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT

CYC 26

PI WO 9520974 A1 950810 (9537)* EN 33 pp
 RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
 W: AU CA CN FI JP NO NZ
 AU 9515979 A 950821 (9547)
 ZA 9500786 A 951227 (9605) 29 pp
 US 5541104 A 960730 (9636) 14 pp
 FI 9603033 A 960731 (9642)
 NO 9603120 A 960930 (9649)
 EP 752876 A1 970115 (9708) EN
 R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE
 JP 09511389 W 971118 (9805) 36 pp
 AU 686314 B 980205 (9813)

ADT WO 9520974 A1 WO 95-US95 950105; AU 9515979 A AU 95-15979 950105; ZA 9500786 A ZA 95-786 950201; US 5541104 A CIP of US 91-705702 910523, CIP of US 91-728838 910709, CIP of US 91-764365 910923, CIP of US 91-807043 911212, CIP of WO 92-US4354 920522, CIP of US 93-37230 930326, US 94-190411 940201; FI 9603033 A WO 95-US95 950105, FI 96-3033 960731; NO 9603120 A WO 95-US95 950105, NO 96-3120 960726; EP 752876 A1 EP 95-907978 950105, WO 95-US95 950105; JP 09511389 W JP 95-520611 950105, WO 95-US95 950105; AU 686314 B AU 95-15979 950105

FDT AU 9515979 A Based on WO 9520974; US 5541104 A CIP of US 5342774; EP

752876 A1 Based on WO 9520974; JP 09511389 W Based on WO 9520974; AU 686314 B Previous Publ. AU 9515979, Based on WO 9520974
PRAI US 94-190411 940201; US 91-705702 910523; US 91-728838 910709;
US 91-764365 910923; US 91-807043 911212; WO 92-US4354 920522;
US 93-37230 930326

AB WO 9520974 A UPAB: 980126
Monoclonal antibody (MAb) that binds specifically to tumour rejection antigen precursor **MAGE-1** is new. Also new are (1) hybridomas that produce MAb; (2) isolated **MAGE-1** deriv. (A) of mol. wt. 20-22 kD; (3) isolated protein (A1) comprising amino acids 57-219 encoded by nucleotides 3931-4761 of the **MAGE-1** gene (sequence of 5674 bp reproduced); and (4) isolated peptides of formulae: Ile Asn Phe Thr Arg Gln Arg Gln Pro Ser Glu Gly Ser Ser (2) Leu Phe Arg Ala Val Ile Thr Lys Lys Val Ala Asp (3) Asp Val Lys Glu Ala Asp Pro Thr Gly His Ser Tyr (4).

USE - MAb, opt. labelled or immobilised, is used to detect **MAGE-1** in samples (e.g. cell lysates) by standard immunoassay methods, e.g. for diagnosis and monitoring of cancer. (A), (A1) and peptides (2)-(4) are useful as immunogens for prodn. of MAb and antisera.

ADVANTAGE - MAb is specific for **MAGE-1**, having no reactivity for MAGE-2 or 3.
Dwg.0/4

L1 ANSWER 7 OF 9 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD

AN 95-090681 [12] WPIDS

DNC C95-041028

TI Human melanoma antigen, **MAGE-1**, peptide(s) -
useful for stimulating immune response against melanoma.

DC B04 D16

IN FIKES, J D; LIVINGSTON, B D; SETTE, A D; SIDNEY, J C

PA (CYTE-N) CYTEL CORP

CYC 57

PI WO 9504542 A1 950216 (9512)* EN 59 pp
RW: AT BE CH DE DK ES FR GB GR IE IT KE LU MC MW NL OA PT SD SE
W: AM AT AU BB BG BR BY CA CH CN CZ DE DK ES FI GB GE HU JP KE
KG KP KR KZ LK LT LU LV MD MG MN MW NL NO NZ PL PT RO RU SD
SE SI SK TJ TT UA US UZ VN

AU 9475534 A 950228 (9524)

EP 721341 A1 960717 (9633) EN

R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE

JP 09502086 W 970304 (9719) 60 pp

NZ 271774 A 980226 (9813)

ADT WO 9504542 A1 WO 94-US8721 940802; AU 9475534 A AU 94-75534 940802;
EP 721341 A1 EP 94-925722 940802, WO 94-US8721 940802; JP 09502086 W
WO 94-US8721 940802, JP 95-506486 940802; NZ 271774 A NZ 94-271774
940802, WO 94-US8721 940802

FDT AU 9475534 A Based on WO 9504542; EP 721341 A1 Based on WO 9504542;
JP 09502086 W Based on WO 9504542; NZ 271774 A Based on WO 9504542

PRAI US 93-103623 930806

AB WO 9504542 A UPAB: 950328

Immunogenic peptides, comprising ca. 9-10 residues from the C-terminal of melanoma antigen protein **MAGE-1** (58 residue sequence given in specification), are new. Also claimed are: (1) isolated DNA encoding the peptides; (2) vectors comprising the DNA; and (3) host cells transformed with the vectors.

USE - The peptides are useful for defining epitopes stimulating HLA-restricted cytotoxic T-lymphocyte activity against **MAGE**-1 antigens (Ags). They are particularly useful for stimulating the immune response of individuals against **MAGE**-1 Ags associated with melanomas. Vaccine compositions containing these peptides can be administered to a patient susceptible to MAGE-associated tumours, eg. melanomas.
Dwg.0/3

L1 ANSWER 8 OF 9 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
AN 94-263764 [32] WPIDS
CR 95-051741 [07]; 95-292948 [38]
DNC C94-120655
TI Treating and detecting, cellular abnormality with specific cytolytic T cells - recognising particular HLA-MAGE - cell surface complex, or with agents which provoke such cells, esp. for melanoma.
DC B04 D16 P31
IN BOON-FALLEUR, T; VAN, DER BRUGGEN P
PA (LUDW-N) LUDWIG INST CANCER RES
CYC 26
PI WO 9416713 A1 940804 (9432)* EN 17 pp
RW: BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE
W: AU CA FI JP NO NZ
AU 9460913 A 940815 (9444)
ZA 9400407 A 941026 (9444) 18 pp
FI 9503534 A 950721 (9542)
NO 9502797 A 950920 (9547)
EP 680330 A1 951108 (9549) EN
R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE
JP 08506015 W 960702 (9650) 16 pp
CN 1096584 A 941221 (9718)
US 5629166 A 970513 (9725) 6 pp
AU 680236 B 970724 (9737)
ADT WO 9416713 A1 WO 94-US688 940118; AU 9460913 A AU 94-60913 940118;
ZA 9400407 A ZA 94-407 940120; FI 9503534 A WO 94-US688 940118, FI
95-3534 950721; NO 9502797 A WO 94-US688 940118, NO 95-2797 950714;
EP 680330 A1 EP 94-907261 940118, WO 94-US688 940118; JP 08506015 W
JP 94-517167 940118, WO 94-US688 940118; CN 1096584 A CN 94-101086
940121; US 5629166 A Cont of US 93-8446 930122, US 94-288977 940811;
AU 680236 B AU 94-60913 940118
FDT AU 9460913 A Based on WO 9416713; EP 680330 A1 Based on WO 9416713;
JP 08506015 W Based on WO 9416713; AU 680236 B Previous Publ. AU
9460913, Based on WO 9416713
PRAI US 93-8446 930122; US 94-288977 940811
AB WO 9416713 A UPAB: 971113
Candidates for treatment with a therapeutic agent (A) specific for complexes (C) of HLA-C-clone 10 and a **MAGE-1** derived peptide are identified by (1) treating an abnormal cell sample from the patient with cytolytic T cells (CTC) specific for (C) and (2) detecting cell lysis to indicate that the subject is suitable for treatment.

Also new are (1) treatment of cellular abnormalities with CTC responsive to (C) or cell surfaces or with an agent inducing such CTC; (2) isolated CTC specific for (C) and (3) detecting abnormal cells having (C) on the surface by detecting lysis induced by these CTC.

USE - The cellular abnormality being treated is cancer, esp.

melanoma, but may also be non-proliferating cells with (C) on the surface, e.g. cells involved in autoimmune disorders. Detection of (C) can be used for diagnosis.

In an example, the melanoma cell line MZ2-MEL43 expresses a protein functionally equiv. (if not identical) to HLA-C-clone 10. A plasmid contg. cDNA for this protein and a second plasmic contg. cDNA for **MAGE-1**, -2 or -3 were used to transfect COS-7 cells. The transformants were then incubated with CTC of clone 81/12 (isolated from patient MZ2 and recognising MZ2-MEL.43) and after 24 hr. the concn. of tumour necrosis factor in the supernatant measured. A tumour rejection antigen derived from **MAGE-1** is presented by HLA-C-clone 10 and recognised by clone 81/12. Expression of MAGE-2 or -3 did not result in antigen presentation.
Dwg.0/1

L1 ANSWER 9 OF 9 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
AN 94-035970 [05] WPIDS
DNC C94-016558
TI Monoclonal antibodies for diagnosis or therapy - directed against conjugate of MHC class I mol and peptide antigen.
DC B04 D16
IN HAEMMERLING, G
PA (DEKR-N) DEUT KREBSFORSCHUNGSZENTRUM
CYC 1
PI DE 4224542 A1 940127 (9405)* 3 pp
ADT DE 4224542 A1 DE 92-4224542 920724
PRAI DE 92-4224542 920724
AB DE 4224542 A UPAB: 940315
Producing monoclonal antibodies directed against a conjugate of a major histocompatibility complex class I mol. (I) and a peptide antigen (II) comprises (a) isolating (I); (b) inserting a (I)-encoding gene into the genome of a mouse to permit expression of the gene; (c) conjugating (I) with (II); (d) immunising the transformed mouse with the conjugate; (e) isolating spleen cells from the mouse; and (f) producing and opt. humanising monoclonal antibodies in known manner.
Process (I) may be isolated from CS7 AL/6 mouse RMA-S tumour cells or human EBV transformed cells, or may be isolated from tissue, or may be produced by recombinant DNA techniques. Step (b) may be omitted if (I) was isolated from the same mouse strain as that to be immunised. (II) may be a viral or tumour antigen, e.g, the human melanoma antigen **MAGE-1** or the tumour antigen produced by the HPV E6 or E7 oncogene.
USE - The antibodies are useful for diagnosis and therapy of tumours and infections, e.g, as a substitute for tumour-specific cytotoxic T cells.
Dwg.0/0

L8 ANSWER 1 OF 8 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
AN 96-433764 [43] WPIDS
DNN N96-365449 DNC C96-136164
TI Anti-lung tumour antigen monoclonal antibody
TB2A36C3 - produced by Epstein-Barr virus transformation of human lung cancer patient B-cells, useful in conjunction with other agents

for lysis of tumours.

DC B04 D16 S03
IN MUKERJEE, S
PA (MEDE-I) MEDENICA R D
CYC 69
PI WO 9628473 A1 960919 (9643)* EN 46 pp
RW: AT BE CH DE DK EA ES FI FR GB GR IE IT KE LS LU MC MW NL OA
PT SD SE SZ UG
W: AL AM AT AU AZ BB BG BR BY CA CH CN CZ DE DK EE ES FI GB GE
HU IS JP KE KG KP KR KZ LK LR LS LT LU LV MD MG MK MN MW MX
NO NZ PL PT RO RU SD SE SG SI SK TJ TM TR TT UA UG UZ VN
AU 9653652 A 961002 (9703)
ADT WO 9628473 A1 WO 96-US3661 960318; AU 9653652 A AU 96-53652 960318
FDT AU 9653652 A Based on WO 9628473
PRAI US 95-405034 950316
AB WO 9628473 A UPAB: 961025
Novel monoclonal antibody (MAB) TB2A36C3 (pref. having the 134
residue amino acid light chain sequence given in the specification),
has high specificity against lung **tumour antigens**
and is produced by an Epstein-Barr virus (EBV) transformed TB945
human B-cell line. Also claimed are: (1) transformed human B-cell
line immortalised by EBV (2) MAB produced by a cell as in (1); (3)
human MAB which shows positive reactivity against small cell lung
cancer (SCLC) and non-SCLC (NSCLC), and no reactivity against
breast, ovary, **melanoma**, leiomyosarcoma and
leukaemia/lymphoma cell lines; (4) MAB which specifically binds to a
32 kD mol. wt. antigen on NCIH 69 cell line, and a cluster
of antigens from 28-106 kD in the NSCLC cell line NCIH661;
and (5) bioreagent for Ab assays comprising a pure peptide fragment
F(ab)'2 of the MAB TB2A36C3.

USE - The MAB can be used for screening serum or tissue samples
for a carcinoma-associated antigen (claimed). It can also be used,
opt. with other agents, for the lysis of tumours in anti-tumour
therapy, and for activating immune competent CD4 or CD8 cells in a
patient's blood system (claimed).
Dwg.0/10

L8 ANSWER 2 OF 8 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
AN 94-025876 [03] WPIDS
CR 92-381780 [46]
DNC C94-011912
TI Inhibiting tumour growth and metastases with mullerian inhibiting
substance - or its C-terminal fragment, opt. introduced by gene
transfer, also for modulating, expression of class 1 MHC antigens,
e.g. in AIDS patients.

DC B04 D16
IN BARKSDALE, E M; CHIN, T W; DONAHOE, P K; EPSTEIN, J; MACLAUGHLIN, D
T; PARRY, R L; RAGIN, R C
PA (GEHO) GEN HOSPITAL CORP
CYC 20
PI WO 9400133 A1 940106 (9403)* EN 165 pp
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
W: CA JP
EP 646010 A1 950405 (9518) EN
R: CH DE DK ES FR GB IE IT LI NL PT SE
EP 646010 A4 970423 (9735)
US 5661126 A 970826 (9740) 63 pp

ADT WO 9400133 A1 WO 93-US5791 930618; EP 646010 A1 EP 93-916585 930618,
WO 93-US5791 930618; EP 646010 A4 EP 93-916585 ; US 5661126 A
CIP of US 89-299158 890119, CIP of US 91-683966 910412, CIP of US
92-901637 920619, Cont of US 93-7125 930121, US 94-271252 940707

FDT EP 646010 A1 Based on WO 9400133

PRAI US 93-7125 930121; US 92-901637 920619; US 89-299158 890119;
US 91-683966 910412; US 94-271252 940707

AB WO 9400133 A UPAB: 971006

Tumour growth is inhibited by admin. of Muellierian inhibiting
substance (MIS), or its C-terminal fragment, opt. used in
conjunction with a chemotherapeutic agent.

Also new are (1) local inhibition of tumour growth by
proteolytic activation (cleavage to 57 and 12.5 kD
fragments) at the tumour site, (2) two DNA sequences (both 327 bp.,
reproduced in the specification) encoding bovine and human MIS
C-terminal fragment (109 amino acids), etc. and (b) method for
increasing (decreasing) expression of mRNA encoding a class I MHC
protein in a cell by contact with MIS (or MIS antagonist).

USE - MIS inhibits both prim. tumour growth and metastasis,
esp. of vulvar epidermoid and cervical carcinoma, endometrial or
ovarian adenocarcinoma, ocular melanoma and tumours of the
prostate, lymphoid tissue, breast, skin and germ cells. The use of
MIS can allow the amt. of (I) needed for tumour treatment to be
reduced. Increasing expression of MHC antigens suppresses
metastases or tumour cells and improves immunodeficiency
e.g. in AIDS patients, pref. when admin. together with interferon.
Reducing MHC expression is esp. with epidermal growth factor and is
used to reduce immunogenicity of transplants.

Dwg.0/27

L8 ANSWER 3 OF 8 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD

AN 94-010204 [02] WPIDS

DNN N94-008206 DNC C94-004140

TI Receptor protein for CSVTCG region of thrombospondin and antibodies
or antisera against it - used as medicaments against, e.g. tumour
cell adhesion and metastasis, thrombosis, and malaria, and as
targetting agents.

DC B04 D16 S03

IN EYAL, J; HAMILTON, B K; TUSZYNSKI, G P; HAMILTON, B

PA (GRAC) GRACE & CO-CONN W R; (MEDI-N) MEDICAL COLLEGE PENNSYLVANIA;
(MEDI-N) MEDICAL COLLEGE PA

CYC 20

PI EP 578342 A2 940112 (9402)* EN 16 pp

R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE

CA 2095404 A 931115 (9406)

US 5367059 A 941122 (9501) 12 pp

EP 578342 A3 940629 (9527)

JP 07138296 A 950530 (9530) 24 pp

ADT EP 578342 A2 EP 93-250135 930511; CA 2095404 A CA 93-2095404 930503;

US 5367059 A US 92-883659 920514; EP 578342 A3 EP 93-250135 930511;

JP 07138296 A JP 93-132353 930512

PRAI US 92-883659 920514

AB EP 578342 A UPAB: 940223

Isolated receptor protein has specific binding affinity for CSVTCG
peptide of sequence Cys-Ser-Val-Thr-Cys-Gly.

Also claimed are (1) an antibody or antisera specifically
reactive to the receptor protein; and (2) a carrier molecule and

biomedical device comprising the antibody or antisera.

USE/ADVANTAGE - CSVTCG receptor protein can be purified from cell extracts of tumour cell lines, pref. **melanoma** or lung cancer cell lines, by passing the extracts through a chromatographic column contg. immobilised CSVTCG peptides. The antibodies or antisera can be used to diagnose carcinoma by reacting them with a tissue sample. They can also be used in the prepn. of a medicament to inhibit tumour cell adhesion or metastasis, or for inhibiting thrombotic activity, atherosclerosis, malarial activity or angiogenesis. The carrier molecule may also comprise toxins, drugs, hormones or imaging agents and can be used to deliver these cpds. to tumour cells for diagnostic or therapeutic purposes. The receptor is specific for the CSVTCG region of thrombospondulin.
Dwg.0/2

L8 ANSWER 4 OF 8 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
AN 92-433665 [52] WPIDS
DNN N92-330897 DNC C92-192572
TI New monoclonal antibody ME20 - specific for cell surface **protein** detectable on human **melanoma** **tumour** cells, for diagnosis and treatment of **melanoma**.
DC B04 D16 S03
IN HELLSTROM, I; HELLSTROM, K E; MARQUARDT, H
PA (BRIM) BRISTOL-MYERS SQUIBB CO
CYC 23
PI WO 9221767 A1 921210 (9252)* EN 38 pp
RW: AT BE CH DE DK ES FR GB GR IT LU MC NL SE
W: AU CA FI JP KR NO
AU 9221706 A 930108 (9315)
ZA 9204068 A 930224 (9316) 35 pp
PT 100568 A 930930 (9342)
ADT WO 9221767 A1 WO 92-US4451 920527; AU 9221706 A AU 92-21706 920527,
WO 92-US4451 920527; ZA 9204068 A ZA 92-4068 920604; PT 100568 A PT
92-100568 920604
FDT AU 9221706 A Based on WO 9221767
PRAI US 91-710613 910605
AB WO 9221767 A UPAB: 940407
An antibody (Ab) or fragment that specifically reacts with a human **melanoma** cell surface protein (I) og mol.wt. 80-120 **kD** and which is present on human **melanoma** tumour cells but not normal cells, is new.
Also new are (1) a purified peptide contg. a region, corresp. to a domain of (I) or a fragment, which can specifically immunoreact with monoclonal Ab ME20 produced by the hybridoma ATCC HB10764 or HB10763; (2) an immunogenic compsn. comprising this peptide and a carrier or an immune responding agent; (3) a kit comprising the Ab or fragment and/or the peptide.
USE/ADVANTAGE - The Ab can be used to determine the presence and location of human **melanoma** cells. It may also be used to treat **melanoma** when administered with a chemotherapeutic agent. The peptide is used to induce an immune response directed towards human **melanoma**. The Ab can be used in in vivo or in vitro assay
Dwg.0/0

L8 ANSWER 5 OF 8 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD

AN 91-353726 [48] WPIDS
DNN N91-270898 DNC C91-152567
TI New 35 **kD** **tumour** associated **protein antigen** - used for immuno-diagnosis, immuno-prognosis and therapy of cancer.
DC B04 D16
IN GUPTA, R K; MORTON, D L; WONG, J H
PA (REGC) UNIV CALIFORNIA
CYC 33
PI WO 9117187 A 911114 (9148)*
RW: AT BE CH DE DK ES FR GB GR IT LU NL OA SE
W: AT BB BG BR CA FI HU JP KP KR LK MC MG MW NO PL RO SD SU
EP 529007 A1 930303 (9309) EN 23 pp
R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE
JP 05506241 W 930916 (9342) 9 pp
ADT EP 529007 A1 EP 91-920948 910417, WO 91-US2638 910417; JP 05506241 W
JP 91-508637 910417, WO 91-US2638 910417
FDT EP 529007 A1 Based on WO 9117187; JP 05506241 W Based on WO 9117187
PRAI US 90-510602 900418
AB WO 9117187 A UPAB: 930928
A purified **tumour**-associated antigenic **protein** has a molecular weight of 35 **kD** by SDS-PAGE under reducing conditions and specifically binds Mab JSI. Also claimed are reagents which specifically bind the protein, reagents which bind JSI, a hybridoma cell line producing JSI, nucleic acid encoding the protein and nucleic acid hybridising to the nucleic acid that encodes the protein.
USE/ADVANTAGE - The protein is used to detect subclinical cancer, to monitor a malignancy, as a vaccine for inducing an immune response to cancers e.g. **melanoma**, sarcoma and carcinoma, especially breast carcinoma. Cancer is detected by enhancing expression of the protein on cancer cells with IFN-gamma, contacting the protein with a reagent (e.g. an antibody) and detecting the presence of the reagent. The reagent may also be used to detect an immune complex containing the protein.
0/1

L8 ANSWER 6 OF 8 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
AN 91-164362 [22] WPIDS
DNN N91-125906 DNC C91-071183
TI New urinary **tumour** associated **antigen** and its sub-units - used for immuno diagnosis, immuno prognosis and therapy of human cancer.
DC B04 D16 S03
IN EUHUS, D M; GUPTA, R K; MORTON, D L; GUPTA, R
PA (EUHU-I) EUHUS D M; (GUPT-I) GUPTA R K; (MORT-I) MORTON D L
CYC 34
PI WO 9106866 A 910516 (9122)* 86 pp
RW: AT BE CH DE DK ES FR GB GR IT LU NL OA SE
W: AT AU BB BG BR CA CH DE DK ES FI GB HU JP KP KR LK LU MC MG
MW NL NO RO SD SE SU
AU 9168753 A 910531 (9135)
EP 498851 A1 920819 (9234) EN 86 pp
R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE
JP 05505596 W 930819 (9338) 31 pp
WO 9106866 A3 910905 (9508)
AU 661816 B 950810 (9540)

EP 678744 A2 951025 (9547) EN 44 pp
 R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE
 EP 498851 B1 960103 (9606) EN 42 pp
 R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE
 DE 69024659 E 960215 (9612)
 EP 678744 A3 951213 (9619)
 ES 2084715 T3 960516 (9627)
 US 5700649 A 971223 (9806) 35 pp
 ADT EP 498851 A1 EP 90-917644 901031, WO 90-US6339 901031; JP 05505596 W
 WO 90-US6339 901031, JP 91-500470 901031; WO 9106866 A3 WO 90-US6339
 901031; AU 661816 B AU 91-68753 901031; EP 678744 A2 EP 95-104918
 901031; EP 498851 B1 EP 90-917644 901031, WO 90-US6339 901031; DE
 69024659 E DE 90-624659 901031, EP 90-917644 901031, WO 90-US6339
 901031; EP 678744 A3 EP 95-104918 901031; ES 2084715 T3 EP 90-917644
 901031; US 5700649 A Div ex US 89-431533 891103, US 95-462264 950605
 FDT EP 498851 A1 Based on WO 9106866; JP 05505596 W Based on WO 9106866;
 AU 661816 B Previous Publ. AU 9168753, Based on WO 9106866; EP
 498851 B1 Based on WO 9106866; DE 69024659 E Based on EP 498851,
 Based on WO 9106866; EP 678744 A3 Related to EP 498851; ES 2084715
 T3 Based on EP 498851
 PRAI US 89-431533 891103; US 95-462264 950605
 AB WO 9106866 A UPAB: 930928
 A new pure antigenic polypeptide subunit of urinary **tumour**
 associated **antigen** (UTAA) is claimed. After reduction by
 beta-mercaptoethanol and separation by SDS-PAGE, the subunit has a
 molecular weight of 90-100 kD. Also claimed are: 1) A
 monoclonal antibody (MAb) produced by isolating antibody producing
 cells from an animal exposed to the polypeptide forming hybridomas
 between these cells and cancer cells, and selecting those producing
 the MAb. 2) Reagents reactive with antibodies that react with UTAA.
 3) An epitope of UTAA on the 45 kD subunit. 4) An epitope
 of UTAA and the 120 kD subunit. 5) An epitope of UTAA on
 the 65 kD subunit. 6) Nucleic acid encoding the subunit;
 and 7) A nucleic acid probe which hybridises with the nucleic acid
 of (5). The MAb is FgG or IgM.
 USE/ADVANTAGE - The MAb is used to detect subclinical cancer,
 UTAA on the tumour cells of a biopsy and breast or lung cancer. Low
 levels of UTAA may be detected. A vaccine against tumour cells is
 also claimed, comprising inactivated tumour cells with a UTAA and at
 least one **tumour-associated antigen** selected
 from GM-2, GD-2, foetal **antigen** or **melanoma**
tumour-associated antigen. Cancers that can be
 vaccinated against include melanomas, sarcomas and carcinomas.
 @ (86pp Dwg.No.1/17)@
 L8 ANSWER 7 OF 8 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
 AN 89-270468 [37] WPIDS
 DNC C89-119828
 TI New continuous cell line for prodn. of monoclonal antibody - reacts
 with **melanoma-associated tumour cell**
antigen, useful for diagnosis and differentiation of
 cancerous diseases.
 DC B04 D16
 IN KHAN, A
 PA (WADL) WADLEY TECHNOLOGIES INC; (CYTO-N) CYTOCLONAL PHARM INC
 CYC 1
 PI US 4851510 A 890725 (8937)* 10 pp

US 5654408 A 970805 (9737) 11 pp
 ADT US 4851510 A US 84-676839 841130; US 5654408 A Div ex US 84-676839
 841130, US 89-341718 890421
 FDT US 5654408 A Div ex US 4851510
 PRAI US 84-676839 841130; US 89-341718 890421
 AB US 4851510 A UPAB: 930923
 A continuous cell line which produces antibodies, which specifically
 bind with at least one site on a **melanoma**-associated
 antigen, but are unreactive with normal human cells, breast or
 ovarian carcinoma cells or H-29 colon carcinoma cells as determined
 by indirect immunofluorescence, is claimed. The site on the antigen
 is not associated with normal human cell surface antigens and the
melanoma-associated antigen is isolatable from G-361
melanoma cells, the isolated antigen having a mol. wt. of
 105000 as determined by sodium dodecyl sulphate gel electrophoresis.
 Also claimed is a continuous cell line producing antibodies
 specific against a **melanoma**-associated antigen of mol. wt.
 38000. Cell line ATCC HB8672 is claimed, and the monoclonal antibody
 WI-MN-1 it produces.
 Also claimed is an antibody produced by (a) obtg. a WI-MN-1
 monoclonal antibody produced by cell line ATCC HB8672; (b) forming a
 complex comprising WI-MN-1 bound to a **tumour** cell
antigen by contacting WI-MN-1 with a **tumour** cell;
 (c) isolating the **tumour** cell **antigen** which
 combines with the WI-MN-1 monoclonal antibody from the complex; (d)
 injecting the **tumour** cell **antigen** into an
 animal; (e) selecting and isolating an antibody-forming cell from
 the animal, the cell capable of producing antibodies specifically
 binding the **tumour** cell **antigen**; (f) fusing the
 antibody-forming cell with a myeloma cell to form a hybridoma; and
 (g) causing the hybridoma to make the claimed antibody.
 Alternatively, the isolated **tumour antigen**
 is injected into an animal, circulating fluids are collected and the
 antibody directed against the antigen is isolated.
 USE/ADVANTAGE - The WI-MN-1 antibody may be used for diagnosis
 and differentiation of cancerous diseases.
 0/0

L8 ANSWER 8 OF 8 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
 AN 86-163227 [26] WPIDS
 DNC C86-069813
 TI Antibody for differentiating between malignant and benign tumours -
 obtd. by contacting malignant tumour cells with gamma-globulin to
 induce antigenicity then using to immunise animal etc..
 DC B04 D16
 IN FERRONE, S; MATSUI, M
 PA (SUNR) SUNTORY LTD
 CYC 13
 PI EP 185135 A 860625 (8626)* EN 15 pp
 R: AT BE CH DE FR GB IT LI LU NL SE
 JP 61148199 A 860705 (8633)
 US 5126262 A 920630 (9229) 7 pp
 ADT EP 185135 A EP 85-110206 850814; JP 61148199 A JP 85-217741 850930;
 US 5126262 A Cont of US 84-684262 841220, Cont of US 88-251980
 880928, US 91-657253 910215
 PRAI US 84-684262 841220
 AB EP 185135 A UPAB: 930922

Antibody specifically differentiating between a malignant and a benign tumour is new when obtd. by: (a) contacting cultured malignant tumour cells with a cytokine or lymphokine antitumour agent (I) to enhance or induce the antigenicity of the cells specific to the malignant tumour; (b) immersing an animal with these cells; (c) obtg. spleen cells from the animal; (d) fusing the spleen cells with immortal cells for hybridoma prodn.; (e) cloning the fused cells for selection of hybridoma cells producing an antibody specific to the malignant tumour; and (f) collecting the antibody from a culture of the selected hybridoma cells.

USE/ADVANTAGE - The antibody is useful for the diagnosis and treatment of human tumour cells and tissues, and esp. for distinguishing malignant melanomas from benign tumours. The target **antigen** does not have to be purified and large amts. of homogeneous antibody can be produced.
0/0

=> fil biosis

FILE 'BIOSIS' ENTERED AT 09:28:46 ON 07 APR 1998
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FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 6 April 1998 (980406/ED)
CAS REGISTRY NUMBERS (R) LAST ADDED: 6 April 1998 (980406/UP)

=> d his

(FILE 'BIOSIS' ENTERED AT 09:23:41 ON 07 APR 1998)

DEL HIS Y
L1 119 S MAGE 1
L2 328823 S SEQUENCE?
L3 19 S L1 AND L2
L4 13 S L1 AND MONOCLONAL
L5 17 S L3 NOT L4
L6 2 S 11540 OR HB11540
L7 26284 S (TUMOR# OR TUMOUR#) (4A) (PROTEIN# OR ANTIGEN#)
L8 1541 S L7 AND MELANOMA?
L9 3105 S (46 OR 34) (2W) (KD OR KDA OR KDS OR KILODALTON# OR KI
L10 7 S L9 AND L8
L11 4 S L1 AND L9
L12 8 S L10 OR L11

FILE 'BIOSIS' ENTERED AT 09:28:46 ON 07 APR 1998

=> d bib ab 14 1-13;d bib ab 15 1-17;d bib ab st 1-8 112

L4 ANSWER 1 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS
AN 97:503587 BIOSIS
DN 99802790
TI Immunohistochemical detection of MAGE tumor-associated antigens in

esophageal squamous cell carcinoma.

AU Schaefer C; Noppen S; Nuernberger H-R; Gudat F; Kocher T; Luescher U; Zuber M; Spagnoli G C; Heberer M

CS Dep. Surg. Res., ZLF, Hebelstrasse 20, CH-4031 Basel, Switzerland

SO Oncology Reports 4 (6). 1997. 1289-1293. ISSN: 1021-335X

LA English

AB Genes of the MAGE family encode tumor-specific antigens recognized by cytotoxic T-lymphocytes in a variety of neoplasms. We investigated the protein expression of these antigens as related to the gene expression, in esophageal squamous cell carcinoma by using **monoclonal** antibodies recognizing MAGE gene products. Esophageal squamous cell carcinomas were found to express both **MAGE-1** (4 out of 15 samples) and **MAGE-3** (7 out of 15 samples) genes, by RT-PCR. Immunoblotting revealed **MAGE-1** and **MAGE-3** gene products in 2 and 6 out of 15 samples, respectively. Immunohistochemistry performed on 12 samples showed **MAGE-1** protein expression, limited to single tumor cells, in 2 cases. **MAGE-3** gene product was detectable in 7 cases: in 5 of them over 50% of neoplastic cells were positive. Considering the high percentages of tumor cells expressing **MAGE-3** antigen, the use of epitope-based vaccines could be envisaged in patients displaying appropriate HLA-class I phenotypes.

L4 ANSWER 2 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS

AN 97:503259 BIOSIS

DN 99802462

TI Heterogeneity of melanoma antigen-1 (**MAGE-1**) gene and protein expression in malignant melanoma.

AU Zuber M; Spagnoli G C; Kocher T; Lusher U; Schaefer C; Noppen C; Gudat F; Harder F; Heberer M

CS Dep. Surg., Univ. Basel, Spitalstr. 21, CH-4031 Basel, Switzerland

SO European Surgical Research 29 (5). 1997. 403-410. ISSN: 0014-312X

LA English

AB Objective: The authors' objective is to identify **MAGE-1** tumor antigen in clinical melanoma specimens and to verify the extent of its expression in tumors where evidence of specific gene transcripts can be obtained. Background data: The **MAGE-1** gene encodes a tumor-associated antigen that can be recognized by specific cytotoxic T lymphocytes. Transcription of the **MAGE-1** gene has previously been demonstrated in various malignancies, but the production of the specific gene product and its distribution in neoplastic tissues have not yet been addressed. Methods: Total cellular mRNA was extracted from six melanoma biopsies, reverse-transcribed and tested in 25-45 cycles of reverse polymerase chain reaction (rtPCR) in the presence of primers' pairs specific for the beta-actin-positive control gene and for the **MAGE-1**-encoding gene. Concurrently, portions of these specimens were lysed and probed for **MAGE-1** protein by immunoblotting. Additional material from the same biopsies was analyzed following immunohistological staining with **MAGE-1**-specific **monoclonal** antibodies. Results: **MAGE-1** gene transcription could be demonstrated following 25 cycles of rtPCR in one out of six biopsies and in three more following 35 cycles of rtPCR. 2/6 samples were negative even after 45 cycles of rtPCR. **MAGE-1** protein production could be detected by immunoblotting in the lysates from biopsies showing evidence of specific gene transcription. Cells

positive for **MAGE-1** protein expression could be identified by immunohistochemistry on snap-frozen sections in three of the four tumors displaying specific transcripts. Distribution of positivity ranged between focal cellular areas and single positive cells in the different tumors. Conclusions: The **MAGE-1** tumor antigen can be detected by specific **monoclonal** antibodies in clinical tumor specimens. The pattern of positivity observed in samples showing evidence of **MAGE-1** gene expression suggests a relevant heterogeneity regarding **MAGE-1** antigen production within individual tumor specimens.

L4 ANSWER 3 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 96:563309 BIOSIS
 DN 99292665
 TI The tumour-associated antigen **MAGE-1** is detectable in formalin-fixed paraffin sections of malignant melanoma.
 AU Gudat F; Zuber M; Durmuller U; Kocher T; Schaefer C; Noppen C; Spagnoli G
 CS Inst. Pathol., Univ. Basel, Schonbeinstrasse 40, CH-4003 Basel, Switzerland
 SO Virchows Archiv 429 (2-3). 1996. 77-81. ISSN: 0945-6317
 LA English
 AB The **MAGE-1** gene encodes a protein encompassing a HLA-A1-restricted target epitope for cytolytic T lymphocytes. **Monoclonal** antibodies directed against the **MAGE-1** protein were tested for usage in immunohistology of routine pathology material. Seven formalin-fixed, paraffin-embedded malignant melanomas were studied by the Avidin-Biotin complex (ABC) method with or without different antigen retrieval methods. Native, frozen tissues from the same tumours were used to validate the results by immunohistochemistry on frozen sections, by PCR for mRNA and by protein demonstration in tissue extracts using western blotting. Of 4 **monoclonal** antibodies tested, mAB 34B and mAB 77B were highly efficient in detecting **MAGE-1** protein in deparaffinized sections with the regular ABC method after microwave pretreatment. In a series of an additional 28 patients 75% expressed **MAGE-1**, 50% in a substantial proportion. Follow-up studies in 6 patients indicate that the expression pattern remains stable but may change substantially within a short range. Immunohistology is thus a rapid and well-established method that might be used to select and monitor HLA-A1 positive patients with malignant melanoma and other candidate tumours for **MAGE-1**-directed immuno-therapy.

L4 ANSWER 4 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 96:415356 BIOSIS
 DN 99137712
 TI **Monoclonal** antibodies against recombinant-**MAGE-1** protein identify a cross-reacting 72-kDa antigen which is co-expressed with **MAGE-1** protein in melanoma cells.
 AU Carrel S; Schreyer M; Spagnoli G; Cerottini J-C; Rimoldi D
 CS Ludwig Inst. Cancer Res., Ch. des Boveresses 155, 1066 Epalinges, Switzerland
 SO International Journal of Cancer 67 (3). 1996. 417-422. ISSN: 0020-7136

LA English

AB The MAGE-I gene codes for tumor-associated peptides recognized by cytolytic T lymphocytes in association with MHC-class-I molecules such as HLA-A I and HLA-Cw16. In the course of a study aiming at the immunohistochemical detection of the MAGE-I gene product in tumor samples, 2 mouse **monoclonal** antibodies (MAbs) directed against a full-length recombinant MAGE-I fusion protein were found to react strongly not only with the 46-kDa MAGE-I protein, but also with a 72-kDa product in immunoblots of lysates obtained from several MAGE1-mRNA-positive melanoma cell lines. Pre-incubation of the antibodies with the recombinant MAGE-I fusion protein abolished their reactivity both with MAGE-I protein and with the 72-kDa product, thus confirming the occurrence of antigenic determinant(s) shared by the 2 proteins. The 72-kDa protein is not an alternative product of MAGE-I, since it was still detected in lysates of a MAGE-I loss variant derived from a MAGE-I-positive melanoma cell line. Moreover, the 72-kDa protein does not appear to be a product of the other members of the MAGE gene family known to be expressed in tumors (such as MAGE-2, -3, -4 and -12). Interestingly, expression of the 72-kDa protein was found to be correlated with that of MAGE-I protein. Thus, in 30 tumor cell lines analyzed by immunoblotting and RT-PCR, the 72-kDa protein was never detected in MAGE-I-mRNA-negative cell lines, while it was co-expressed with MAGE-I protein in 12 out of 15 cell lines expressing MAGE-I. Furthermore, the 72-kDa protein was detected in lysates of human testis, the only normal tissue known to express MAGE-I. Finally, treatment of **MAGE-1** -mRNA-negative cell lines with 5-Aza-2'-deoxycytidine, a hypomethylating agent known to induce MAGE- I expression, resulted in the expression of the 72-kDa protein. Taken collectively, these findings suggest that expression of the gene encoding the 72-kDa protein identified in this study through antigenic determinant(s) shared with MAGE-I protein is regulated in a way similar to that of MAGE-I.

L4 ANSWER 5 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS

AN 96:257272 BIOSIS

DN 98813401

TI **Monoclonal** antibodies against full-length **MAGE-**

1 protein identify a crossreacting 72 kDa antigen which is coexpressed with **MAGE-1** melanoma cells.

AU Carrel S; Salvi S; Hartmann F; Rimoldi D; Schreyer M; Spagnoli G

CS Ludwig Inst. Cancer Res., Lausanne Branch, Univ. Lausanne, 1066 Epalinges, Switzerland

SO 87th Annual Meeting of the American Association for Cancer Research, Washington, D.C., USA, April 20-24, 1996. Proceedings of the American Association for Cancer Research Annual Meeting 37 (0). 1996. 465. ISSN: 0197-016X

DT Conference

LA English

L4 ANSWER 6 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS

AN 96:46201 BIOSIS

DN 98618336

TI A 72kDa protein coexpressed in melanoma cells with **MAGE-**

1, revealed by anti-recombinant **MAGE-1** **monoclonal** antibodies.

AU Carrel S; Hartmann F; Salvi S; Spagnoli G; Schreyer M; Rimoldi D

CS Ludwig Inst. Cancer Research, Lausanne Branch, Univ. Lausanne, 1066
Epalinges, Switzerland
SO Fifth International Conference of Anticancer Research, Corfu, Greece,
October 17-22, 1995. Anticancer Research 15 (5A). 1995. 1672. ISSN:
0250-7005
DT Conference
LA English

L4 ANSWER 7 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS

AN 95:551277 BIOSIS

DN 98565577

TI Establishment of an enzyme-linked immunosorbent assay (ELISA) for
measuring cellular MAGE-4 protein on human cancers.

AU Shichijo S; Tsunosue R; Kubo K; Kuramoto T; Tanaka Y; Hayashi A; Itoh
K

CS Dep. Immunol., Kurume Univ. Sch. Med., Kurume 830, Japan

SO Journal of Immunological Methods 186 (1). 1995. 137-149. ISSN:
0022-1759

LA English

AB The MAGE genes encoding tumor-rejection antigens are expressed on
various human cancers. An enzyme-linked immunosorbent assay (ELISA)
was established for measuring cellular MAGE-4 protein (MAGE-4a and/or
-4b) expressed on human tumor cells using a **monoclonal**
antibody (mAb) and polyclonal Ab to recombinant MAGE-4b protein. Both
the R5 mAb (IgG1) and the polyclonal Ab recognized a 45 kDa protein
in extracts of MAGE-4 mRNA positive cancers, and showed no apparent
cross-reactivity to the other MAGE gene products (**MAGE-**

1, -2, -3, -6, and -12) by the immunoblot analyses. The R5
mAb and the polyclonal Ab primarily recognized one (the position
119-133) and two oligopeptides (the positions 119-133 and 259-273),
respectively, among a series of 31 different MAGE-4b oligopeptides.
The amino acid sequences of these two peptides were identical to
those of MAGE-4a and -4b, but differed from those of all the other
MAGE proteins (**MAGE-1**, -2, -3, -6, and -12).
Substitution of glycine for amino acid in position 123 (arginine, R),
124 (lysine, K), 126 (R) or 128 (K) in a MAGE-4b oligopeptide of the
position 119-132 severely decreased the reactivity of the R5 mAb to
the oligopeptide. This ELISA also showed no apparent cross-reactivity
with the other MAGE gene products (**MAGE-1**, -2 -3,
-6, and -12). The minimum detectable level of MAGE-4 protein was
determined to be 10 pg/well (100 pg/ml). The results suggest that
this ELISA is a reliable and quantitative method to measure cellular
MAGE-4 protein that is a potential target molecule for specific
immunotherapy of human cancers.

L4 ANSWER 8 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS

AN 95:487231 BIOSIS

DN 98501531

TI Expression of the MAGE gene family in human lymphocytic leukemia.

AU Schichijo S; Tsunosue R; Masuoka K; Natori H; Tamai M; Miyajima J;
Sagawa K; Itoh K

CS Dep. Immunol., Kurume Univ. Sch. Med., 67-Asahi-machi, Kurume,
Fukuoka 830, Japan

SO Cancer Immunology Immunotherapy 41 (2). 1995. 95-103. ISSN:
0340-7004

LA English

AB The MAGE gene family, encoding tumor-rejection antigens recognized by

cytotoxic T lymphocytes, is frequently expressed in human solid cancers. However, its expression in leukemia has not been well studied. We have investigated MAGE gene expression at the mRNA level in human leukemia. The MAGE gene family was expressed in 17 of 34 (50%) examples of T cell leukemia (12/21 patients' peripheral blood mononuclear cells and 5/13 cell lines), in 7 of 16 (44%) cases of B cell leukemia (1/8 and 6/8 respectively), but in none of 23 myelomonocytic leukemia cases (0/16 and 0/7), as evaluated by the primers common to the **MAGE-1**, -3, -4 (-4a and/or -4b), and -6 genes and the semi-quantificative reverse transcription/polymerase chain reaction method. None of a panel of normal lymphoid cells expressed the MAGE gene family. As revealed by the primers specific for each of the MAGE genes, the **MAGE-1**, -2, -3, -4 or -6 gene was expressed in 8, 8, 6, 2, or 6 respectively out of 23 types of leukemia cell lines. Expression of the **MAGE-1** protein in both the cell lines and patients' cells was confirmed by immunoblot analysis with the polyclonal antibody to recombinant **MAGE-1** protein. Cellular MAGE-4 protein in the cell lines was measured by an enzyme-linked immunosorbent assay with the polyclonal and **monoclonal** antibodies to recombinant MAGE-4b protein. In summary, the MAGE gene family was found to be expressed in the substantial proportion of T cell leukemias, but in no case of myelomonocytic leukemia. Antigens coded by the MAGE gene family could be important molecules for understanding specific immunity against lymphocytic leukemia.

L4 ANSWER 9 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS

AN 95:411919 BIOSIS

DN 98426219

TI Detection of MAGE-4 protein in lung cancers.

AU Shichijo S; Hayashi A; Takamori S; Tsunosue R; Hoshino T; Sakata M; Kuramoto T; Oizumi K; Itoh K

CS Dep. Immunol., Kurume Univ. Sch. Med., 67 Asahi-machi, Kurume 830, Japan

SO International Journal of Cancer 64 (3). 1995. 158-165. ISSN: 0020-7136

LA English

AB Expression of genes of the MAGE family, which encode tumor-rejection antigens recognized on HLA-A1 and -Cw1601 by cytotoxic T lymphocytes (CTL), was investigated in lung cancers at the mRNA (**MAGE-1**, -2, -3/-6, and -4 (4a and/or 4b)) and protein (**MAGE-4**) levels. **MAGE-1**, -2, -3/-6 and -4 genes were expressed, respectively, at the mRNA level in 6, 7, 20 and 7 of 53 lung cancers (50 non-small-cell lung cancers and 3 small-cell lung cancers) by the reverse transcription-polymerase chain reaction (RT-PCR) method. Polyclonal antibody (Ab) and **monoclonal** antibody (MAb) against recombinant MAGE-4b protein were developed to detect MAGE-4 protein. Both the polyclonal Ab and the RS MAb recognized a 45-kDa protein in extracts of MAGE-4 mRNA-positive lung cancers, and showed no apparent cross-reactivity with the other MAGE gene products except with MAGE-4a by immunoblot analyses and transfection experiments. MAGE-4 protein was detected in 13 of 44 (30%) lung cancers (18 to 55,989 pg/mg) by ELISA with the polyclonal Ab and RS MAb. These 13 lung cancers consisted of 6 of 6 MAGE-4 mRNA-detectable and 7 of 38 MAGE-4 mRNA undetectable lung cancers. Histologically, these comprised 7 of 10 squamous-cell carcinomas, 4

of 30 adenocarcinomas and 2 of 3 small-cell lung cancers. The proportions of MAGE gene-positive samples, at both the mRNA and protein levels, correlated with the size of the primary tumors and with regional node involvement. These results should provide important information on specific immunotherapy of lung cancers using MAGE gene products.

L4 ANSWER 10 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 95:317017 BIOSIS
 DN 98331317
 TI Identification and intracellular location of MAGE-3 gene product.
 AU Kocher T; Schultz-Thater E; Gudat F; Schaefer C; Casorati G; Juretic A; Willimann T; Harder F; Heberer M; Spagnoli G C
 CS Surg. Res. Lab., 20 Hebelstrasse 4031 Basel, Switzerland
 SO Cancer Research 55 (11). 1995. 2236-2239. ISSN: 0008-5472
 LA English
 AB The human MAGE-3 gene encodes a melanoma antigenic epitope recognized by specific cytotoxic T lymphocytes, but its gene product has not been identified thus far. We produced a recombinant MAGE-3 gene product by expression cloning of the entire reading frame in the context of a fusion protein characterized by a 10-histidine tail, allowing purification by metal chelation on a nickel Sepharose column. The semipurified product was used to generate MAGE-3-specific **monoclonal** antibodies. One reagent could identify by immunoblotting the native MAGE-3 gene product as a M, 48,000 protein in lysates of cell lines showing evidence of MAGE-3 gene expression. No apparent cross-reactivity with recombinant or native **MAGE-1** gene product was observed. Immunohistochemistry shows that, closely resembling the **MAGE-1** gene product, MAGE-3 is a cytoplasmic protein.

L4 ANSWER 11 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 95:187036 BIOSIS
 DN 98201336
 TI Immunohistochemical localization of **MAGE-1** in melanoma cell lines by **monoclonal** anti-**MAGE-1** antibodies.
 AU Carrel S; Hartmann F; Salvi S; Spagnoli G; Schreyer M; Rimoldi D
 CS Ludwig Inst. Cancer Res., Lausanne Branch, Univ. Lausanne, 1066 Epalinges, Switzerland
 SO Eighty-sixth Annual Meeting of the American Association for Cancer Research, Toronto, Ontario, Canada, March 18-22, 1995. Proceedings of the American Association for Cancer Research Annual Meeting 36 (0). 1995. 479. ISSN: 0197-016X
 DT Conference
 LA English

L4 ANSWER 12 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 94:548546 BIOSIS
 DN 98008094
 TI **MAGE-1** gene product is a cytoplasmic protein.
 AU Schultz-Thater E; Juretic A; Dellabona P; Luscher U; Siegrist W; Harder F; Heberer M; Zuber M; Spagnoli G C
 CS Z.L.F., Surgical Res. Lab., 20 Hebelstrasse, CH-4031 Basel, Switzerland
 SO International Journal of Cancer 59 (3). 1994. 435-439. ISSN: 0020-7136

LA English

AB **MAGE-1** gene encodes a human melanoma antigen, recognized by syngeneic cytotoxic T lymphocytes (CTL). **MAGE-1** transcripts are also detectable in breast cancers, in non-small-cell lung carcinomas and in central nervous system tumors. In order to identify, in cellular preparations, the protein encompassing the antigenic peptide, we generated a panel of **monoclonal** antibodies (MAbs) against the **MAGE-1** gene product by using, as immunogen, a full-length recombinant preparation (rMAGE1), obtained through expression cloning of the relevant gene in *E. coli*. Four reagents were obtained recognizing both rMAGE-1 and the 46-kDa native protein in cell lines expressing **MAGE-1** mRNA. No positivity could be detected in **MAGE-1**-mRNA-negative melanoma lines. No surface labelling of **MAGE-1**-positive cell lines could be observed. In contrast, on permeabilization of MZ2 melanoma cells, all 4 MAbs induced efficient staining, as detected by cytofluorography. Fluorescence microscopy shows that **MAGE-1** gene product is a cytoplasmic protein clustered in paranuclear organelle-like structures. Thus, **MAGE-1** protein location closely resembles that of P91A and P198 murine-tumor antigens.

L4 ANSWER 13 OF 13 BIOSIS COPYRIGHT 1998 BIOSIS

AN 94:129901 BIOSIS

DN 97142901

TI Identification of the **MAGE-1** gene product by **monoclonal** and polyclonal antibodies.

AU Chen Y-T; Stockert E; Chen Y; Garin-Chesa P; Rettig W J; Van Der Bruggen P; Boon T; Old L J

CS Ludwig Inst. Cancer Res., New York Unit, New York Hosp.-Cornell Med. Cent., New York, NY 10021, USA

SO Proceedings of the National Academy of Sciences of the United States of America 91 (3). 1994. 1004-1008. ISSN: 0027-8424

LA English

AB The human **MAGE-1** gene encodes a melanoma peptide antigen recognized by autologous cytotoxic T lymphocytes. To produce antibodies against the **MAGE-1** gene product, several approaches were taken. Three oligopeptides were synthesized based on predicted **MAGE-1** amino acid sequences and were used to generate rabbit anti-peptide antisera. In addition, a truncated **MAGE-1** cDNA was cloned into an *Escherichia coli* expression vector, and recombinant protein was produced and purified. All three rabbit anti-peptide antisera showed reactivity against the immunizing peptide, and one reacted with the recombinant **MAGE-1** protein by immunoblotting, but none reacted with cell lysates from **MAGE-1** mRNA-positive cells. The recombinant **MAGE-1** protein was then used for the generation of mouse **monoclonal** and rabbit polyclonal antibodies. One IgG1 **monoclonal** antibody, MA454, as well as rabbit polyclonal antisera recognized a 46-kDa protein in extracts of **MAGE-1** mRNA-positive melanoma cell lines. The antibodies showed no apparent crossreactivity with products of the closely related **MAGE-2** and **MAGE-3** genes. Serological typing of normal and tumor cell lysates was in full agreement with mRNA analysis, showing expression of **MAGE-1** protein in **MAGE-1**

mRNA-positive testis and a subset of melanomas but not in **MAGE-1** mRNA-negative normal or tumor tissues.
Transfection of the **MAGE-1** gene into a **MAGE-1** mRNA-negative melanoma cell line resulted in the expression of the 46-kDa protein, confirming the identity of this protein as the **MAGE-1** gene product.

L5 ANSWER 1 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
AN 98:93450 BIOSIS
DN 01093450
TI Two members of the human MAGEB gene family located in Xp21.3 are expressed in tumors of various histological origins.
AU Lurquin C; De Smet C; Brasseur F; Muscatelli F; Martelange V; De Plaen E; Brasseur R; Monaco A P; Boon T
CS Ludwig Inst. Cancer Res., 74 avenue Hippocrate, UCL 74.59, B-1200 Brussels, Belgium
SO Genomics 46 (3). 1997. 397-408. ISSN: 0888-7543
LA English
AB Genes of the MAGE family direct the expression of tumor antigens recognized on a human melanoma by autologous cytolytic T lymphocytes. Twelve closely related MAGE genes are located in the Xq28 region. These genes share 60-98% nucleotide identity in their coding region. The presence of homologous genes in a region of Xp21.3 has been reported previously. We obtained the complete **sequence** of a 42-kb stretch of this region. It contains four MAGE-related genes, which we propose to name MAGE-B1, B2, B3, and B4 (HGMW-approved symbols MAGEB1, MAGEB2, MAGEB3, and MAGEB4). The coding regions of these genes share 66-81% nucleotide identity and show 4563% identity with those of the MAGE genes located in Xq28. Like the MAGE genes located in Xq28, the MAGEB genes are silent in normal tissues with the exception of testis. Like **MAGE-1**, 2, 3, 4, 6 and 12 (HGMW-approved symbols MAGEA1, 2, 3, 4, 6, and 12), genes MAGE-B1 and MAGE-B2 are expressed in a significant fraction of tumors of various histological types. The transcription of MAGE-B1 and MAGE-B2 can be induced by 5-aza-2'-deoxycytidine, suggesting that the activation of these genes in tumors results from a demethylation process.

L5 ANSWER 2 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
AN 97:180328 BIOSIS
DN 99472041
TI Alternative promoters of gene MAGE4a.
AU De Plaen E; Naerhuyzen B; De Smet C; Szikora J-P; Boon T
CS Ludwig Inst. Cancer Res., Brussels Branch, 74 avenue Hippocrate, UCL 74.59, B1200 Brussels, Belgium
SO Genomics 40 (2). 1997. 305-313. ISSN: 0888-7543
LA English
AB Gene MAGE-4 (HGMW-approved symbol MAGE4) is expressed in several types of tumors, but not in normal tissues, except testis and placenta. The 5' end of this gene contains eight homologous exons spread over a 5.8-kb region. These exons are alternatively spliced to a unique second exon and a unique third exon, which encodes a protein of 317 amino acids. The analysis of transcripts found in testis, placenta, and a sarcoma cell line showed that each of the alternative first exons is used in at least one of these tissues. Various regions

of the promoter of the fifth alternative exon (1.5) were cloned in a luciferase reporter plasmid, and the constructs were transfected in a sarcoma cell line that expresses MAGE-4. Two Ets motifs located between positions -70 and -29 relative to the transcription start site were found to drive 55% of the promoter activity. A region containing a Sp1 consensus binding site located upstream of the two Ets motifs was found to be responsible for 44% of the transcriptional activity. MAGE-4a promoters 1.4 and 1.6, which also contain the Sp1 and the two Ets binding motifs, supported a level of transcription comparable to that of promoter 1.5, whereas promoter 1.1, which contains only one Ets binding site, was sixfold less active. In line with observations made with gene **MAGE-1** (HGMW-approved symbol MAGE1), we found that promoter 1.5 stimulated a high level of transcription in a melanoma cell line that does not express MAGE-4. This suggests that the tumor-specific expression of MAGE genes is not determined by the presence of specific transcription factors.

L5 ANSWER 3 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 97:19666 BIOSIS
 DN 99318869
 TI Methylated CpG points identified within **MAGE-1**
 promoter are involved in gene repression.
 AU Serrano A; Gracia A; Abril E; Garrido F; Ruiz-Cabello F
 CS Serv. Analisis Clinicos Inmunologia, Hospital Universitario Virgen de
 las Nieves, Univ. Granada, Avda. Constitucion s/n, 18014 Granada,
 Spain
 SO International Journal of Cancer 68 (4). 1996. 464-470. ISSN:
 0020-7136
 LA English
 AB The **MAGE-1** gene, expressed in some tumors of
 different histological origins, codes for a tumor antigen recognized
 by cytotoxic T lymphocytes. The gene is not expressed in normal
 tissues with the exception of testes. The present study was designed
 to investigate the relationship between methylation of the
MAGE-1 promoter and inactivation of the
MAGE-1 gene. We examined the extent to which
MAGE-1 B'B promoter sequences are
 methylated in tumor-cell lines, in order to determine whether
 methylation correlates with **MAGE-1** expression.
 Using methylation-sensitive restriction analysis followed by
 polymerase chain reaction (PCR), we found an inverse correlation
 between methylation of the **MAGE-1** B'B region and
MAGE-1 expression. An unmethylated state was
 identified in DNA from sperm and some tumor-cell lines of different
 origins. In contrast, a hypermethylation state was found in
 leukocytes and other **MAGE-1** non-expressing cells.
 Furthermore, treatment with 5-aza-2'-deoxycytidine, a demethylating
 agent, induced **MAGE-1** expression in tumor-cell
 lines in which we found no direct relation between transcriptional
 activity of the B'B region and **MAGE-1** expression.
 Binding of the nuclear factors to the B'-methylated probe was
 strongly inhibited, indicating that methylation of cytosine
 interferes directly in the binding of transcriptional factors.

L5 ANSWER 4 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 96:511599 BIOSIS

DN 99233955
 TI Conserved TCR usage by HLA-Cw* 1601-restricted T cell clones recognizing melanoma antigens.
 AU Farina C; Van Der Bruggen P; Boel P; Parmiani G; Sensi M
 CS Div. Exp. Oncol. D, Istituto Nazionale per lo Studio e la Cura dei Tumori, Via Venezian 1, 20133 Milano, Italy
 SO International Immunology 8 (9). 1996. 1463-1466. ISSN: 0953-8178
 LA English
 AB In this study we determined TCR alpha and beta chain nucleotide **sequences** of HLA-Cw*1601-restricted cytotoxic T lymphocyte (CTL) clones obtained from the peripheral blood lymphocytes (PBL) of a melanoma patient. These clones were previously shown to be involved in the recognition of melanoma-associated antigenic epitopes SAYGEPRKL and AARAVFLAL encoded by gene **MAGE-1** and BAGE respectively. All (3/3) anti-**MAGE-1** CTL clones displayed TCRBV5 usage and one clonotype was found twice, gt 1 year apart, in patient's PBL. Two out of three anti-BAGE CTL clones showed the same TCRAV/AJ and TCRBV/BJ combinations and differed in the a chain CDR3 for two residues and in the beta chain CDR3 for a single nucleotide which, however, did not change translation. These results suggest a pattern of TCR conservation in CTL selected for recognition of **MAGE-1** or BAGE peptides on the autologous melanoma.

L5 ANSWER 5 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 96:383076 BIOSIS
 DN 99105432
 TI Identification of peptide epitopes of **MAGE-1**, -2, -3 that demonstrate HLA-A3-specific binding.
 AU McIntyre C A; Rees R C; Platts K E; Cooke C J; Smith M O; Mulcahy K A; Murray A K
 CS Inst. Cancer Stud., Univ. Sheffield Med. Sch., Beech Hill Road, Sheffield S10 2RX, UK
 SO Cancer Immunology Immunotherapy 42 (4). 1996. 246-250. ISSN: 0340-7004
 LA English
 AB The MAGE gene family of tumour antigens are expressed in a wide variety of human cancers. We have identified 43 nonamer peptide **sequences**, from **MAGE-1**, -2 and -3 proteins that contain binding motifs for HLA-A3 MHC class I molecules. The T2 cell line, transfected with the cDNA for the HLA-A3 gene, was used in a MHC class I stabilisation assay performed at 37 degree C and 26 degree C. At 37 degree C, 2 peptides were identified that stabilised HLA-A3 with high affinity (fluorescence ratio, FR gt 1.5), 4 peptides with low affinity (FR 1.11-1.49) and 31 peptides that did not stabilise this HLA haplotype (FR lt 1.1). At 26 degree C, 12 peptides were identified that stabilised HLA-A3 with high affinity, 8 peptides with low affinity and 17 peptides that did not stabilise this HLA haplotype. Two peptides stabilised HLA-A3 at both temperatures. Small changes in one to three amino acids at positions distinct from the anchor residues altered peptide affinity. Data were compared to a similar study in which a peptide competition assay was used to investigate **MAGE-1** peptide binding to several HLA haplotypes. This study demonstrates that anchor residues do not accurately predict peptide binding to specific HLA haplotypes, changes in one to three amino acids at positions distinct from anchor residues influence peptide binding and alternative methods of

determining peptide binding yield different results. We are currently investigating the ability of these peptides to induce antitumour cytotoxic T lymphocyte activity as they may be of potential therapeutic value.

L5 ANSWER 6 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 96:333217 BIOSIS
 DN 99055573
 TI Epitope specificity of anti-HIV antibodies in human and murine autoimmune diseases.
 AU Fraziano M; Montesano C; Lombardi V R M; Sammarco I; De Pisa D; Mattei M; Valesini G; Pittoni V; Colizzi V
 CS Dep. Biol., Univ. Rome "Tor Vergata", Via della Ricerca Scientifica 00133 Rome, Italy
 SO AIDS Research and Human Retroviruses 12 (6). 1996. 491-496. ISSN: 0889-2229
 LA English
 AB This article reports the HIV epitope specificity of antibodies present in the sera of HIV-negative patients with autoimmune diseases. Recombinant gp120 and a panel of synthetic peptides derived from the amino acid consensus **sequences** of either related (gp120, gp41, and p24) or unrelated (**Mage-1**, necdin, heat shock protein (65 kDa), and amyloid) HIV proteins were tested by a specific ELISA. The first set of experiments performed on four patients with Sjogren's syndrome (SjS) and four patients with systemic lupus erythematosus (SLE) revealed a significant anti-gp120 antibody reactivity in autoimmune patients when compared to healthy HIV-negative controls. Moreover, such binding could be almost completely inhibited by preincubation with free gp120. A significant anti-p24 reactivity was observed in 18 of 29 sera from SjS patients and in 13 of 25 sera from SLE patients, while anti-gp41 was observed only in 3 of 14 SjS and in 2 of 20 SLE-affected patients. Similar analyses were performed in the murine model of autoimmunity, showing that sera from MRL/lpr mice were able to bind all HIV-related peptides in an age-dependent manner. The analysis of a panel of HIV unrelated peptides showed that SLE as well as MRL/lpr sera bind both HIV-related and unrelated peptides, while SjS sera failed to do so, revealing the polyclonal nature of the SLE and MRL/lpr repertoire and the oligoclonal reactivity of SjS sera. This is also supported by inhibition experiments, which showed that SLE, but not SjS, sera competitively inhibited the binding to HIV gp120 peptide of sera from autoimmune MRL/lpr mice. These results indicate that an overlapping polyclonal repertoire is present in both SLE and MRL/lpr sera, while the oligoclonal specificity of SjS antibodies may be related to a specific, nonpolyclonal, activation against putative retroviral antigens.

L5 ANSWER 7 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 96:257365 BIOSIS
 DN 98813494
 TI Immunization of melanoma patients with melanoma cell vaccine induces anti-**MAGE-1** immunity.
 AU Okamoto T; Yuzuki D; Morton D L; Hoon D S B
 CS John Wayne Cancer Inst., Saint John's Hosp., Santa Monica, CA, USA
 SO 87th Annual Meeting of the American Association for Cancer Research, Washington, D.C., USA, April 20-24, 1996. Proceedings of the American Association for Cancer Research Annual Meeting 37 (0). 1996.

- 478-479. ISSN: 0197-016X
DT Conference
LA English
- L5 ANSWER 8 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
AN 96:110455 BIOSIS
DN 98682590
TI **MAGE-1**-specific precursor cytotoxic T-lymphocytes
present among tumor-infiltrating lymphocytes from a patient with
breast cancer: Characterization and antigen-specific activation.
AU Toso J F; Oei C; Oshidari F; Tartaglia J; Paoletti E; Lysterly H K;
Talib S; Weinhold K J
CS Dep. Surg., Box 2926, Duke Univ. Med. Cent., Durham, NC 27710-2926,
USA
SO Cancer Research 56 (1). 1996. 16-20. ISSN: 0008-5472
LA English
AB A potential target for development of tumor-specific
immunotherapeutic strategies is the **MAGE-1** gene.
We have utilized a recently developed recombinant canarypox (ALVAC)
virus vector containing the **MAGE-1** gene (vCP235)
to activate CTLs from a breast cancer patient bearing a **MAGE**
-1+ tumor. Tumor-infiltrating lymphocytes (TILs) obtained
from the tumor of a patient were stimulated in vitro with irradiated
autologous peripheral blood mononuclear cells acutely infected with
the vCP235 construct. These TILs preferentially expanded
approximately 6-fold over a 16-day culture period and specifically
recognized an allogeneic transformed B-cell line acutely infected
with a vaccinia-**MAGE-1** recombinant targeting
vector (vP1188) in the context of HLA-A2 and/or B7. TCR V-beta
analysis of in vitro expanded T cells by a quantitative multiprobe
RNase protection assay revealed preferential expansion of TCR
V-beta-6.3 and V-beta-6.4. In addition, homologous T-cell receptor
beta CDR3 joining **sequences** were found in the in vitro
stimulated cultures. These results suggest that tumor
antigen-specific, MHC-restricted CTLs may be derived from precursor
CTLs present in TILs obtained from patients with **MAGE-**
1+ tumors by in vitro stimulation with recombinant avipox
MAGE-1 virus-infected autologous cells.
Collectively, these findings provide a rationale for tumor-associated
antigen-based immunization as a means of activating precursor CTLs
residing in patients with tumors expressing defined tumor-associated
antigens such as **MAGE-1**.
- L5 ANSWER 9 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
AN 96:63419 BIOSIS
DN 98635554
TI Human neoplasms elicit multiple specific immune responses in the
autologous host.
AU Sahin U; Tuereci O; Schmitt H; Cochlovius B; Johannes T; Schmits R;
Luo F S G; Schobert I; Pfreundschuh M
CS Med. Klinik Poliklinik, Innere Med. I, Univ. Saarlandes, D-66421
Homburg, Germany
SO Proceedings of the National Academy of Sciences of the United States
of America 92 (25). 1995. 11810-11813. ISSN: 0027-8424
LA English
AB Expression of cDNA libraries from human melanoma, renal cancer,
astrocytoma, and Hodgkin disease in Escherichia coli and screening

for clones reactive with high-titer IgG antibodies in autologous patient serum lead to the discovery of at least four antigens with a restricted expression pattern in each tumor. Besides antigens known to elicit T-cell responses, such as **MAGE-1** and tyrosinase, numerous additional antigens that were overexpressed or specifically expressed in tumors of the same type were identified.

Sequence analyses suggest that many of these molecules, besides being the target of a specific immune response, might be of relevance for tumor growth. Antibodies to a given antigen were usually confined to patients with the same tumor type. The unexpected frequency of human tumor antigens, which can be readily defined at the molecular level by the serological analysis of autologous tumor cDNA expression cloning, indicates that human neoplasms elicit multiple specific immune responses in the autologous host and provides diagnostic and therapeutic approaches to human cancer.

- L5 ANSWER 10 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 95:551288 BIOSIS
 DN 98565588
 TI Expression of the MAGE gene family in human head-and-neck squamous-cell carcinomas.
 AU Eura M; Ogi K; Chikamatsu K; Lee K D; Nakano K; Masuyama K; Itoh K; Ishikawa T
 CS Dep. Otolaryngol., Kumamoto Univ. Sch. Med., Honjo 1-1-1, Kumamoto 860, Japan
 SO International Journal of Cancer 64 (5). 1995. 304-308. ISSN: 0020-7136
 LA English
 AB The MAGE genes encode certain tumor-associated antigens recognized by cytotoxic T lymphocytes. We investigated the expression of the **MAGE-1**, -2, -3, -4, -41 and -6 genes in 88 head-and-neck squamous-cell carcinomas (83 fresh tumor samples and 5 cell lines), using a reverse-transcription-polymerase-chain-reaction assay, followed by dot-blot hybridization with **sequence**-specific oligonucleotides and/or restriction-enzyme-pattern analysis. The **MAGE-1**, -2, -3, -4, -41 and -6 genes were expressed at the mRNA level in 27, 34, 36, 22, 16 and 35, respectively, of 83 fresh tumor samples. At least one of these genes was expressed in 59 of the 83 samples. Neither non-tumor inflammatory cells nor normal tissues were positive for these genes. The **MAGE-1** gene was expressed relatively frequently in SCC of the oropharynx, hypopharynx and maxillary sinus, but at lower rates in SCC of the larynx and of the tongue and oral cavity. **MAGE-1** was frequently expressed in poorly differentiated SCC, somewhat less frequently in moderately differentiated SCC, and only infrequently in well-differentiated SCC. The expression levels of the other MAGE genes also varied with the anatomic site as well as the degree of differentiation. Our results suggest that specific immunotherapy against MAGE gene products may be useful for patients with head-and-neck carcinomas.

- L5 ANSWER 11 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 95:487219 BIOSIS
 DN 98501519
 TI Multiple specificities in the repertoire of a melanoma patient's cytolytic T lymphocytes directed against tumor antigen **MAGE**-1.A1.

- AU Romero P; Pannetier C; Herman J; Jongeneel C V; Cerottini J-C; Coulie P G
 CS Ludwig Inst. Cancer Res., Ch. des Boveresses 155, CH-1066 Epalinges, Switzerland
 SO Journal of Experimental Medicine 182 (4). 1995. 1019-1028. ISSN: 0022-1007
 LA English
 AB Peptide **MAGE-1.A1** is a nonamer derived from protein **MAGE-1** that can associate with the HLA-A1 molecule. It was shown previously to be recognized by an antitumor cytolytic T lymphocyte (CTL) clone derived from the blood of melanoma patient MZ2. We derived two other anti-**MAGE-1.A1** CTL clones from different blood samples of the same patient and compared the fine specificity of recognition of the three CTL by testing them on variant **MAGE-1.A1** peptides incorporating different amino acid substitutions. The epitopes recognized by the CTL proved to be different. While modifications of residues at positions 5, 6, or 7 in the antigenic peptide affected recognition by the three CTL, each of the modifications of residues at positions 1, 4, or 8 affected recognition by one CTL only. The **sequences** of both the alpha and beta chains of the T cell antigen receptor of the three CTL were completely different. The results indicate a long-lasting diversity in terms of fine specificity and of T cell antigen receptor structure in the repertoire of antitumor CTL derived From the blood of a melanoma patient and directed against a defined tumor antigen.
- L5 ANSWER 12 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 95:440692 BIOSIS
 DN 98454992
 TI **Sequence** analysis of the MAGE gene family encoding human tumor-rejection antigens.
- AU Imai Y; Shichijo S; Yamada A; Katayama T; Yano H; Itoh K
 CS Dep. Immunol., Kurume Univ. Sch. Med., Kurume 830, Japan
 SO Gene (Amsterdam) 160 (2). 1995. 287-290. ISSN: 0378-1119
 LA English
 AB The MAGE multigene family, which includes the **MAGE-1** and -3 genes that encode tumor-rejection antigens on HLA-A1 recognized by cytotoxic T-lymphocytes (CTL), is preferentially expressed at the mRNA level on human malignant cells, but not on normal cells. However, little is known about the MAGE-4, -41 and -6 genes. In this study, we have amplified 1040 bp (**MAGE-1**), 1061 bp (**MAGE-3** and -6) and 1064 bp (**MAGE-4** and -41) cDNA fragments, including the entire coding **sequences** (927-951 bp), using the reverse transcription-polymerase chain reaction (RT-PCR) method followed by nucleotide (nt) sequencing. One member had greater than 80 or 66% homology with the other members at the nt or deduced amino acid (aa) levels, respectively. Higher homology was found between MAGE-3 and -6 (98% at the nt level) and also between MAGE-4 and -41 (98%). The results of this investigation demonstrated high homology, as well as the clear differences between the members of the MAGE family at the coding **sequence** level.
- L5 ANSWER 13 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 95:317508 BIOSIS
 DN 98331808
 TI Presentation of synthetic peptide antigen encoded by the **MAGE**

- 1 gene by granulocyte-macrophage-colony-stimulating-factor-cultured macrophages from HLA-A1 melanoma patients.
- AU Yamasaki S; Okino T; Chakraborty N G; Adkisson W O; Sampieri A; Padula S J; Mauri F; Mukherji B
- CS Dep. Med., Univ. Conn. Health Cent., Farmington, CT 06030-3210, USA
- SO Cancer Immunology Immunotherapy 40 (4). 1995. 268-271. ISSN: 0340-7004
- LA English
- AB The recent identification of the **sequences** of the peptides derived from a number of human melanoma-associated antigens has presented opportunities for developing a specific-peptide-based vaccine in this form of cancer. Since antigen-presenting cells (APC) play a crucial role in the induction of the T-cell-mediated immune response, we examined whether or not ex vivo cultured APC, bearing the appropriate MHC restricting elements, when pulsed with a relevant melanoma-specific cytotoxic-T-lymphocyte(CTL)-determined peptide, can present the peptide to the CTL. Here we show that a population of cells, derived from the monocyte/macrophage lineage from peripheral blood and grown in granulocyte/macrophage-colony-stimulating factor, exhibit many essential characteristics of "professional" APC (dendritic-type morphology with a proportion of the population, the B7 molecule, and high levels of MHC class I and class II molecules, CD11b and CD54 molecules) and are capable of efficiently presenting the nonapeptide, EADPTGHSY, encoded by the melanoma antigen **MAGE-1** gene, to the **MAGE-1**-specific CTL clone, 82/30. These results suggest that this type of autologous ex vivo cultured population of professional APC, when pulsed with the relevant-CTL-determined peptide, can serve as a novel type of candidate vaccine for active specific immunization against HLA-A1-positive patients with melanoma expressing the **MAGE-1** antigen.
- L5 ANSWER 14 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
- AN 95:128084 BIOSIS
- DN 98142384
- TI Identification of potential CTL epitopes of tumor-associated antigen **MAGE-1** for five common HLA-A alleles.
- AU Celis E; Fikes J; Wentworth P; Sidney J; Southwood S; Maewal A; Del Guercio M-F; Sette A; Livingston B
- CS 3525 John Hopkins Court, Cytel Corp., San Diego, CA 92121, USA
- SO Molecular Immunology 31 (18). 1994. 1423-1430. ISSN: 0161-5890
- LA English
- AB Identification of CTL epitopes for tumor-specific responses is important for the development of immunotherapies to treat cancer patients. We have developed a strategy to identify potential CTL epitopes based on screening of **sequences** of target proteins for presence of specific motifs recognized by the most common HLA-A alleles, and identification of high affinity binding peptides using in vitro quantitative assays. A systematic analysis using the **sequence** of the product of the tumor-associated **MAGE-1** gene has been carried out. All possible peptides of nine and ten residues, containing binding motifs for HLA-A1, -A2.1, A-3.2, -A11 and -A24 were synthesized and tested for binding using a quantitative assay. Out of 237 possible peptide/MHC combinations, 47 cases demonstrated good binding affinity (K_d ltoreq 500 nM). Several peptides were identified as good MHC binders for each one of the five HLA-A alleles studied (five for HLA-A1, 11 for HLA-A2.1, 10 for

HLA-A3.2, 16 for HLA-A11 and five for HLA-A24. Furthermore, eight of these peptides were found to bind well to more than one HLA-A allele. These results have important implications for the development of immunotherapeutic vaccines to treat malignant melanoma.

L5 ANSWER 15 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 94:545758 BIOSIS
 DN 98005306
 TI Structure, chromosomal localization, and expression of 12 genes of the MAGE family.
 AU De Plaen E; Arden K; Traversari C; Gaforio J J; Szikora J-P; De Smet C; Brasseur F; Van Der Bruggen P; Lethe B; Lurquin C; Brasseur R; Chomez P; De Backer O; Cavenee W; Boon T
 CS Ludwig Inst. Cancer Res., Brussels Branch, 74 Ave. Hippocrate, B-1200 Brussels, Belgium
 SO Immunogenetics 40 (5). 1994. 360-369. ISSN: 0093-7711
 LA English
 AB We reported previously that human gene **MAGE-1** directs the expression of a tumor antigen recognized on a melanoma by autologous cytolytic T lymphocytes. Probing cosmid libraries with a **MAGE-1 sequence**, we identified 11 closely related genes. The analysis of hamster-human somatic cell hybrids indicated that the 12 MAGE genes are located in the q terminal region of chromosome X. Like **MAGE-1**, the 11 additional MAGE genes have their entire coding **sequence** located in the last exon, which shows 64%-85% identity with that of MAGE1. The coding **sequences** of the MAGE genes predict the same main structural features for all MAGE proteins. In contrast, the promoters and first exons of the 12 MAGE genes show considerable variability, suggesting that the existence of this gene family enables the same function to be expressed under different transcriptional controls. The expression of each MAGE gene was evaluated by reverse transcription and polymerase chain reaction amplification. Six genes of the MAGE family including **MAGE-1** were found to be expressed at a high level in a number of tumors of various histological types. None was expressed in a large panel of healthy tissues, with the exception of testis and placenta.

L5 ANSWER 16 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 94:393049 BIOSIS
 DN 97406049
 TI Cloning and analysis of **MAGE-1**-related genes.
 AU Ding M; Beck R J; Keller C J; Fenton R G
 CS NCI-FCRDC, P.O. Box B, Bldg. 567, Room 207, Frederick, MD 21702, USA
 SO Biochemical and Biophysical Research Communications 202 (1). 1994. 549-555. ISSN: 0006-291X
 LA English
 AB The spectrum of MAGE gene expression in the human melanoma cell line DM150 was examined using reverse transcription polymerase chain reaction and cDNA cloning. We have isolated five full-length cDNAs from DM150 which were identified as **MAGE-1**, **MAGE-3**, **MAGE-12** and two previously undescribed MAGE genes, **MAGE-3b** and **MAGE-X2**. DNA **sequence** analysis of the coding regions of the **MAGE-3b** and **MAGE-X2** genes revealed 83% and 88% identity with **MAGE-1**, while **MAGE-3b** was 98% homologous with the full length **MAGE-3** clone. The predicted amino acid **sequences** of **MAGE-X2** and **MAGE-3b** contain consensus HLA-A1 peptide binding

motifs, suggesting that, like **MAGE-1**, they may code for tumor-associated antigens. In addition, a nonamer peptide encoded by both the **MAGE-3** and **MAGE-12** genes was shown by direct binding studies to contain an aggretope for HLA-A2.

L5 ANSWER 17 OF 17 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 94:180223 BIOSIS
 DN 97193223
 TI Human gene **MAGE-3** codes for an antigen recognized on a melanoma by autologous cytolytic T lymphocytes.
 AU Gaugler B; Van Den Eynde B; Van Der Bruggen P; Romero P; Gaforio J J; De Plaen E; Lethe B; Brasseur F; Boon T
 CS Ludwig Institute for Cancer Research, Brussels Branch, 74 Ave. Hippocrate, UCL 74-59, B-1200 Brussels, BEL
 SO Journal of Experimental Medicine 179 (3). 1994. 921-930. ISSN: 0022-1007
 LA English
 AB Human melanoma cell line MZ2-MEL expresses several antigens recognized by autologous cytolytic T lymphocyte (CTL) clones. We reported previously the identification of a gene, named **MAGE-1**, that codes for one of these antigens named MZ2-E. We show here that antigen MZ2-D, which is present on the same tumor, is encoded by another member of the **MAGE** gene family named **MAGE-3**. Like **MAGE-1**, **MAGE-3** is composed of three exons and the large open reading frame is entirely located in the third exon. Its **sequence** shows 73% identity with **MAGE-1**.
 Like MZ2-E, antigen MZ2-D is presented by HLA-A1. The antigenic peptide of MZ2-D is a nonapeptide that is encoded by the **sequence** of **MAGE-3** that is homologous to the **MAGE-1 sequence** coding for the MZ2-E peptide.
 Competition experiments using single Ala-substituted-peptides indicated that amino acid residues Asp in position 3 and Tyr in position 9 were essential for binding of the **MAGE-1** peptide to HLA-A1. Gene **MAGE-3** is expressed in many tumors of several types, such as melanoma, head and neck squamous cell carcinoma, lung carcinoma and breast carcinoma, but not in normal tissues except for testes. It is expressed in a larger proportion of melanoma samples than **MAGE-1**. **MAGE-3** encoded antigens may therefore have a wide applicability for specific immunotherapy of melanoma patients.

*Published
March
1994
ML*

L12 ANSWER 1 OF 8 BIOSIS COPYRIGHT 1998 BIOSIS
 AN 98:168613 BIOSIS
 DN 01168613
 TI Identification of a human VPF-VEGF 3' untranslated region mediating hypoxia-induced mRNA stability.
 AU Claffey K P; Shih S-C; Mullen A; Dziennis S; Cusick J L; Abrams K R; Lee S W; Detmar M
 CS Dep. Pathol., Beth Israel Deaconess Med. Cent., Boston, MA 02215, USA
 SO Molecular Biology of the Cell 9 (2). 1998. 469-481. ISSN: 1059-1524
 LA English
 AB Hypoxia is a prominent feature of malignant tumors that are characterized by angiogenesis and vascular hyperpermeability. Vascular permeability factor/vascular endothelial growth factor (VPF/VEGF) has been shown to be up-regulated in the vicinity of

necrotic tumor areas, and hypoxia potently induces VPF/VEGF expression in several tumor cell lines in vitro. Here we report that hypoxia-induced VPF/VEGF expression is mediated by increased transcription and mRNA stability in human M21 **melanoma** cells. RNA-binding/electrophoretic mobility shift assays identified a single 125-bp AU-rich element in the 3' untranslated region that formed hypoxia-inducible RNA-protein complexes. Hypoxia-induced expression of chimeric luciferase reporter constructs containing this 125-bp AU-rich hypoxia stability region were significantly higher than constructs containing an adjacent 3' untranslated region element without RNA-binding activity. Using UV-cross-linking studies, we have identified a series of hypoxia-induced proteins of 90/88 kDa, 72 kDa, 60 kDa, 56 kDa, and **46 kDa** that bound to the hypoxia stability region element. The 90/88-kDa and 60-kDa species were specifically competed by excess hypoxia stability region RNA. Thus, increased VPF/VEGF mRNA stability induced by hypoxia is mediated, at least in part, by specific interactions between a defined mRNA stability sequence in the 3' untranslated region and distinct mRNA-binding **proteins** in human **tumor** cells.

ST RESEARCH ARTICLE; HUMAN; HYPOXIA; MESSENGER RNA STABILITY; VASCULAR PERMEABILITY FACTOR; VASCULAR ENDOTHELIAL GROWTH FACTOR; MICROVASCULAR PERMEABILITY; ANGIOGENESIS; VASCULAR HYPERPERMEABILITY; TUMOR; TUMOR BIOLOGY; NEOPLASTIC DISEASE

L12 ANSWER 2 OF 8 BIOSIS COPYRIGHT 1998 BIOSIS

AN 97:111308 BIOSIS

DN 99410511

TI The expression of the secreted protein acidic and rich in cysteine (SPARC) is associated with the neoplastic progression of human **melanoma**.

AU Ledda F; Bravo A I; Adris S; Bover L; Mordoh J; Podhajcer O L

CS Instituto de Investigaciones Bioquimicas Luis F. Leloir "Fundacion Campomar", Av. Patricias Argentinas 435, 1405 Buenos Aires, Argentina

SO Journal of Investigative Dermatology 108 (2). 1997. 210-214. ISSN: 0022-202X

LA English

AB SPARC (secreted protein acidic and rich in cysteine) is an extracellular protein associated with tissues exhibiting high rates of cell proliferation and matrix remodeling. The current work shows that the human **melanoma** cell lines IIB-MEL-LES, IIB-MEL-IAN, and IIB-MEL-J and different human metastatic **melanomas** expressed high levels of SPARC mRNA and protein. By western blot analysis we detected a single secreted 42-kDa band in human diploid fibroblasts-conditioned medium and a 45-to 40-kDa doublet in the three **melanoma** cell lines and all the metastatic **melanomas** tested. Part of the **melanoma** samples and cell lines showed an additional doublet of 36-34 **kDa**. SPARC mRNA was expressed by the three established cell lines, 14 metastatic **melanoma** samples, and tumors raised in nude mice, and no spliced variants were found. The heterogeneous pattern of SPARC secreted by human **melanoma** cells is the result of post-translational glycosylation and a specific extracellular leupeptin-inhibitable cleavage. Unlike human fibroblasts, **melanoma** cells did not overexpress SPARC on addition of TGF-beta. Immunohistochemical analysis showed that SPARC was strongly expressed in 100% of primary **melanomas** (7 of

7) and metastatic **melanomas** (29 of 29), moderately expressed in most of the positive dysplastic nevi (13 of 14), and only weakly expressed in nevocellular nevi (4 of 25). Normal melanocytes did not express SPARC. The data suggest that the expression of SPARC is associated with the neoplastic progression of human **melanoma**.

ST RESEARCH ARTICLE; NUDE MOUSE; IIB-MEL-LES CELL LINE; IIB-MEL-IAN CELL LINE; IIB-MEL-J CELL LINE; HUMAN **MELANOMA** CELLS;

MELANOMA; INTEGUMENTARY SYSTEM; **TUMOR** BIOLOGY; SECRETED **PROTEIN** ACIDIC AND RICH IN CYSTEINE; EXPRESSION; DERMAL FIBROBLAST; IMMUNOHISTOCHEMISTRY; NEVUS; BIOCHEMISTRY AND BIOPHYSICS; METASTASES; NEOPLASTIC DISEASE; INTEGUMENTARY SYSTEM; IMMUNOLOGICAL METHOD; DYSPLASTIC; INTEGUMENTARY SYSTEM DISEASE; NEVOCELLULAR

L12 ANSWER 3 OF 8 BIOSIS COPYRIGHT 1998 BIOSIS

AN 96:415356 BIOSIS

DN 99137712

TI Monoclonal antibodies against recombinant-**MAGE-1** protein identify a cross-reacting 72-kDa antigen which is co-expressed with **MAGE-1** protein in **melanoma** cells.

AU Carrel S; Schreyer M; Spagnoli G; Cerottini J-C; Rimoldi D

CS Ludwig Inst. Cancer Res., Ch. des Boveresses 155, 1066 Epalinges, Switzerland

SO International Journal of Cancer 67 (3). 1996. 417-422. ISSN: 0020-7136

LA English

AB The **MAGE-I** gene codes for tumor-associated peptides recognized by cytolytic T lymphocytes in association with MHC-class-I molecules such as HLA-A I and HLA-Cw16. In the course of a study aiming at the immunohistochemical detection of the **MAGE-I** gene product in tumor samples, 2 mouse monoclonal antibodies (MAbs) directed against a full-length recombinant **MAGE-I** fusion protein were found to react strongly not only with the **46-kDa** **MAGE-I** protein, but also with a 72-kDa product in immunoblots of lysates obtained from several **MAGE1**-mRNA-positive **melanoma** cell lines. Pre-incubation of the antibodies with the recombinant **MAGE-I** fusion protein abolished their reactivity both with **MAGE-I** protein and with the 72-kDa product, thus confirming the occurrence of antigenic determinant(s) shared by the 2 proteins. The 72-kDa protein is not an alternative product of **MAGE-I**, since it was still detected in lysates of a **MAGE-I** loss variant derived from a **MAGE-I**-positive **melanoma** cell line. Moreover, the 72-kDa protein does not appear to be a product of the other members of the **MAGE** gene family known to be expressed in tumors (such as **MAGE-2**, -3, -4 and -12). Interestingly, expression of the 72-kDa protein was found to be correlated with that of **MAGE-I** **protein**. Thus, in 30 **tumor** cell lines analyzed by immunoblotting and RT-PCR, the 72-kDa protein was never detected in **MAGE-I**-mRNA-negative cell lines, while it was co-expressed with **MAGE-I** protein in 12 out of 15 cell lines expressing **MAGE-I**. Furthermore, the 72-kDa protein was detected in lysates of human testis, the only normal tissue known to express **MAGE-I**. Finally, treatment of **MAGE-1** -mRNA-negative cell lines with 5-Aza-2'-deoxycytidine, a hypomethylating agent known to induce **MAGE-I** expression, resulted in the expression of the 72-kDa protein. Taken collectively, these

findings suggest that expression of the gene encoding the 72-kDa protein identified in this study through antigenic determinant(s) shared with MAGE-I protein is regulated in a way similar to that of MAGE-I.

- ST RESEARCH ARTICLE; HUMAN; MOUSE; MESSENGER RNA; HLA ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX; CYTOLYTIC T-LYMPHOCYTES; 5-AZA-2'-DEOXYCYTIDINE; METABOLIC-DRUG
- L12 ANSWER 4 OF 8 BIOSIS COPYRIGHT 1998 BIOSIS
AN 96:110561 BIOSIS
DN 98682696
TI Expression of **MAGE-1**, MAGE-2, MAGE-3--6, and MAGE-4a--4b genes in ovarian tumors.
AU Yamada A; Kataoka A; Shichijo S; Kamura T; Imai Y; Nishida T; Itoh K
CS Dep. Immunol., Kurume Univ. Sch. Med., 67 Asahi-machi, Kurume 830, Japan
SO International Journal of Cancer 64 (6). 1995. 388-393. ISSN: 0020-7136
LA English
AB MAGE genes encoding tumor-rejection antigens recognized by cytotoxic T lymphocytes are expressed at the mRNA level in various malignant tumors. We have investigated the expression of genes **MAGE-1**, -2, -3/-6 and -4a/-4b at the mRNA level in malignant and non-malignant ovarian tumors as well as in normal ovaries by reverse transcription-polymerase chain reaction. **MAGE-1**, -2, -3/-6 and -4a/-4b were expressed in 12, 5, 11 and 4 of 58 malignant tumors, respectively- The majority of these MAGE-mRNA-positive tumors were histologically surface-epithelial-stromal tumors, in particular serous adenocarcinomas. They mostly consisted of either advanced-stage or recurrent tumors. In contrast, neither benign tumors nor normal ovaries expressed any of the MAGE genes investigated. A 46-kDa **MAGE-1** protein was identified in **MAGE-1**-mRNA-positive serous adenocarcinomas by immunoblot analysis with polyclonal anti-**MAGE-1** antibody. These results provide important information for specific immunotherapy of ovarian serous e products.
- ST RESEARCH ARTICLE; HUMAN; MESSENGER RNA; STAGING; ADENOCARCINOMA
- L12 ANSWER 5 OF 8 BIOSIS COPYRIGHT 1998 BIOSIS
AN 94:548546 BIOSIS
DN 98008094
TI **MAGE-1** gene product is a cytoplasmic protein.
AU Schultz-Thater E; Juretic A; Dellabona P; Luscher U; Siegrist W; Harder F; Heberer M; Zuber M; Spagnoli G C
CS Z.L.F., Surgical Res. Lab., 20 Hebelstrasse, CH-4031 Basel, Switzerland
SO International Journal of Cancer 59 (3). 1994. 435-439. ISSN: 0020-7136
LA English
AB **MAGE-1** gene encodes a human melanoma antigen, recognized by syngeneic cytotoxic T lymphocytes (CTL). **MAGE-1** transcripts are also detectable in breast cancers, in non-small-cell lung carcinomas and in central nervous system tumors. In order to identify, in cellular preparations, the protein encompassing the antigenic peptide, we generated a panel of monoclonal antibodies (MAbs) against the **MAGE-1**

gene product by using, as immunogen, a full-length recombinant preparation (rMAGE1), obtained through expression cloning of the relevant gene in E. coli. Four reagents were obtained recognizing both rMAGE-1 and the 46-kDa native protein in cell lines expressing MAGE-1 mRNA. No positivity could be detected in MAGE-1-mRNA-negative melanoma lines. No surface labelling of MAGE-1-positive cell lines could be observed. In contrast, on permeabilization of MZ2 melanoma cells, all 4 MAbs induced efficient staining, as detected by cytofluorography. Fluorescence microscopy shows that MAGE-1 gene product is a cytoplasmic protein clustered in paranuclear organelle-like structures. Thus, MAGE-1 protein location closely resembles that of P91A and P198 murine-tumor antigens.

ST RESEARCH ARTICLE; ESCHERICHIA COLI; HUMAN; MOUSE; MELANOMA ANTIGEN; BREAST; LUNG; CENTRAL NERVOUS SYSTEM TUMORS; T-LYMPHOCYTE RECOGNITION; MESSENGER RNA; MZ-2 CELL LINE

L12 ANSWER 6 OF 8 BIOSIS COPYRIGHT 1998 BIOSIS

AN 94:303423 BIOSIS

DN 97316423

TI Characterization of cluster 13: The epithelial-carcinoma antigen recognized by MAb RS7.

AU Stein R; Basu A; Goldenberg D M; Lloyd K O; Mattes M J

CS Center Mol. Med. Immunol., One Bruce St., Newark, NJ 07103, USA

SO International Journal of Cancer 0 (SUPPL. 8). 1994. 98-102. ISSN: 0020-7136

LA English

AB Cluster 13 was defined by 2 independently derived murine monoclonal antibodies (MAbs), RS7 (IgG-1) and MR54 (IgG-2a), which were raised against human squamous-cell carcinoma of the lung and a human ovarian-carcinoma cell line, respectively. Immunologic and biochemical evidence demonstrated that RS7 and MR54, as well as 2 additional MAbs, MR6 (IgG-2a) and MR23 (IgG-1), generated in the same fusion as MR54, recognize the same antigen, a 46- to 48-

kDa glycoprotein. Evaluation of the expression of antigen on the surface of tumor cell lines, Western blotting analyses, competitive binding studies, and double-determinant ELISA assays, support this conclusion. Two distinct epitopes are defined by these MAbs. In order to further characterize this antigen, amino-acid-sequence analyses were performed on peptides derived from antigen purified by affinity chromatography with MAb RS7. The sequence data obtained from 2 peptides, which were independently generated by CNBr cleavage and trypsin digestion respectively indicated identity to GA733-1. The GA733-1 genomic DNA sequence predicted a type-1 membrane protein of 35 kDa, with 4 potential N-linked glycosylation sites. The GA733-1 protein product has not been identified previously, and MAbs to this tumor-associated antigen were not previously known.

ST RESEARCH ARTICLE; HUMAN; MONOCLONAL ANTIBODY; LUNG; OVARIAN CANCER CELLS; ELISA; IMMUNOLOGICAL METHOD; MELANOMA; COLON; PANCREATIC; CERVICAL CANCER CELLS; GLYCOPROTEIN

L12 ANSWER 7 OF 8 BIOSIS COPYRIGHT 1998 BIOSIS

AN 94:129901 BIOSIS

DN 97142901

published
6/94
PL

TI Identification of the **MAGE-1** gene product by monoclonal and polyclonal antibodies.

AU Chen Y-T; Stockert E; Chen Y; Garin-Chesa P; Rettig W J; Van Der Bruggen P; Boon T; Old L J

CS Ludwig Inst. Cancer Res., New York Unit, New York Hosp.-Cornell Med. Cent., New York, NY 10021, USA

SO Proceedings of the National Academy of Sciences of the United States of America 91 (3). 1994. 1004-1008. ISSN: 0027-8424

LA English

AB The human **MAGE-1** gene encodes a **melanoma** peptide antigen recognized by autologous cytotoxic T lymphocytes. To produce antibodies against the **MAGE-1** gene product, several approaches were taken. Three oligopeptides were synthesized based on predicted **MAGE-1** amino acid sequences and were used to generate rabbit anti-peptide antisera. In addition, a truncated **MAGE-1** cDNA was cloned into an Escherichia coli expression vector, and recombinant protein was produced and purified. All three rabbit anti-peptide antisera showed reactivity against the immunizing peptide, and one reacted with the recombinant **MAGE-1** protein by immunoblotting, but none reacted with cell lysates from **MAGE-1** mRNA-positive cells. The recombinant **MAGE-1** protein was then used for the generation of mouse monoclonal and rabbit polyclonal antibodies. One IgG1 monoclonal antibody, MA454, as well as rabbit polyclonal antisera recognized a **46-kDa** protein in extracts of **MAGE-1** mRNA-positive **melanoma** cell lines. The antibodies showed no apparent crossreactivity with products of the closely related **MAGE-2** and **MAGE-3** genes. Serological typing of normal and tumor cell lysates was in full agreement with mRNA analysis, showing expression of **MAGE-1** protein in **MAGE-1** mRNA-positive testis and a subset of **melanomas** but not in **MAGE-1** mRNA-negative normal or tumor tissues. Transfection of the **MAGE-1** gene into a **MAGE-1** mRNA-negative **melanoma** cell line resulted in the expression of the **46-kDa** protein, confirming the identity of this protein as the **MAGE-1** gene product.

ST RESEARCH ARTICLE; HUMAN **MELANOMA** CELLS; RABBIT; MOUSE; **TUMOR-REJECTION ANTIGEN**

L12 ANSWER 8 OF 8 BIOSIS COPYRIGHT 1998 BIOSIS

AN 90:471686 BIOSIS

DN BA90:111106

TI MOLECULAR CLONING OF COMPLEMENTARY DNA FOR THE HUMAN **TUMOR**-ASSOCIATED **ANTIGEN** CO-029 AND IDENTIFICATION OF RELATED TRANSMEMBRANE ANTIGENS.

AU SZALA S; KASAI Y; STEPLEWSKI Z; RODECK U; KOPROWSKI H; LINNENBACH A J

CS WISTAR INST. ANAT. BIOL., 3601 SPRUCE ST., PHILADELPHIA, PA. 19104.

SO PROC NATL ACAD SCI U S A 87 (17). 1990. 6833-6837. CODEN: PNASA6 ISSN: 0027-8424

LA English

AB The human **tumor-associated antigen** CO-029 is a monoclonal antibody-defined cell surface glycoprotein of **27-34 kDa**. By using the high-efficiency COS cell expression system, a full-length cDNA clone for CO-029 was isolated. When transiently expressed in COS cells, the cDNA clone directed the

synthesis of an antigen reactive to monoclonal antibody CO-029 in mixed hemadsorption and immunoblot assays. Sequence analysis revealed that CO-029 belongs to a family of cell surface antigens that includes the **melanoma**-associated antigen ME491, the leukocyte cell surface antigen CD37, and the Sm23 antigen of the parasitic helminth *Schistosoma mansoni*. CO-029 and ME491 antigen expression and the effect of their corresponding monoclonal antibodies on cell growth were compared in human tumor cell lines of various histologic origins.

ST SCHISTOSOMA-MANSONI SM23 ANTIGEN **MELANOMA**-ASSOCIATED ME491
ANTIGEN LEUKOCYTE CD37 ANTIGEN MONOCLONAL ANTIBODY MOLECULAR SEQUENCE
DATA AMINO ACID SEQUENCE NUCLEOTIDE SEQUENCE GENBANK-M35252

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L13 18 SEA FILE=WPIDS ABB=ON (46 OR 34) (3W) KDA
L14 1 SEA FILE=WPIDS ABB=ON L13 AND (MAGE OR MELANOMA)

=> d bib ab

L14 ANSWER 1 OF 1 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD
AN 93-035688 [04] WPIDS
DNC C93-016134
TI Vaccine against swine dysentery - contains *Treponema hyodysenteriae*
haemolysin, opt. with immunogenic protein.
DC B04 C03 D16
IN MCCAMAN, M; SLOMIANY, R
PA (MLTE-N) ML TECHNOLOGY VENTURES LP
CYC 1
PI US 5176910 A 930105 (9304)* 4 pp
ADT US 5176910 A US 89-296958 890117
PRAI US 89-296958 890117
AB US 5176910 A UPAB: 931119
Vaccine for protection against swine dysentery comprises *Treponema*
hyodysenteriae hemolysin (I) free of *T. hyodysenteriae* cells and a
carrier. The vaccine pref. also contains at least one protein (II)
which elicits antibodies which recognise a *T. hyodysenteriae* antigen
of mol. wt. 19-90 kda.
(II) elicits an antibody which recognises at least one of the
19 kda, 29 kda, 30 kda, 31 kda, **34 kda**, 36
kda, 38 kda, 39 kda, 42 kda, 44 kda, and 60 kdaT.

hyodysenterial antigens.

USE - In addn. to its use as a vaccine. (I) has been shown to act like an enterotoxin when applied to isolated swine mucosal tissue. (I) has also been shown to be cytopathic to CHO cells, Bowes melanoma cells and RBC
Dwg.0/0

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(FILE 'HCAPLUS' ENTERED AT 09:31:23 ON 07 APR 1998)

DEL HIS Y

L1 163 S (46 OR 34) (L) KDA
L2 2536 S ((46 OR 34) (2W) KDA)/AB
L3 2563 S L1 OR L2
L4 4 S L3 AND MAGE
L5 4 S L3 AND (TUMOR# OR TUMOUR#) AND MELANOMA?
L6 8 S L4 OR L5

=> d .ca 1-8

L6 ANSWER 1 OF 8 HCAPLUS COPYRIGHT 1998 ACS
AN 1997:710404 HCAPLUS
DN 127:357528
TI Keratin 17: immunohistochemical mapping of its distribution in human epithelial tumors and its potential applications
AU Miettinen, Markku; Nobel, Michael P.; Tuma, Bodil T.; Kovatich, Albert J.
CS Department of Soft Tissue Pathology, Armed Forces Institute of Pathology, Washington, DC, 20306-6000, USA
SO Appl. Immunohistochem. (1997), 5(3), 152-159
CODEN: APIMEH; ISSN: 1062-3345
PB Lippincott-Raven

DT Journal
 LA English
 AB The distribution of keratin 17 (K17), mol. wt. (MW) **46 kDa**, was immunohistochem. evaluated in a series of >500 formaldehyde-fixed, paraffin-embedded human epithelial and selected nonepithelial tumor specimens using a specific monoclonal antibody (clone E3). In normal epithelial tissues, K17 reactivity was found in a subset of hair shaft cells, sebaceous gland reserve cells, and respiratory and prostate basal epithelial cells. Furthermore, variable and inconsistent K17 expression was found in myoepithelia of sweat, salivary, and mammary glands. Although normal epidermis and other squamous epithelia were K17-neg., regenerative epithelia, e.g., at the site of ulceration or acute inflammation, were pos. Furthermore, K17 was present in dysplastic but not in normal squamous epithelia of skin and internal organs. Most squamous-cell carcinomas showed K17-pos. cells that were more numerous in more well-differentiated tumors. About 50% of pulmonary and >50% of pancreatic adenocarcinomas showed K17-pos. cells. Although K17-pos. cells, in some cases, reflected adenosquamous differentiation, this was not the case in all K17-pos. adenocarcinomas. Approx. one third of mammary ductal carcinomas showed K17-pos. cells, whereas lobular carcinomas were invariably K17-neg. In situ lobular and ductal carcinomas often showed prominent K17-pos. myoepithelial cells; such cells showed even greater positivity when present with in situ carcinoma or proliferative conditions, as compared with normal ducts. Other adenocarcinomas often showing K17-pos. cells included endometrial, ovarian, and, to a lesser degree, gastric carcinomas. K17-neg. tumors, almost without exception, included colon, prostate, renal, and hepatocellular carcinomas and neuroendocrine tumors. Synovial sarcomas typically showed K17-pos. epithelial cells in biphasic but not in monophasic spindle cell tumors. The obsd. distribution of K17 indicates that this marker may be helpful in evaluating abnormalities of squamous epithelia and in the subtyping of epithelial tumors.

CC 14-1 (Mammalian Pathological Biochemistry)
 ST keratin 17 epithelium **tumor**
 IT Thyroid carcinoma
 (anaplastic; immunohistochem. mapping of distribution keratin 17
 in human epithelial **tumors**)

IT Prostate
 Respiratory tract
 (basal epithelium; immunohistochem. mapping of distribution
 keratin 17 in human epithelial **tumors**)

IT Carcinoid
 (bronchial; immunohistochem. mapping of distribution keratin 17
 in human epithelial **tumors**)

IT Squamous cell carcinoma
 (cervical; immunohistochem. mapping of distribution keratin 17 in
 human epithelial **tumors**)

IT Digestive system **tumors**
 (cholangioma; immunohistochem. mapping of distribution keratin 17
 in human epithelial **tumors**)

IT **Tumors** (animal)
 (chordoma; immunohistochem. mapping of distribution keratin 17 in
 human epithelial **tumors**)

IT Gastric **tumors**
 (colon carcinoma-like; immunohistochem. mapping of distribution

- keratin 17 in human epithelial **tumors**)
- IT Breast carcinoma
(ductal, infiltrating; immunohistochem. mapping of distribution
keratin 17 in human epithelial **tumors**)
- IT Testicular **tumors**
(embryonal carcinoma; immunohistochem. mapping of distribution
keratin 17 in human epithelial **tumors**)
- IT Sarcoma
(epithelioid; immunohistochem. mapping of distribution keratin 17
in human epithelial **tumors**)
- IT Squamous cell carcinoma
(esophageal; immunohistochem. mapping of distribution keratin 17
in human epithelial **tumors**)
- IT Basal cell carcinoma
Colon adenocarcinoma
Dermatitis
Endometrial adenocarcinoma
Epidermis (skin)
Epithelium
Follicular carcinoma (thyroid)
Gastric adenocarcinoma
Hepatoma
Lung adenocarcinoma
Medullary thyroid carcinoma
Melanoma
Pancreatic adenocarcinoma
Papillary carcinoma (thyroid)
Prostatic adenocarcinoma
Renal cell carcinoma
Small-cell carcinoma (lung)
Squamous cell carcinoma
Squamous cell carcinoma (lung)
Squamous cell carcinoma (skin)
(immunohistochem. mapping of distribution keratin 17 in human
epithelial **tumors**)
- IT Breast **tumors**
(infiltrating lobular; immunohistochem. mapping of distribution
keratin 17 in human epithelial **tumors**)
- IT Pancreatic **tumors**
(islet of Langerhans; immunohistochem. mapping of distribution
keratin 17 in human epithelial **tumors**)
- IT Keratins
RL: BOC (Biological occurrence); BIOL (Biological study); OCCU
(Occurrence)
(keratin 17; immunohistochem. mapping of distribution keratin 17
in human epithelial **tumors**)
- IT Squamous cell carcinoma
(larynx; immunohistochem. mapping of distribution keratin 17 in
human epithelial **tumors**)
- IT Mammary epithelium
Salivary gland
Sweat gland
(myoepithelium; immunohistochem. mapping of distribution keratin
17 in human epithelial **tumors**)
- IT Neural **tumors**
(peripheral, sheath; immunohistochem. mapping of distribution
keratin 17 in human epithelial **tumors**)

- IT Salivary gland diseases
(pleomorphic adenoma; immunohistochem. mapping of distribution
keratin 17 in human epithelial **tumors**)
- IT Lung **tumors**
(pleura, mesothelioma; immunohistochem. mapping of distribution
keratin 17 in human epithelial **tumors**)
- IT Sebaceous gland
(reserve cell; immunohistochem. mapping of distribution keratin
17 in human epithelial **tumors**)
- IT Adenoma
(salivary gland pleomorphic; immunohistochem. mapping of
distribution keratin 17 in human epithelial **tumors**)
- IT **Tumors** (animal)
(salivary gland, parotid adenoid cystic carcinoma;
immunohistochem. mapping of distribution keratin 17 in human
epithelial **tumors**)
- IT Synovial membrane
(sarcoma, biphasic; immunohistochem. mapping of distribution
keratin 17 in human epithelial **tumors**)
- IT Synovial membrane
(sarcoma, monophasic spindle cell; immunohistochem. mapping of
distribution keratin 17 in human epithelial **tumors**)
- IT Testicular **tumors**
(seminoma; immunohistochem. mapping of distribution keratin 17 in
human epithelial **tumors**)
- IT Ovarian **tumors**
(serous cystadenoma; immunohistochem. mapping of distribution
keratin 17 in human epithelial **tumors**)
- IT Ovarian carcinoma
(serous papillary carcinoma; immunohistochem. mapping of
distribution keratin 17 in human epithelial **tumors**)
- IT Hair
(shaft cell; immunohistochem. mapping of distribution keratin 17
in human epithelial **tumors**)
- IT Ulcer
(skin; immunohistochem. mapping of distribution keratin 17 in
human epithelial **tumors**)
- IT Intestinal **tumors**
(small intestine, carcinoid; immunohistochem. mapping of
distribution keratin 17 in human epithelial **tumors**)
- IT Intestinal **tumors**
(small intestine, colon carcinoma-like; immunohistochem. mapping
of distribution keratin 17 in human epithelial **tumors**)
- IT Larynx
(squamous cell carcinoma; immunohistochem. mapping of
distribution keratin 17 in human epithelial **tumors**)
- IT Bladder carcinoma
- IT Cervical carcinoma
- IT Esophageal carcinoma
(squamous cell; immunohistochem. mapping of distribution keratin
17 in human epithelial **tumors**)
- IT Sarcoma
(synovial membrane, biphasic; immunohistochem. mapping of
distribution keratin 17 in human epithelial **tumors**)
- IT Sarcoma
(synovial membrane, monophasic spindle cell; immunohistochem.
mapping of distribution keratin 17 in human epithelial

tumors)
 IT Lymphoma
 Thymus tumors
 (thymoma; immunohistochem. mapping of distribution keratin 17 in
 human epithelial tumors)
 IT Bladder carcinoma
 (transition cell; immunohistochem. mapping of distribution
 keratin 17 in human epithelial tumors)
 IT Pleural diseases
 (tumor, mesothelioma; immunohistochem. mapping of
 distribution keratin 17 in human epithelial tumors)
 IT Small intestine
 (tumors, carcinoid; immunohistochem. mapping of
 distribution keratin 17 in human epithelial tumors)
 IT Biliary tract
 (tumors, cholangioma; immunohistochem. mapping of
 distribution keratin 17 in human epithelial tumors)
 IT Small intestine
 (tumors, colon carcinoma-like; immunohistochem. mapping
 of distribution keratin 17 in human epithelial tumors)
 IT Salivary gland diseases
 (tumors, parotid adenoid cystic carcinoma;
 immunohistochem. mapping of distribution keratin 17 in human
 epithelial tumors)
 IT Islet of Langerhans
 (tumors; immunohistochem. mapping of distribution
 keratin 17 in human epithelial tumors)
 IT Skin diseases
 (ulcer; immunohistochem. mapping of distribution keratin 17 in
 human epithelial tumors)
 IT Ovarian carcinoma
 (undifferentiated; immunohistochem. mapping of distribution
 keratin 17 in human epithelial tumors)

L6 ANSWER 2 OF 8 HCAPLUS COPYRIGHT 1998 ACS
 AN 1996:517504 HCAPLUS
 DN 125:192240
 TI Monoclonal antibodies against recombinant **MAGE-1** protein
 identify a cross-reacting 72-kDa antigen which is co-expressed with
 MAGE-1 protein in melanoma cells
 AU Carrel, Stefan; Schreyer, Magali; Spagnoli, Giulio; Cerottini,
 Jean-Charles; Rimoldi, Donata
 CS Ludwig Institute Cancer Research, University Lausanne, Epalinges,
 1066, Switz.
 SO Int. J. Cancer (1996), 67(3), 417-422
 CODEN: IJCNAW; ISSN: 0020-7136
 DT Journal
 LA English
 AB The MAGE-1 gene codes for tumor-assocd. peptides recognized by
 cytolytic T lymphocytes in assocn. with MHC class I mols. such as
 HLA-A1 and HLA-Cw16. In the course of a study aimed at the
 immunohistochem. detection of the MAGE-1 gene product in tumor
 samples, 2 mouse monoclonal antibodies (MAbs) directed against a
 full-length recombinant MAGE-1 fusion protein were found to react
 strongly not only with the **46-kDa** MAGE-1
 protein, but also with a 72-kDa product in immunoblots of lysates
 obtained from several MAGE-1-mRNA-pos. melanoma cell lines.

Pre-incubation of the antibodies with the recombinant MAGE-1 fusion protein abolished their reactivity both with MAGE-1 protein and with the 72-kDa product, thus confirming the occurrence of antigenic determinant(s) shared by the 2 proteins. The 72-kDa protein is not an alternative product of MAGE-1, since it was still detected in lysates of a MAGE-1 loss variant derived from a MAGE-1-pos. melanoma cell line. Moreover, the 72-kDa protein does not appear to be a product of the other members of the MAGE gene family known to be expressed in tumors (such as MAGE-2, -3, -4 and -12). Interestingly, expression of the 72-kDa protein was correlated with that of MAGE-1 protein. Thus, in 30 tumor cell lines analyzed by immunoblotting and RT-PCR, the 72-kDa protein was never detected in MAGE-1-mRNA-neg. cell lines, while it was co-expressed with MAGE-1 protein in 12 out of 15 cell lines expressing MAGE-1. Furthermore, the 72-kDa protein was detected in lysates of human testis, the only normal tissue known to express MAGE-1. Finally, treatment of MAGE-1 mRNA-neg. cell lines with 5-aza-2'-deoxycytidine, a hypomethylating agent known to induce MAGE-1 expression, resulted in the expression of the 72-kDa protein. Taken collectively, these findings suggest that expression of the gene encoding the 72-kDa protein identified in this study through antigenic determinant(s) shared with MAGE-1 protein is regulated in a way similar to that of MAGE-1.

CC 14-1 (Mammalian Pathological Biochemistry)

IT Antigens

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)

(MAGE-1; monoclonal antibodies to MAGE-1 cross-react with 72 kDa protein in melanoma cells)

IT Testis

(monoclonal antibodies to MAGE-1 cross-react with 72 kDa protein in)

IT Melanoma

(monoclonal antibodies to MAGE-1 cross-react with 72 kDa protein in melanoma cells)

IT Proteins, specific or class

RL: BOC (Biological occurrence); BPR (Biological process); MFM (Metabolic formation); PRP (Properties); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence); PROC (Process)
(72,000-mol.-wt., monoclonal antibodies to MAGE-1 cross-react with 72 kDa protein in melanoma cells)

IT Antibodies

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)

(monoclonal, monoclonal antibodies to MAGE-1 cross-react with 72 kDa protein in melanoma cells)

L6 ANSWER 3 OF 8 HCAPLUS COPYRIGHT 1998 ACS

AN 1996:150834 HCAPLUS

DN 124:228283

TI Expression of MAGE-1, MAGE-2, MAGE

-3/-6 and MAGE-4a/-4b genes in ovarian tumors

AU Yamada, Akira; Kataoka, Akio; Shichijo, Shigeki; Kamura, Toshiharu; Imai, Yasuhisa; Nishida, Takashi; Itoh, Kyogo

CS School of Medicine, Kurume University, Kurume, 830, Japan

SO Int. J. Cancer (1995), Volume Date 1995, 64(6), 388-93

CODEN: IJCNAW; ISSN: 0020-7136

DT Journal

LA English

AB MAGE genes encoding tumor-rejection antigens recognized by cytotoxic T lymphocytes are expressed at the mRNA level in various malignant tumors. The authors have investigated the expression of genes MAGE-1, -2, -3/-6, and -4a/-4b at the mRNA level in malignant and non-malignant ovarian tumors as well as in normal ovaries by reverse transcription-polymerase chain reaction. MAGE-1, -2, -3/-6, and -4a/-4b were expressed in 12, 5, 11, and 4 of 58 malignant tumors, resp. The majority of these MAGE-mRNA-pos. tumors were histol. surface-epithelial-stromal tumors, in particular serous adenocarcinomas. They mostly consisted of either advanced-stage or recurrent tumors. In contrast, neither benign tumors nor normal ovaries expressed any of the MAGE genes investigated. A 46 -kDa MAGE-1 protein was identified in MAGE-1-mRNA-pos. serous adenocarcinomas by immunoblot anal. with polyclonal anti-MAGE-1 antibody. These results provide important information for specific immunotherapy of ovarian serous adenocarcinomas with MAGE gene products.

CC 14-1 (Mammalian Pathological Biochemistry)
Section cross-reference(s): 3, 15

ST MAGE gene expression ovary tumor

IT Gene, animal
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(MAGE-1; expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)

IT Gene, animal
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(MAGE-2; expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)

IT Gene, animal
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(MAGE-3; expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)

IT Gene, animal
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(MAGE-4a; expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)

IT Gene, animal
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(MAGE-4b; expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)

IT Gene, animal

- RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
 (MAGE-6; expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)
- IT Ovary, neoplasm
 (expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)
- IT Proteins, specific or class
 RL: BOC (Biological occurrence); BIOL (Biological study); OCCU (Occurrence)
 (gene MAGE-1; expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)
- IT Ovary, neoplasm
 (arrhenoblastoma, expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)
- IT Ovary, neoplasm
 (clear cell carcinoma, expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)
- IT Ovary, neoplasm
 (dysgerminoma, expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)
- IT Ovary, neoplasm
 (endometrioid carcinoma, expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)
- IT Ovary, neoplasm
 (granulosa cell, expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)
- IT Ovary, neoplasm
 (metastasis, expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)
- IT Ovary, neoplasm
 (mucinous adenocarcinoma, expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)
- IT Mesonephros
 (neoplasm, ovarian yolk sac tumor, expression of MAGE-1, -2, -3/-6, and -4a/-4b genes in human ovarian tumors with the preferential expression of MAGE-1 and MAGE-3/-6 genes in serous adenocarcinomas)

-3/-6 genes in serous adenocarcinomas)
 IT Ovary, neoplasm
 (serous adenocarcinoma, expression of **MAGE-1**, -2,
 -3/-6, and -4a/-4b genes in human ovarian tumors with the
 preferential expression of **MAGE-1** and **MAGE**
 -3/-6 genes in serous adenocarcinomas)

L6 ANSWER 4 OF 8 HCAPLUS COPYRIGHT 1998 ACS
 AN 1995:995009 HCAPLUS
 DN 124:127118
 TI Delipidated purified polysaccharidic compound D25 preparation, and
 injectable composition comprising same
 IN Binz, Hans; Durand, Jacques; Cudennec, Claude-Alain; Normier,
 Gerard; Le Pape, Alain
 PA Pierre Fabre Medicament, Fr.
 SO PCT Int. Appl., 56 pp.
 CODEN: PIXXD2
 PI WO 9525128 A1 950921
 DS W: AU, CA, JP, NZ, US
 RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
 AI WO 95-FR311 950315
 PRAI FR 94-3072 940316
 DT Patent
 LA French
 AB A polysaccharide compd. D25, with a mol. wt. of .apprx.34
 kDa, extd. from the membrane proteoglycans of Klebsiella
 pneumoniae, is delipidated and purified so that an aq. soln. contg.
 the compd. no longer contains any C16 fatty acids or peptides
 whether free or combined with the said compd. The use of said
 prepn. in imaging, given the targeting properties of said compd., is
 also disclosed. Thus an injectable formulation comprised the
 purified carbohydrate 1.0 mg in an aq. soln. contg. NaCl at 1.0 mg.
 Such a soln. was labeled with 99mTc by the SnF2 method with ascorbic
 acid as stabilizing agent and was used for imaging of melanoma.

IC ICM C08B037-00
 ICS A61K051-00; A61K031-715
 CC 63-6 (Pharmaceuticals)
 IT **Melanoma**
 (polysaccharidic formulation for imaging and diagnosis of)
 IT Macrophage
 (targeting properties of injectable formulation contg.
 polysaccharide for **tumor** imaging)

L6 ANSWER 5 OF 8 HCAPLUS COPYRIGHT 1998 ACS
 AN 1995:222942 HCAPLUS
 DN 122:262435
 TI **MAGE-1** gene product is a cytoplasmic protein
 AU Schultz-Thater, Elke; Juretic, Antonio; Dellabona, Paolo; Luescher,
 Urs; Siegrist, Walter; Harder, Felix; Heberer, Michael; Zuber,
 Markus; Spagnoli, Giulio C.
 CS Department of Surgery, University of Basel, Basel, Switz.
 SO Int. J. Cancer (1994), 59(3), 435-9
 CODEN: IJCNAW; ISSN: 0020-7136
 DT Journal
 LA English
 AB **MAGE-1** gene encodes a human melanoma antigen, recognized by
 syngeneic cytotoxic T lymphocytes (CTL). **MAGE-1** transcripts are

also detectable in breast cancers, in non-small cell lung carcinomas and in central nervous system tumors. To identify, in cellular prepn., the protein encompassing the antigenic peptide, the authors generated a panel of monoclonal antibodies (MAbs) against the MAGE-1 gene product by using, as immunogen, a full-length recombinant prepn. (rMAGE-1), obtained through expression cloning of the relevant gene in E. coli. Four reagents were obtained recognizing both rMAGE-1 and the **46-kDa** native protein in cell lines expressing MAGE-1 mRNA. No positivity could be detected in MAGE-1-mRNA-neg. melanoma lines. No surface labeling of MAGE-1-pos. cell lines could be obsd. In contrast, on permeabilization of MZ2 melanoma cells, all 4 MAbs induced efficient staining, as detected by cytofluorog. Fluorescence microscopy shows that MAGE-1 gene product is a cytoplasmic protein clustered in paranuclear organelle-like structures. Thus, MAGE-1 protein location closely resembles that of P91A and P198 murine-tumor antigens.

CC 14-1 (Mammalian Pathological Biochemistry)
Section cross-reference(s): 15

IT Gene, animal
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**MAGE-1**; human **MAGE-1** gene antigen is
cytoplasmic protein in melanoma)

IT Antigens
RL: ANT (Analyte); BOC (Biological occurrence); ANST (Analytical
study); BIOL (Biological study); OCCU (Occurrence)
(gene **MAGE-1**; human **MAGE-1** gene antigen is
cytoplasmic protein in melanoma)

IT Cytoplasm
Melanoma
(human **MAGE-1** gene antigen is cytoplasmic protein in
melanoma)

IT Antibodies
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL
(Biological study); PREP (Preparation); USES (Uses)
(monoclonal, to gene **MAGE-1** antigen; human **MAGE-1**
-1 gene antigen is cytoplasmic protein in melanoma)

L6 ANSWER 6 OF 8 HCAPLUS COPYRIGHT 1998 ACS
AN 1994:131751 HCAPLUS
DN 120:131751
TI Identification of the **MAGE-1** gene product by monoclonal
and polyclonal antibodies
AU Chen, Yao Tseng; Stockert, Elisabeth; Chen, Yachi; Garin-Chesa,
Pilar; Rettig, Wolfgang J.; Van der Bruggen, P.; Boon, Thierry; Old,
Lloyd J.
CS New York Unit, Ludwig Inst. Cancer Res., New York, NY, 10021, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1994), 91(3), 1004-8
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The human MAG-1 gene encodes a melanoma peptide antigen recognized
by autologous cytotoxic T lymphocytes. To produce antibodies
against the MAGE-1 gene product, several approaches were taken.
Three oligopeptides were synthesized based on predicted MAGE-1 amino
acid sequences and were used to generate rabbit anti-peptide
anti-sera. In addn., a truncated MAGE-1 cDNA was cloned into an

Escherichia coli expression vector, and recombinant protein was produced and purified. All three rabbit anti-peptide antisera showed reactivity against the immunizing peptide, and one reacted with the recombinant MAGE-1 protein by immunoblotting, but none reacted with cell lysates from MAGE-1 mRNA-pos. cells. The recombinant MAGE-1 protein was then used for the generation of mouse monoclonal and rabbit polyclonal antibodies. One IgG1 monoclonal antibody, MA454, as well as rabbit polyclonal antisera recognized a **46-kDa** protein in exts. of MAGE-1 mRNA-pos. melanoma cell lines. The antibodies showed no apparent cross-reactivity with products of the closely related MAGE-2 and MAGE-3 genes. Serol. typing of normal and tumor cell lysates was in full agreement with mRNA anal., showing expression of MAGE-1 protein in MAGE-1 mRNA-pos. testis and a subset of melanomas but not in MAGE-1 mRNA-neg. normal or tumor tissues. Transfection of the MAGE-1 gene into a MAGE-1 mRNA-neg. melanoma cell line resulted in the expression of the **46-kDa** protein, confirming the identity of this protein as the MAGE-1 gene product.

CC 15-2 (Immunocytochemistry)

IT Proteins, specific or class

RL: PREP (Preparation)

(gene **MAGE-1**, monoclonal and polyclonal antibodies to, prepn. and reactivity of)

IT Antibodies

RL: PREP (Preparation)

(to **MAGE-1** gene product, prepn. and reactivity of)

IT Antibodies

RL: PREP (Preparation)

(monoclonal, to **MAGE-1** gene product, prepn. and reactivity of)

L6 ANSWER 7 OF 8 HCAPLUS COPYRIGHT 1998 ACS

AN 1994:125072 HCAPLUS

DN 120:125072

TI The melanocyte-stimulating hormone (MSH) receptor in M2R mouse

melanoma tumors: solubilization and properties of the receptor-MSH complex and its covalently crosslinked conjugate

AU Shafir, I.; Schmidt-Sole, J.; Shai, E.; Salomon, Y.

CS Dep. Horm. Res., Weizmann Inst. Sci., Rehovot, 76100, Israel

SO Melanoma Res. (1993), 3(3), 157-68

CODEN: MREEEH; ISSN: 0960-8931

DT Journal

LA English

AB Several properties of the MSH receptor in solid melanotic and amelanotic mouse M2R tumor isografts were studied in C57BL mice. Using cell membrane fractions prepd. from such tumors and the superpotent [Nle4,D-Phe7].alpha.MSH analog, the affinity and receptor contents of the two tumor variants were similar. When occupied by MSH, the receptor-MSH complex (R.cntdot.MSH) was readily sol. in cholate. In the solubilized form, R.cntdot.MSH was extremely stable and dissocd. to an extent of only 30% within 12 days at 4.degree.. While this high stability can be maintained in the pH range of 7.0-8.5, the solubilized R.cntdot.MSH complex becomes increasingly unstable below pH 7.0 and totally dissocd. at a pH <6.0. In the membrane-bound form, the R.cntdot.MSH complex shows a parallel pH stability profile which is shifted down by approx. two pH units. In addn. to low pH, the R.cntdot.MSH complex becomes

unstable and totally dissoecs. in the presence of 10 mM EGTA, suggesting that the calcium-sensitive function of the receptor is still assocd. with the receptor in the detergent-sol. state. The R.cntdot.MSH complexes in the sol. and membrane-bound forms are also totally resistant to proteolytic digestion by V8 protease, but were slowly digested by trypsin. Treatment of R.cntdot.MSH with 1-ethyl-3-(3-dimethylamino-propyl)carbodiimide hydrochloride or bis(sulfosuccinimidyl) suberate led to covalent crosslinking of MSH to the receptor mol. The electrophoretic mobility on SDS-PAGE of the 43/46 kDa doublet of the receptor-MSH conjugate (R*MSH) was identical to the photoaffinity labeled MSH receptor product described earlier in cultured M2R cells. However, the efficiency of prodn. of the crosslinked product was .apprx.30%, much higher than that achieved previously by photoaffinity labeling. Using rabbit polyclonal anti-.alpha.MSH antibodies, the R*MSH conjugate was identifiable on Western immunoblots. These results provide a basis for further development of procedures for purifn. of the MSH receptor mol. and studying its protein structure.

CC 2-1 (Mammalian Hormones)
 Section cross-reference(s): 14
 ST MSH receptor **melanoma** solubilization
 IT Receptors
 RL: PROC (Process)
 (MSH, from **melanoma**, solubilization of, in complexes
 with ligand and crosslinked conjugate)

IT **Melanoma**
 (amelanotic, MSH receptor of, solubilization of)

IT **Melanoma**
 (melanotic, MSH receptor of, solubilization of)

IT 9002-79-3, Melanocyte-stimulating hormone
 RL: ANST (Analytical study)
 (receptor for, solubilization of, from **melanomas** in
 complexes with ligand and crosslinked conjugate)

L6 ANSWER 8 OF 8 HCAPLUS COPYRIGHT 1998 ACS

AN 1990:53087 HCAPLUS

DN 112:53087

TI Synthesis of vitamin K-dependent proteins by cultured human
tumor cells

AU Al-Mondhiry, Hamid; Wallin, Reidar

CS Coll. Med., Pennsylvania State Univ., Hershey, PA, 17033, USA

SO Thromb. Haemostasis (1989), 62(2), 661-6

CODEN: THHADQ; ISSN: 0340-6245

DT Journal

LA English

AB The observation that warfarin inhibits the growth and metastasis of certain types of clin. and exptl. tumors suggests a role for vitamin K in tumor biol. The synthesis of vitamin K-dependent proteins was investigated in four malignant (lung epidermoid carcinoma, melanoma, colon adenocarcinoma, and breast adenocarcinoma) and three normal (colon epithelium, breast epithelium, and fibroblasts) cell lines of human origin grown in tissue cultures. The results show the following: 1) vitamin K-dependent carboxylase activity is present in all of the malignant and normal cell lines studied; 2) the malignant, as well as normal, cell lines synthesize a family of vitamin K-dependent proteins, and microsomal precursors of these proteins with apparent mol. masses of 74, 62, and 34

kDa are common to all malignant and normal cell lines, whereas precursors of higher and lower mol. mass seem to be synthesized by some but not all tumor cell lines; and 3) the 74-kDa precursor synthesized by colon carcinoma and breast carcinoma was pos. identified as a precursor of protein S.

CC 14-1 (Mammalian Pathological Biochemistry)

Section cross-reference(s): 13

ST vitamin K protein formation **tumor** cell

IT **Melanoma**

Neoplasm, metabolism
 (vitamin K-dependent protein formation by, of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)

IT Intestine, neoplasm
 (colon, adenocarcinoma, vitamin K-dependent protein formation by, of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)

IT Lung, neoplasm
 (epidermoid carcinoma, vitamin K-dependent protein formation by, of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)

IT Mammary gland
 (neoplasm, adenocarcinoma, vitamin K-dependent protein formation by, of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)

IT Proteins, specific or class
 RL: BIOL (Biological study)
 (.gamma.-carboxyglutamic acid-contg., 34,000-mol.-wt., formation of vitamin K-dependent, by neoplastic and normal cells of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)

IT Proteins, specific or class
 RL: BIOL (Biological study)
 (.gamma.-carboxyglutamic acid-contg., 62,000-mol.-wt., formation of vitamin K-dependent, by neoplastic and normal cells of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)

IT Proteins, specific or class
 RL: BIOL (Biological study)
 (.gamma.-carboxyglutamic acid-contg., 74,000-mol.-wt., formation of vitamin K-dependent, by neoplastic and normal cells of humans, **tumor** growth and metastasis and **tumor**-assocd. hypercoagulable states in relation to)

MSRCH_PP

(TM)

Release 2.1d John F. Collins, BioComputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:43:30 1998; MasPar time 2.22 Seconds
Tubular output not generated.

Title: >US-08-190-411A-2
Description: (1-14) from 5541104.ppe
Perfect Score: 93
Sequence: 1 INTRORPSEGSS 14

Scoring table: PAM 150
Gap 15

Searched: 60183 seqs, 5492030 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: a-issued
1-back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:CT90
10:PC91 11:PC92 12:PC93 13:PC94 14:PC95 15:PC96

Statistics: Mean 16.616; Variance 48.328; scale 0.344

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	93	100.0	14	6	US-08-190- Sequence 2, Applicatio	1.51e+04
2	53	57.0	420	7	US-08-391- Sequence 10, Applicati	1.13e+01
3	53	57.0	420	7	US-08-391- Sequence 2, Applicatio	1.13e+01
4	53	57.0	599	7	US-08-463- Sequence 3, Applicatio	1.13e+01
5	53	57.0	613	7	US-08-405- Sequence 1, Applicatio	1.13e+01
6	53	57.0	614	14	PCT-US95-0 Sequence 1, Applicatio	1.13e+01
7	53	57.0	614	7	US-08-225- Sequence 1, Applicatio	1.13e+01
8	53	57.0	637	6	US-08-235- Sequence 16, Applicatio	1.13e+01
9	53	57.0	637	6	US-08-235- Sequence 8, Applicatio	1.13e+01
10	51	54.8	834	5	US-07-977- Sequence 5, Applicatio	1.90e+01
11	51	54.8	834	10	PCT-US91-0 Sequence 8, Applicatio	1.90e+01
12	50	53.8	311	6	US-07-917- Sequence 6, Applicatio	2.46e+01
13	50	53.8	311	7	US-08-479- Sequence 6, Applicatio	2.46e+01
14	50	53.8	311	6	US-07-917- Sequence 5, Applicatio	2.46e+01
15	50	53.8	311	7	US-08-479- Sequence 5, Applicatio	2.46e+01
16	50	53.8	889	7	US-08-118- Sequence 4, Applicatio	2.46e+01
17	48	51.6	355	7	US-08-366- Sequence 34, Applicatio	4.09e+01
18	48	51.6	355	8	US-08-681- Sequence 34, Applicatio	4.09e+01
19	47	50.5	369	6	US-07-688- Sequence 31, Applicatio	5.26e+01
20	47	50.5	369	10	PCT-US91-0 Sequence 32, Applicatio	5.26e+01
21	47	50.5	527	14	PCT-US95-0 Sequence 10, Applicatio	5.26e+01
22	47	50.5	599	6	US-08-391- Sequence 4, Applicatio	5.26e+01

96 41 44.1 738 7 US-08-530- Sequence 3, Applicatio 2.29e+02
97 41 44.1 738 7 US-08-530- Sequence 11, Applicati 2.29e+02
98 41 44.1 869 7 US-08-646- Sequence 32, Applicati 2.29e+02
99 41 44.1 890 8 US-08-445- Sequence 2, Applicatio 2.29e+02
100 41 44.1 1203 12 PCT-US93-1 Sequence 103, Applicat 2.29e+02

ALIGNMENTS

RESULT 1
ID US-08-190-411A-2 STANDARD; PRT; 14 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 2, Application US/08190411A.
XX CC Patent No. 5541104
XX CC GENERAL INFORMATION:
CC APPLICANT: Chen, Yao-Tsang; Stockert, Elisabeth;
CC APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
CC APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
CC APPLICANT: Old, Lloyd J.
CC TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
CC TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBI
CC NANT MAGE-1.
CC TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felife & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/190,411A
CC FILING DATE: 01-FEBRUARY-1994
CC CLASSIFICATION: 436
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 037,230
CC FILING DATE: 26-MARCH-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/04354
CC FILING DATE: 22-MAY-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/807,043
CC FILING DATE: 12-DECEMBER-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/764,364
CC FILING DATE: 23-SEPTEMBER-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/728,838
CC APPLICATION NUMBER: 9-JULY-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/705,702
CC FILING DATE: 23-MAY-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5541104man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5354
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC 'LENGTH: 14 amino acid residues

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 14 AA; 1607 MW; 1134 CN;
Query Match 100.0%; Score 93; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.51e-04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 INFTRQRPSEGSS 14
| | | | | | | | | | | | | | | |
Qy 1 INFTRQRPSEGSS 14
| | | | | | | | | | | | | | | |

RESULT 2
ID US-08-391-259-10 STANDARD; PRT; 420 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 10, Application US/08391259.
XX CC Sequence 10, Application US/08391259
XX CC Patent No. 5621078
XX CC GENERAL INFORMATION:
CC APPLICANT: Riemen, Mark W
CC APPLICANT: Stirlivant, Steven M
CC TITLE OF INVENTION: Modified PE40
CC NUMBER OF SEQUENCES: 11
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Merck & Co., Inc.
CC STREET: 126 Lincoln Avenue
CC CITY: Rahway
CC STATE: New Jersey
CC COUNTRY: U.S.
CC ZIP: 07065
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/391,259
CC FILING DATE:
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/120,698
CC FILING DATE:
CC APPLICATION NUMBER: US/07/879,037
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Grassler, Frank P
CC REGISTRATION NUMBER: 31,164
CC REFERENCE/DOCKET NUMBER: 178791A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (908) 594-3462
CC TELEFAX: (908) 594-4720
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 420 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 420 AA; 45129 MW; 823636 CN;
Query Match 57.0%; Score 53; DB 7; Length 420;
Best Local Similarity 85.7%; Pred. No. 1.13e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 79 FTRHRQP 85
| | | | | | | | | | | | | | | |

QY 3 FTRQRP 9

RESULT 3
ID US-08-391-259-2 STANDARD: PRT: 420 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 2, Application US/08391259.

XX Sequence 2, Application US/08391259
Patent No. 5621078

CC GENERAL INFORMATION:

CC APPLICANT: Riemen, Mark W

CC APPLICANT: Stirdivant, Steven M

CC TITLE OF INVENTION: Modified PE40

CC NUMBER OF SEQUENCES: 11

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Merck & Co., Inc.

CC STREET: 126 Lincoln Avenue

CC CITY: Rahway

CC STATE: New Jersey

CC COUNTRY: U.S.

CC ZIP: 07065

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/391,259

CC FILING DATE:

CC CLASSIFICATION: 530

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US/08/120,698

CC FILING DATE:

CC APPLICATION NUMBER: US/07/879,037

CC FILING DATE:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Grassler, Frank P

CC REGISTRATION NUMBER: 31,164

CC REFERENCE/DOCKET NUMBER: 17879IA

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (908) 594-3462

CC TELEFAX: (908) 594-4720

CC INFORMATION FOR SEQ ID NO: 2:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 420 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

SQ SEQUENCE 420 AA; 45179 MW; 824920 CN;

Query Match 57.0%; Score 53; DB 7; Length 420;
Best Local Similarity 85.7%; Pred. No. 1.13e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 79 FTRHRQP 85

|||||

QY 3 FTRQRP 9

RESULT 4
ID US-08-463-163-3 STANDARD: PRT: 599 AA.

XX xxxxxx

DT 01-JAN-1900

XX Sequence 3, Application US/08463163.

XX

CC Sequence 3, Application US/08463163

CC Patent No. 5696237

CC GENERAL INFORMATION:

CC APPLICANT: Fitzgerald, David J.

CC APPLICANT: Chaudhary, Vijay K.

CC APPLICANT: Pastan, Ira H.

CC APPLICANT: Waldmann, Thomas A.

CC APPLICANT: Queen, Cary L.

CC TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein

CC NUMBER OF SEQUENCES: 12

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Townsend and Townsend and Crew

CC STREET: One Market Plaza, Steuart Street Tower

CC CITY: San Francisco

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94105-1492

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.30

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/463,163

CC FILING DATE: 05-JUN-1995

CC CLASSIFICATION: 536

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 06/227,227

CC FILING DATE: 22-JAN-1981

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 06/911,227

CC FILING DATE: 24-SEP-1986

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/341,361

CC FILING DATE: 21-APR-1989

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/865,722

CC FILING DATE: 08-APR-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Weber, Ellen L.

CC REGISTRATION NUMBER: 32,762

CC REFERENCE/DOCKET NUMBER: 015280-12211

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 543-9600

CC TELEFAX: (415) 543-5043

CC INFORMATION FOR SEQ ID NO: 3:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 599 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

SQ SEQUENCE 599 AA; 64018 MW; 1732802 CN;

Query Match 57.0%; Score 53; DB 7; Length 599;
Best Local Similarity 85.7%; Pred. No. 1.13e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 258 FTRHRQP 264

|||||

QY 3 FTRQRP 9

RESULT 5
ID US-08-405-615-1 STANDARD: PRT: 613 AA.

XX xxxxxx

AC xxxxxx

XX 01-JAN-1900

DT 01-JAN-1900

XX Sequence 1, Application US/08405615.

DE Sequence 1, Application US/08405615

XX Sequence 1, Application US/08405615

CC Sequence 1, Application US/08405615

CC Patent No. 5602095
CC GENERAL INFORMATION:
CC APPLICANT: Pastan, Ira
CC APPLICANT: Fitzgerald, David J.
CC TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
CC TITLE OF INVENTION: Increased Activity
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Ellen L. Weber
CC STREET: One Market Plaza, Steuart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/405,615
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/07/901,709
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Weber, Ellen L.
CC REGISTRATION NUMBER: 32,762
CC REFERENCE/DOCKET NUMBER: 15280-36
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 613 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 613 AA; 66827 MW; 1767040 CN;

Db 272 FTRHRQP 278
Oy 3 FTRQRQP 9

RESULT 6
ID PCT-US95-04468-1 STANDARD; PRT; 614 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE Sequence 1, Application PC/TUS9504468.
XX Sequence 1, Application PC/TUS9504468
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
CC TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
CC NUMBER OF SEQUENCES: 59
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/04468

CC FILING DATE: 07-APR-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/225,224
CC FILING DATE: 08-APR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Weber, Ellen L.
CC REGISTRATION NUMBER: 32,762
CC REFERENCE/DOCKET NUMBER: 15280-193-1PC
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 614 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..614
CC OTHER INFORMATION: /label= native-PE
CC SEQUENCE 614 AA; 66959 MW; 1772843 CN;

Query Match 57.0%; Score 53; DB 14; Length 614;
Best Local Similarity 85.7%; Pred. No. 1.13e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 273 FTRHRQP 279
Oy 3 FTRQRQP 9

RESULT 7
ID US-08-225-224-1 STANDARD; PRT; 614 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE Sequence 1, Application US/08225224.
XX Sequence 1, Application US/08225224.
CC Patent No. 5635599
CC GENERAL INFORMATION:
CC APPLICANT: PASTAN, Ira
CC APPLICANT: KREITMAN, Robert J.
CC TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
CC TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,224
CC FILING DATE: 8-APR-1994
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Weber, Ellen L.
CC REGISTRATION NUMBER: 32,762
CC REFERENCE/DOCKET NUMBER: 15280-193
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600

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CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 614 amino acids
CC TYPE: amino acid
CC TOPOLOGY: unknown
CC STRANDEDNESS: unknown
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..614
CC OTHER INFORMATION: /label= native-PE
CC SEQUENCE 614 AA; 66959 MW; 1772843 CN;

Query Match 57.0%; Score 53; DB 7; Length 614;
Best Local Similarity 85.7%; Pred. No. 1.13e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 273 FTRHRQP 279
QY 3 FTRORQP 9
|||:||||
|||:||||

RESULT 8
ID US-08-235-838-16 STANDARD; PRT; 637 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 16, Application US/08235838.
XX
CC Sequence 16, Application US/08235838
CC Patent No. 5571894
CC GENERAL INFORMATION:
CC APPLICANT: Wels, Winfried S.
CC APPLICANT: Hynes, Nancy E.
CC APPLICANT: Harwerth, Ina-Maria
CC APPLICANT: Groner, Bernd
CC APPLICANT: Hardman, No. 5571894man
CC APPLICANT: Zwickl, Markus
CC TITLE OF INVENTION: Recombinant Antibodies Specific for a
CC TITLE OF INVENTION: Growth Factor Receptor
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CIBA-GEIGY Corporation
CC STREET: 7 Skyline Drive
CC CITY: Hawthorne
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10532
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION NUMBER: US/08/235,838
CC FILING DATE: TBA
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/828,832
CC FILING DATE: 31-JAN-1992
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/235,838
CC FILING DATE: TBA
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/828,832
CC FILING DATE: 31-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GB 91-810079.3
CC FILING DATE: 05-FEB-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Elmer, James Scott
CC REGISTRATION NUMBER: 36,129
CC REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (919)541-8614
CC TELEFAX: (919)541-8689

CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 637 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 637 AA; 68361 MW; 1955217 CN;

Query Match 57.0%; Score 53; DB 6; Length 637;
Best Local Similarity 85.7%; Pred. No. 1.13e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 296 FTRHRQP 302
QY 3 FTRORQP 9
|||:||||
|||:||||

RESULT 9
ID US-08-235-838-14 STANDARD; PRT; 637 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 14, Application US/08235838.
XX
CC Sequence 14, Application US/08235838
CC Patent No. 5571894
CC GENERAL INFORMATION:
CC APPLICANT: Wels, Winfried S.
CC APPLICANT: Hynes, Nancy E.
CC APPLICANT: Harwerth, Ina-Maria
CC APPLICANT: Groner, Bernd
CC APPLICANT: Hardman, No. 5571894man
CC APPLICANT: Zwickl, Markus
CC TITLE OF INVENTION: Recombinant Antibodies Specific for a
CC TITLE OF INVENTION: Growth Factor Receptor
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CIBA-GEIGY Corporation
CC STREET: 7 Skyline Drive
CC CITY: Hawthorne
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10532
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION NUMBER: US/08/235,838
CC FILING DATE: TBA
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/828,832
CC FILING DATE: 31-JAN-1992
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: GB 91-810079.3
CC FILING DATE: 05-FEB-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Elmer, James Scott
CC REGISTRATION NUMBER: 36,129
CC REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (919)541-8614
CC TELEFAX: (919)541-8689

CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 637 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
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SQ SEQUENCE 637 AA; 68441 MW; 1957762 CN;
Query Match 57.0%; Score 53; DB 6; Length 637;
Best Local Similarity 85.7%; Pred.No. 1.13e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 296 FTRHRQP 302
111:111
QY 3 FTRORQP 9

RESULT 10
ID US-07-977-434-8 STANDARD; PRT; 834 AA.
XX AC xxxxxx
XX 01-JAN-1900
Sequence 8, Application US/07977434.
Sequence 8, Application US/07977434
Patent No. 5466591
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,434
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
-4 FILING DATE:

SQ SEQUENCE 834 AA; 94055 MW; 3318124 CN;
Query Match 54.8%; Score 51; DB 5; Length 834;
Best Local Similarity 44.4%; Pred.No. 1.90e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 258 VDFARREP 266
:::|::|
QY 1 INFTRORQP 9

RESULT 11
ID PCT-US91-07035-8 STANDARD; PRT; 834 AA.
XX AC xxxxxx
XX 01-JAN-1900
Sequence 8, Application PC/TUS9107035.
Sequence 8, Application PC/TUS9107035
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-third Street
CITY: Emeryville
STATE: California
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07035
FILING DATE: 19910930
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
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CC APPLICANT: Yajima, Kazuyoshi
CC TITLE OF INVENTION: PROCESS FOR PRODUCTION OF D-ALPHA-AMINO
CC TITLE OF INVENTION: ACIDS
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Wegner, Cantor, Mueller & Player
CC STREET: 1233 20th Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC ZIP: 20036-8218
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US 07/917,111
CC FILING DATE: 07-AUG-1992
CC APPLICATION NUMBER: JP 400848/1990
CC FILING DATE: 07-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 407922/1990
CC FILING DATE: 27-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 078840/1991
CC FILING DATE: 11-APR-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Player Esq., William E.
CC REGISTRATION NUMBER: 31,409
CC REFERENCE/DOCKET NUMBER: P-500-23486
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-887-0400
CC TELEFAX: 202-835-0605
CC TELEX: 440706
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 311 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: Pseudomonas
CC STRAIN: NK 003A (FERM BP-3181)
CC SEQUENCE 311 AA; 35307 MW; 480721 CN;

Query Match 53.8%; Score 50; DB 7; Length 311;
Best Local Similarity 44.4%; Pred. No. 2.46e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 286 FDFARHREP 294
:::|:|:
Qy 1 INFTRQRP 9

RESULT 14
ID US-07-917-111-5 STANDARD; PRT; 311 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 5, Application US/07917111.
XX DE Sequence 5, Application US/07917111
CC CC Patent No. 5565344

CC GENERAL INFORMATION:
CC APPLICANT: Nanba, Hirokazu
CC APPLICANT: Yamada, Yukio
CC APPLICANT: Takano, Masayuki
CC APPLICANT: Ikenaka, Yasuhiro
CC APPLICANT: Takahashi, Satomi
CC APPLICANT: Yajima, Kazuyoshi
CC TITLE OF INVENTION: PROCESS FOR PRODUCTION OF D-ALPHA-AMINO
CC TITLE OF INVENTION: ACIDS
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Wegner, Cantor, Mueller & Player
CC STREET: 1233 20th Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC ZIP: 20036-8218
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/917,111
CC FILING DATE: 19920807
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 400848/1990
CC FILING DATE: 07-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 407922/1990
CC FILING DATE: 27-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 078840/1991
CC FILING DATE: 11-APR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/JP91/01696
CC FILING DATE: 06-DEC-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Player Esq., William E.
CC REGISTRATION NUMBER: 31,409
CC REFERENCE/DOCKET NUMBER: P-500-23486
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-887-0400
CC TELEFAX: 202-835-0605
CC TELEX: 440706
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 311 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 311 AA; 35307 MW; 480721 CN;

Query Match 53.8%; Score 50; DB 6; Length 311;
Best Local Similarity 44.4%; Pred. No. 2.46e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 286 FDFARHREP 294
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Qy 1 INFTRQRP 9

RESULT 15
ID US-08-479-638-5 STANDARD; PRT; 311 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 5, Application US/08479638.
XX DE Sequence 5, Application US/08479638
CC CC Patent No. 5695968

CC GENERAL INFORMATION:
CC APPLICANT: Nanba, Hirokazu
CC APPLICANT: Yamada, Yukio
CC APPLICANT: Takano, Masayuki
CC APPLICANT: Ikenaka, Yasuhiro
CC APPLICANT: Takahashi, Satoshi
CC APPLICANT: Yajima, Kazuyoshi
CC TITLE OF INVENTION: PROCESS FOR PRODUCTION OF D-ALPHA-AMINO
CC ACIDS
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Wegner, Cantor, Mueller & Player
CC STREET: 1233 20th Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC ZIP: 20036-8218
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/479,638
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/917,111
CC FILING DATE: 07-AUG-1992
CC APPLICATION NUMBER: JP 400848/1990
CC FILING DATE: 07-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 407922/1990
CC FILING DATE: 27-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 078840/1991
CC FILING DATE: 11-APR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/JP91/01696
CC FILING DATE: 06-DEC-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Player Esq., William E.
CC REGISTRATION NUMBER: 31,409
CC REFERENCE/DOCKET NUMBER: P-500-23486
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-887-0400
CC TELEFAX: 202-835-0605
CC TELEX: 440706
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 311 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 311 AA; 35307 MW; 480721 CN;
SQ
Query Match 53.8%; Score 50; DB 7; Length 311;
Best Local Similarity 44.4%; Pred. No. 2.46e+01;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Db 286 DDFARHP 294
QY 1 INFTQRQP 9
RESULT 16
ID US-08-118-101A-4 STANDARD; PRT; 889 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 4, Application US/08118101A.
CC

CC Sequence 4, Application US/08118101A
CC Patent No. 5620892
CC GENERAL INFORMATION:
CC APPLICANT: Kurtz, Stephen E.
CC APPLICANT: Knickerbocker, Aron M.
CC APPLICANT: McCullough, John R.
CC TITLE OF INVENTION: A STRAIN OF SACHAROMYCES CEREVISIAE
CC EXPRESSING THE GENE ENCODING POTASSIUM TRANSPORTER
R MINK
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Burton Rodney
CC STREET: P.O. Box 4000
CC CITY: Princeton
CC STATE: New Jersey
CC COUNTRY: U.S.A.
CC ZIP: 08543-4000
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/118,101A
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Gaul, Timothy J.
CC REGISTRATION NUMBER: 33,111
CC REFERENCE/DOCKET NUMBER: DC27
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (609) 252-5901
CC TELEFAX: (609) 252-4526
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 889 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 889 AA; 101086 MW; 4294395 CN;
SQ
Query Match 53.8%; Score 50; DB 7; Length 889;
Best Local Similarity 60.0%; Pred. No. 2.46e+01;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 233 NFSSKROPSD 242
QY 2 NFTRQRPSE 11
RESULT 17
ID US-08-196-218-34 STANDARD; PRT; 355 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 34, Application US/08196218.
XX
CC Sequence 34, Application US/08196218
CC Patent No. 5614619
CC GENERAL INFORMATION:
CC APPLICANT: Piepersberg, Wolfgang
CC APPLICANT: Stockmann, Michael
CC APPLICANT: Taleghani, Kamiz Mansouri
CC APPLICANT: Distler, Jurgen
CC APPLICANT: Grabley, Susanne
CC APPLICANT: Sichel, Petra
CC APPLICANT: Brau, Barbara
CC TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
CC FROM Actinomycetes, Method of Isolating Them, and
CC Their TITLE OF INVENTION: Use.
CC

CC NUMBER OF SEQUENCES: 34
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
CC ADDRESSEE: Dunner
CC STREET: 1300 I Street, N.W.
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: United States
CC ZIP: 20005-3315
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/196,218
CC FILING DATE: 25-AUG-1994
CC CLASSIFICATION: 435
CC PRIORITY/DOCKET NUMBER: 02481.1372-00000
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ogden, Stasia L.
CC REGISTRATION NUMBER: 36,228
CC REFERENCE/DOCKET NUMBER: 02481.1372-00000
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-408-4000
CC TELEFAX: 202-408-4400
CC INFORMATION FOR SEQ ID NO: 34:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 355 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 355 AA; 37616 MW; 642264 CN;
SQ
Query Match 51.6%; Score 48; DB 7; Length 355;
Best Local Similarity 50.0%; Pred. No. 4.09e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Db 120 EFTRRPAAQ 129
QY 2 NTRQRPSE 11
RESULT 18
ID US-08-681-953-34 STANDARD; PRT; 355 AA.
XX xxxxxx
DT 01-JAN-1900
DE Sequence 34, Application US/08681953.
XX Sequence 34, Application US/08681953
CC Patent No. 5710032
CC GENERAL INFORMATION:
CC APPLICANT: Piepersberg, Wolfgang
CC APPLICANT: Stockmann, Michael
CC APPLICANT: Taleghani, Kamiz Mansouri
CC APPLICANT: Distler, Jurgen
CC APPLICANT: Grabley, Susanne
CC APPLICANT: Sichel, Petra
CC APPLICANT: Brau, Barbara
CC TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
CC TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them, and
Their
CC TITLE OF INVENTION: Use.
CC NUMBER OF SEQUENCES: 34
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
CC ADDRESSEE: Dunner
CC STREET: 1300 I Street, N.W.
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: United States

CC ZIP: 20005-3315
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/681,953
CC FILING DATE: 30-JUL-1996
CC CLASSIFICATION: 435
CC PRIORITY/DOCKET NUMBER: 02481.1372-00000
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Ogden, Stasia L.
CC REGISTRATION NUMBER: 36,228
CC REFERENCE/DOCKET NUMBER: 02481.1372-00000
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-408-4000
CC TELEFAX: 202-408-4400
CC INFORMATION FOR SEQ ID NO: 34:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 355 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 355 AA; 37616 MW; 642264 CN;
SQ
Query Match 51.6%; Score 48; DB 8; Length 355;
Best Local Similarity 50.0%; Pred. No. 4.09e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Db 120 EFTRRPAAQ 129
QY 2 NTRQRPSE 11
RESULT 19
ID US-07-688-352C-32 STANDARD; PRT; 369 AA.
XX xxxxxx
DT 01-JAN-1900
DE Sequence 32, Application US/07688352C.
XX Sequence 32, Application US/07688352C
CC Patent No. 5527896
CC GENERAL INFORMATION:
CC APPLICANT: Wigler, Michael H.
CC APPLICANT: Colicelli, John J.
CC TITLE OF INVENTION: Cloning by Complementation and Related
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Bicknell
CC STREET: Two First National Plaza, 20 South Clark
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/688,352C
CC FILING DATE: 19910419
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/511,715
CC FILING DATE: 20-APR-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Borun, Michael F.
CC REGISTRATION NUMBER: 25447
CC REFERENCE/DOCKET NUMBER: 27805/30197
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 346-5750
CC TELEFAX: (312) 984-9740
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 32:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 369 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 369 AA; 40466 MW; 592164 CN;

Query Match 50.5%; Score 47; DB 6; Length 369;
Best Local Similarity 60.0%; Pred. No. 5.26e+01;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 296 RQRPREDGN 305
QY 5 RQRPSEGSS 14

RESULT 20
ID PCT-US91-02714-31 STANDARD; PRT; 369 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 31, Application PC/TUS9102714.
XX
XX Sequence 31, Application PC/TUS9102714
CC GENERAL INFORMATION:
CC APPLICANT: Wigler, Michael H.
CC APPLICANT: Colicelli, John J.
CC TITLE OF INVENTION: Cloning by Complementation and Related
CC NUMBER OF SEQUENCES: 55
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Bicknell
CC STREET: Two First National Plaza, 20 South Clark
CC STREET: Street
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US91/02714
CC FILING DATE: 19910419
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/511,715
CC FILING DATE: 20-APR-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Borun, Michael F.
CC REGISTRATION NUMBER: 25447
CC REFERENCE/DOCKET NUMBER: 27805/30197
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 346-5750
CC TELEFAX: (312) 984-9740
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 31:

CC APPLICATION NUMBER: US 07/511,715
CC FILING DATE: 20-APR-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Borun, Michael F.
CC REGISTRATION NUMBER: 25447
CC REFERENCE/DOCKET NUMBER: 27805/30197
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312) 346-5750
CC TELEFAX: (312) 984-9740
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 31:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 369 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 369 AA; 40466 MW; 592164 CN;

Query Match 50.5%; Score 47; DB 10; Length 369;
Best Local Similarity 60.0%; Pred. No. 5.26e+01;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 296 RQRPREDGN 305
QY 5 RQRPSEGSS 14

RESULT 21
ID PCT-US95-05008-10 STANDARD; PRT; 527 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 10, Application PC/TUS9505008.
XX
XX Sequence 10, Application PC/TUS9505008
CC GENERAL INFORMATION:
CC APPLICANT: Sugen, Inc.
CC APPLICANT: 515 Galveston Drive
CC APPLICANT: Redwood City, California 94063-4720
CC APPLICANT: United States of America
CC APPLICANT: Wissenschaften E.V.
CC APPLICANT: Hofgarten Str. 2
CC APPLICANT: Munchen 80539
CC APPLICANT: Germany
CC TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
CC NUMBER OF SEQUENCES: 21
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: U.S.A.
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/05008
CC FILING DATE: 24-APR-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/232,545
CC FILING DATE: 22-APR-1994
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Coruzzi, Laura A.
CC REGISTRATION NUMBER: 30,742
CC REFERENCE/DOCKET NUMBER: 7683-074
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212)790-9090
CC TELEFAX: (212)869-9741
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 527 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein

SQ SEQUENCE 527 AA; 61556 MW; 1469994 CN;

Query Match 50.5%; Score 47; DB 14; Length 527;
Best Local Similarity 75.0%; Pred. No. 5.26e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 347 LNFLRQRQ 354
:|||||
QY 1 INFTRQRQ 8

RESULT 22

ID US-08-391-615-4 STANDARD; PRT: 599 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 4, Application US/08391615.

XX CC Sequence 4, Application US/08391615

XX CC Patent No. 5550054

XX CC GENERAL INFORMATION:

XX CC APPLICANT: Witte, Owen

XX CC APPLICANT: Tsukada, Satoshi

XX CC APPLICANT: Saffran, Douglas

XX CC APPLICANT: Rawlings, David

XX CC TITLE OF INVENTION: HEMATOPOIETIC RESTRICTED TYROSINE KINASE

XX CC TITLE OF INVENTION:

XX CC NUMBER OF SEQUENCES: 7

XX CC CORRESPONDENCE ADDRESS:

XX CC ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

XX CC STREET: 4 Embarcadero Center, Suite 3400

XX CC CITY: San Francisco

XX CC STATE: California

XX CC COUNTRY: USA

XX CC ZIP: 94111-4187

XX CC COMPUTER READABLE FORM:

XX CC MEDIUM TYPE: Floppy disk

XX CC COMPUTER: IBM PC compatible

XX CC OPERATING SYSTEM: PC-DOS/MS-DOS

XX CC SOFTWARE: Patentin Release #1.0, Version #1.25

XX CC CURRENT APPLICATION DATA:

XX CC APPLICATION NUMBER: US/08/391.615

XX CC FILING DATE:

XX CC CLASSIFICATION: 435

XX CC PRIOR APPLICATION DATA:

XX CC APPLICATION NUMBER: US 08/006.449

XX CC FILING DATE: 21-JAN-1993

XX CC ATTORNEY/AGENT INFORMATION:

XX CC NAME: Rowland, Bertram I

XX CC REGISTRATION NUMBER: 20,015

XX CC REFERENCE/DOCKET NUMBER: A-57583-1/BIR UCLA 232-1

XX CC TELECOMMUNICATION INFORMATION:

XX CC TELEPHONE: (415) 781-1989

XX CC TELEFAX: (415) 398-3249

XX CC TELEX: 910 277299 FHT UR

XX CC INFORMATION FOR SEQ ID NO: 4:

XX CC SEQUENCE CHARACTERISTICS:

XX CC LENGTH: 599 amino acids

XX CC TYPE: amino acid

XX CC STRANDEDNESS: single

XX CC TOPOLOGY: linear

XX CC MOLECULE TYPE: peptide

SQ SEQUENCE 599 AA; 69815 MW; 1897283 CN;

Query Match 50.5%; Score 47; DB 6; Length 599;
Best Local Similarity 75.0%; Pred. No. 5.26e+01;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 425 LNFLRQRQ 432
:|||||
QY ' ' 1 INFTRQRQ 8

RESULT 23

ID PCT-US94-06430-2 STANDARD; PRT: 249 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 2, Application PC/TUS9406430.

XX CC Sequence 2, Application PC/TUS9406430

XX CC GENERAL INFORMATION:

XX CC APPLICANT: The Upjohn Company

XX CC TITLE OF INVENTION: Lettuce Infectious Yellow Virus Genes

XX CC NUMBER OF SEQUENCES: 25

XX CC CORRESPONDENCE ADDRESS:

XX CC ADDRESSEE: The Upjohn Company, Corp. Intellectual

XX CC ADDRESSEE: Property Law

XX CC STREET: 301 Henrietta Street

XX CC CITY: Kalamazoo

XX CC STATE: Michigan

XX CC COUNTRY: USA

XX CC ZIP: 49001

XX CC COMPUTER READABLE FORM:

XX CC MEDIUM TYPE: Floppy disk

XX CC COMPUTER: IBM PC compatible

XX CC OPERATING SYSTEM: PC-DOS/MS-DOS

XX CC SOFTWARE: Patentin Release #1.0, Version #1.25

XX CC CURRENT APPLICATION DATA:

XX CC APPLICATION NUMBER: PCT/US94/06430

XX CC FILING DATE:

XX CC CLASSIFICATION:

XX CC ATTORNEY/AGENT INFORMATION:

XX CC NAME: Barnley Jr., James D.

XX CC REGISTRATION NUMBER: 33,673

XX CC TELECOMMUNICATION INFORMATION:

XX CC TELEPHONE: 616-385-5210

XX CC TELEFAX: 616-385-6897

XX CC TELEX: 224401

XX CC INFORMATION FOR SEQ ID NO: 2:

XX CC SEQUENCE CHARACTERISTICS:

XX CC LENGTH: 249 amino acids

XX CC TYPE: amino acid

XX CC STRANDEDNESS: single

XX CC TOPOLOGY: linear

SQ SEQUENCE 249 AA; 27770 MW; 295210 CN;

Query Match 49.5%; Score 46; DB 13; Length 249;
Best Local Similarity 50.0%; Pred. No. 6.75e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 82 INFMRKDPN 91
||| |::|:
QY 1 INFTRQRQ 10

RESULT 24

ID US-08-479-638-3 STANDARD; PRT: 303 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 3, Application US/08479638.

XX CC Sequence 3, Application US/08479638

XX CC Patent No. 5695968

XX CC GENERAL INFORMATION:

XX CC APPLICANT: Namba, Hirokazu

XX CC APPLICANT: Yamada, Yukio

XX CC APPLICANT: Takano, Masayuki

XX CC APPLICANT: Ikenaka, Yasuhiro

CC APPLICANT: Takahashi, Satomi
CC APPLICANT: Yajima, Kazuyoshi
CC TITLE OF INVENTION: PROCESS FOR PRODUCTION OF D-ALPHA-AMINO
CC TITLE OF INVENTION: ACIDS
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Wegner, Cantor, Mueller & Player
CC STREET: 1233 20th Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC ZIP: 20036-8218
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA: US 07/917,111
CC FILING DATE: 07-AUG-1992
CC APPLICATION NUMBER: JP 400848/1990
CC FILING DATE: 07-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 407922/1990
CC FILING DATE: 27-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 078840/1991
CC FILING DATE: 11-APR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/JP91/01696
CC FILING DATE: 06-DEC-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Player Esq., William E.
CC REGISTRATION NUMBER: 31,409
CC REFERENCE/DOCKET NUMBER: P-500-23486
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-887-0400
CC TELEFAX: 202-835-0605
CC TELEX: 440706
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 303 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: Agrobacterium radiobacter
CC STRAIN: KNK 712 (FERM BP-1900)
CC SEQUENCE 303 AA; 34154 MW; 451356 CN;

Query Match 49.5%; Score 46; DB 7; Length 303;
Best Local Similarity 55.8%; Pred. No. 6.75e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 286 FNFKQHRQP 294
:|| :|||
QY 1 INFTQRQP 9

RESULT 25
ID US-07-917-111-2 STANDARD; PRT; 303 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application US/07917111.
XX
CC Sequence 2, Application US/07917111

CC Patent No. 5565344
CC GENERAL INFORMATION:
CC APPLICANT: Nanba, Hirokazu
CC APPLICANT: Yamada, Yukio
CC APPLICANT: Takano, Masayuki
CC APPLICANT: Ikenaka, Yasuhiro
CC APPLICANT: Takahashi, Satomi
CC APPLICANT: Yajima, Kazuyoshi
CC TITLE OF INVENTION: PROCESS FOR PRODUCTION OF D-ALPHA-AMINO
CC TITLE OF INVENTION: ACIDS
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Wegner, Cantor, Mueller & Player
CC STREET: 1233 20th Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC ZIP: 20036-8218
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA: US/07/917,111
CC FILING DATE: 19920807
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA: JP 400848/1990
CC APPLICATION NUMBER: JP 400848/1990
CC FILING DATE: 07-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 407922/1990
CC FILING DATE: 27-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 078840/1991
CC FILING DATE: 11-APR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/JP91/01696
CC FILING DATE: 06-DEC-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Player Esq., William E.
CC REGISTRATION NUMBER: 31,409
CC REFERENCE/DOCKET NUMBER: P-500-23486
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-887-0400
CC TELEFAX: 202-835-0605
CC TELEX: 440706
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 303 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 303 AA; 34154 MW; 451356 CN;

Query Match 49.5%; Score 46; DB 6; Length 303;
Best Local Similarity 55.6%; Pred. No. 6.75e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 286 FNFKQHRQP 294
:|| :|||
QY 1 INFTQRQP 9

RESULT 26
ID US-07-917-111-3 STANDARD; PRT; 303 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 3, Application US/07917111.
XX
CC Sequence 3, Application US/07917111

CC Patent No. 5565344
CC GENERAL INFORMATION:
CC APPLICANT: Nanba, Hirokazu
CC APPLICANT: Yamada, Yukio
CC APPLICANT: Takano, Masayuki
CC APPLICANT: Ikenaka, Yasuhiro
CC APPLICANT: Takahashi, Satomi
CC APPLICANT: Yajima, Kazuyoshi
CC TITLE OF INVENTION: PROCESS FOR PRODUCTION OF D-ALPHA-AMINO
CC TITLE OF INVENTION: ACIDS
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Wegner, Cantor, Mueller & Player
CC STREET: 1233 20th Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC ZIP: 20036-8218
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/917,111
CC FILING DATE: 07-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 407922/1990
CC FILING DATE: 27-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 400848/1990
CC FILING DATE: 07-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 407922/1990
CC FILING DATE: 11-APR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/JP91/01696
CC FILING DATE: 06-DEC-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Player Esq., William E.
CC REGISTRATION NUMBER: 31,409
CC REFERENCE/DOCKET NUMBER: P-500-23486
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-887-0400
CC TELEFAX: 202-835-0605
CC TELEX: 440706
CC INFORMATION FOR SEQ ID NO: 3:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 303 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: Agrobacterium radiobacter
CC STRAIN: KNK 712 (FERM BP-1900)
CC SEQUENCE 303 AA; 34154 MW; 451356 CN;

Query Match 49.5%; Score 46; DB 6; Length 303;
Best Local Similarity 55.6%; Pred. No. 6.75e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 286 FNFKQHRQP 294
:|:|:|:|
Qy 1 INFTRQRP 9

RESULT 27
ID US-08-479-638-2 STANDARD; PRT; 303 AA.
XX xxxxxx
XX '01-JAN-1900
DT

XX Sequence 2, Application US/08479638.
DE Sequence 2, Application US/08479638
XX Patent No. 5695968
CC GENERAL INFORMATION:
CC APPLICANT: Nanba, Hirokazu
CC APPLICANT: Yamada, Yukio
CC APPLICANT: Takano, Masayuki
CC APPLICANT: Ikenaka, Yasuhiro
CC APPLICANT: Takahashi, Satomi
CC APPLICANT: Yajima, Kazuyoshi
CC TITLE OF INVENTION: PROCESS FOR PRODUCTION OF D-ALPHA-AMINO
CC TITLE OF INVENTION: ACIDS
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Wegner, Cantor, Mueller & Player
CC STREET: 1233 20th Street, N.W., Suite 300
CC CITY: Washington
CC STATE: D.C.
CC ZIP: 20036-8218
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/479,638
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/917,111
CC FILING DATE: 07-AUG-1992
CC APPLICATION NUMBER: JP 400848/1990
CC FILING DATE: 07-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 407922/1990
CC FILING DATE: 27-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 078840/1991
CC FILING DATE: 11-APR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/JP91/01696
CC FILING DATE: 06-DEC-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Player Esq., William E.
CC REGISTRATION NUMBER: 31,409
CC REFERENCE/DOCKET NUMBER: P-500-23486
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-887-0400
CC TELEFAX: 202-835-0605
CC TELEX: 440706
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 303 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 303 AA; 34154 MW; 451356 CN;

Query Match 49.5%; Score 46; DB 7; Length 303;
Best Local Similarity 55.8%; Pred. No. 6.75e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 286 FNFKQHRQP 294
:|:|:|:|
Qy 1 INFTRQRP 9

RESULT 28
ID US-07-977-434-6 STANDARD; PRT; 830 AA.
XX xxxxxx
AC

XX 01-JAN-1900
DT Sequence 6, Application US/07977434.
DE Sequence 6, Application US/07977434
XX Patent No. 5466591
CC GENERAL INFORMATION:
CC APPLICANT: Gelfand, David H.
CC APPLICANT: Abramson, Richard D.
CC TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
CC TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
CC NUMBER OF SEQUENCES: 38
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Hoffmann-La Roche Inc.
CC STREET: 340 Kingsland Street
CC CITY: Nutley
CC STATE: New Jersey
CC ZIP: 07110-1199
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: 7
CC SOFTWARE: WordPerfect 2.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/977,434
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 590,490
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 590,466
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 523,394
CC FILING DATE: 15-MAY-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 143,441
CC FILING DATE: 12-JAN-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 063,509
CC FILING DATE: 17-JUN-1987
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 590,213
CC FILING DATE: 22-AUG-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 746,121
CC FILING DATE: 15-AUG-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: WO PCT/US90/07641
CC FILING DATE: 21-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 585,471
CC FILING DATE: 20-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 455,611
CC FILING DATE: 22-DEC-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 609,157
CC FILING DATE: 02-NOV-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 557,517
CC FILING DATE: 24-JUL-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Luann Cserr
CC REGISTRATION NUMBER: 31,822
CC REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (510) 814-2972

CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 830 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 830 AA; 93347 MW; 3328578 CN;
Query Match 49.5%; Score 46; DB 5; Length 830;
Best Local Similarity 33.3%; Pred. No. 6.75e+01;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Db 254 VDFAKREP 262
QY :::::|:|
1 INFTRQRP 9
RESULT 29
ID PCT-US91-07035-6 STANDARD; PRT; 830 AA.
XX
AC xxxxxx
XX 01-JAN-1900
DT Sequence 6, Application PC/TUS9107035.
DE
XX Sequence 6, Application PC/TUS9107035
CC GENERAL INFORMATION:
CC APPLICANT: Gelfand, David H.
CC APPLICANT: Abramson, Richard D.
CC TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
CC TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
CC NUMBER OF SEQUENCES: 38
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Cetus Corporation
CC STREET: 1400 Fifty-third Street
CC CITY: Emeryville
CC STATE: California
CC ZIP: 94608
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Wordperfect 5.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US91/07035
CC FILING DATE: 19910930
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 590,490
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 590,466
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 590,213
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 523,394
CC FILING DATE: 15-MAY-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 143,441
CC FILING DATE: 12-JAN-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 063,509
CC FILING DATE: 17-JUN-1987
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,241
CC FILING DATE: 22-AUG-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 746,121
CC FILING DATE: 15-AUG-1991
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: WO PCT/US90/07641
CC FILING DATE: 21-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 585,471
CC FILING DATE: 20-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 455,611
CC FILING DATE: 22-DEC-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 609,157
CC FILING DATE: 02-NOV-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 557,517
CC FILING DATE: 24-JUL-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Sias Ph.D, Stacey R.
CC REGISTRATION NUMBER: 32,630
CC REFERENCE/DOCKET NUMBER: Case No. 2580
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-420-3300
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 830 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 830 AA; 93347 MW; 3328578 CN;

Query Match 49.5%; Score 46; DB 10; Length 830;
Best Local Similarity 33.3%; Pred. No. 6.75e+01;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 254 VDFAKRREP 262
QY 1 INFTRQRP 9

RESULT 30
ID US-07-977-434-2 STANDARD; PRT; 832 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application US/07977434.
XX
CC Sequence 2, Application US/07977434
CC Patent No. 5466591
CC GENERAL INFORMATION:
CC APPLICANT: Gelfand, David H.
CC APPLICANT: Abramson, Richard D.
CC TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
CC TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
CC NUMBER OF SEQUENCES: 38
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Hoffmann-La Roche Inc.
CC STREET: 340 Kingsland Street
CC CITY: Nutley
CC STATE: New Jersey
CC ZIP: 07110-1199
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: 7
CC SOFTWARE: WordPerfect 2.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/977,434
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION NUMBER: US 590,490
CC FILING DATE: 28-SEP-1990
CC ** PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 590,466
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 590,213
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 523,394
CC FILING DATE: 15-MAY-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 143,441
CC FILING DATE: 12-JAN-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 063,509
CC FILING DATE: 17-JUN-1987
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,241
CC FILING DATE: 22-AUG-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 746,121
CC FILING DATE: 15-AUG-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: WO PCT/US90/07641
CC FILING DATE: 21-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 585,471
CC FILING DATE: 20-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 455,611
CC FILING DATE: 22-DEC-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 609,157
CC FILING DATE: 02-NOV-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 557,517
CC FILING DATE: 24-JUL-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Luann Cserr
CC REGISTRATION NUMBER: 31,822
CC REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (510) 814-2972
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 832 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 832 AA; 93909 MW; 3296737 CN;

Query Match 49.5%; Score 46; DB 5; Length 832;
Best Local Similarity 33.3%; Pred. No. 6.75e+01;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 256 VDFAKRREP 264
QY 1 INFTRQRP 9

RESULT 31
ID US-08-156-020-6 STANDARD; PRT; 832 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 6, Application US/08156020.
XX
CC Sequence 6, Application US/08156020
CC Patent No. 5474920
CC GENERAL INFORMATION:
CC APPLICANT: Moses M.D., Robb E.
CC TITLE OF INVENTION: Modified Thermo-Resistant DNA
CC ** TITLE OF INVENTION: Polymerases

CC NUMBER OF SEQUENCES: 15
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Allegretti & Witcoff
CC STREET: 10 South Wacker Drive
CC CITY: Chicago
CC STATE: IL
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Macintosh
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/156,020
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Greenfield Ph.D., Michael S.
CC REGISTRATION NUMBER: 37,142
CC REFERENCE/DOCKET NUMBER: 93,413
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312)715-1000
CC TELEFAX: (312)715-1234
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 832 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 832 AA; 93806 MW; 3296848 CN;
Query Match 49.5%; Score 46; DB 5; Length 832;
Best Local Similarity 33.3%; Pred. No. 6.75e+01;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Db 256 VDFAKRREP 264
QY 1 INFTQRQP 9
RESULT 32
ID US-08-156-020-8 STANDARD; PRT; 832 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 8, Application US/08156020.
XX Sequence 8, Application US/08156020
CC Patent No. 5474920
CC GENERAL INFORMATION:
CC APPLICANT: Moses M.D., Robb E.
CC TITLE OF INVENTION: Modified Thermo-Resistant DNA
CC TITLE OF INVENTION: Polymerases
CC NUMBER OF SEQUENCES: 15
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Allegretti & Witcoff
CC STREET: 10 South Wacker Drive
CC CITY: Chicago
CC STATE: IL
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Macintosh
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/156,020
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Greenfield Ph.D., Michael S.
CC REGISTRATION NUMBER: 37,142
CC REFERENCE/DOCKET NUMBER: 93,413
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312)715-1000
CC TELEFAX: (312)715-1234
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 832 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 832 AA; 93859 MW; 3296773 CN;
Query Match 49.5%; Score 46; DB 5; Length 832;
Best Local Similarity 33.3%; Pred. No. 6.75e+01;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

CC ATTORNEY/AGENT INFORMATION:
CC NAME: Greenfield Ph.D., Michael S.
CC REGISTRATION NUMBER: 37,142
CC REFERENCE/DOCKET NUMBER: 93,413
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312)715-1000
CC TELEFAX: (312)715-1234
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 832 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 832 AA; 93840 MW; 3297291 CN;
Query Match 49.5%; Score 46; DB 5; Length 832;
Best Local Similarity 33.3%; Pred. No. 6.75e+01;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Db 256 VDFAKRREP 264
QY 1 INFTQRQP 9
RESULT 33
ID US-08-156-020-4 STANDARD; PRT; 832 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 4, Application US/08156020.
XX Sequence 4, Application US/08156020
CC Patent No. 5474920
CC GENERAL INFORMATION:
CC APPLICANT: Moses M.D., Robb E.
CC TITLE OF INVENTION: Modified Thermo-Resistant DNA
CC TITLE OF INVENTION: Polymerases
CC NUMBER OF SEQUENCES: 15
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Allegretti & Witcoff
CC STREET: 10 South Wacker Drive
CC CITY: Chicago
CC STATE: IL
CC COUNTRY: USA
CC ZIP: 60606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Macintosh
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/156,020
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Greenfield Ph.D., Michael S.
CC REGISTRATION NUMBER: 37,142
CC REFERENCE/DOCKET NUMBER: 93,413
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (312)715-1000
CC TELEFAX: (312)715-1234
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 832 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 832 AA; 93859 MW; 3296773 CN;
Query Match 49.5%; Score 46; DB 5; Length 832;
Best Local Similarity 33.3%; Pred. No. 6.75e+01;

Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 256 VDFAKRREP 264
:|:|:|:|
QY 1 INFTRQRP 9

RESULT 34

ID US-08-073-384C-4 STANDARD; PRT; 832 AA.

XX AC xxxxxx

DT 01-JAN-1900

XX Sequence 4, Application US/08073384C.

CC Sequence 4, Application US/08073384C

CC Patent No. 5541311

CC GENERAL INFORMATION:

CC APPLICANT: Dahlberg, James E.

CC APPLICANT: Lyamichev, Victor I.

CC TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA

CC NUMBER OF SEQUENCES: 29

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL

CC STREET: 220 Montgomery Street, Suite 2200

CC CITY: San Francisco

CC STATE: California

CC COUNTRY: United States of America

CC ZIP: 94104

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/073,384C

CC FILING DATE: 04-JUN-1993

CC CLASSIFICATION: 536

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/986,330

CC FILING DATE: 07-DEC-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Carroll, Peter G.

CC REGISTRATION NUMBER: 32,837

CC REFERENCE/DOCKET NUMBER: FORS-00613

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 415/705-8410

CC TELEFAX: 415/397-8338

CC INFORMATION FOR SEQ ID NO: 4:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 832 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 832 AA; 93909 MW; 3296737 CN;

Query Match 49.5%; Score 46; DB 6; Length 832;
Best Local Similarity 33.3%; Pred. No. 6.75e+01;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 256 VDFAKRREP 264

:|:|:|:|

QY 1 INFTRQRP 9

RESULT 35

ID US-08-254-359A-4 STANDARD; PRT; 832 AA.

XX AC 'xxxxx'

XX 01-JAN-1900

DE Sequence 4, Application US/08254359A.

XX Sequence 4, Application US/08254359A

CC Patent No. 5614402

CC GENERAL INFORMATION:

CC APPLICANT: DAHLBERG, JAMES E.

CC APPLICANT: LYAMICHEV, VICTOR I.

CC APPLICANT: BROW, MARY ANN D.

CC TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE

CC NUMBER OF SEQUENCES: 40

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL

CC STREET: 220 MONTGOMERY STREET, SUITE 2200

CC CITY: SAN FRANCISCO

CC STATE: CALIFORNIA

CC COUNTRY: UNITED STATES OF AMERICA

CC ZIP: 94104

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/254,359A

CC FILING DATE:

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/073,384

CC FILING DATE: 06-JUN-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/986,330

CC FILING DATE: 07-DEC-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: CARROLL, PETER G.

CC REGISTRATION NUMBER: 32,837

CC REFERENCE/DOCKET NUMBER: FORS-01000

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 705-8410

CC TELEFAX: (415) 397-8338

CC INFORMATION FOR SEQ ID NO: 4:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 832 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 832 AA; 93909 MW; 3296737 CN;

Query Match 49.5%; Score 46; DB 7; Length 832;
Best Local Similarity 33.3%; Pred. No. 6.75e+01;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 256 VDFAKRREP 264

:|:|:|:|

QY 1 INFTRQRP 9

Search completed: Tue Apr 7 08:43:40 1998
Job time : 10 secs.

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:39:04 1998; MasPar time 2.05 Seconds
115.783 Million cell updates/sec
Tabular output not generated.

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Title:
Description:
Perfect Score:
Sequence:

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Scoring table:  PAM 150
                  Gap 15

Searched:      111725 seqs, 16919825 residues

Post-processing: Minimum Match 0%
                  Listing first 100 summaries

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Database: a-geneseq30
1:a-geneseq1

Statistics: Mean 20.114: Variance 30.066: scale 0.669

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match	Mismatch					
1	93	100.0	40	1	R80618		Immunogenic peptide of	1.92e-09
2	93	100.0	335	1	R70909		Human melanoma antigen	1.92e-09
3	57	61.3	935	1	R50092		Humanised anti-CEA sFv	1.46e-01
4	55	59.1	122	1	R81863		Sequence encoded by IA	3.62e-01
5	53	57.0	35	1	R65121		MAGE 1 immunogenic pep	8.86e-01
6	53	57.0	122	1	R12258		HIV-1 strain OVI open	8.86e-01
7	53	57.0	368	1	R95034		TGF-a-DETA-DGAL4 multi	8.86e-01
8	53	57.0	440	1	R36807		Pseudomonas exotoxin d	8.86e-01
9	53	57.0	440	1	R32455		PE amino acids 2-414.	8.86e-01
10	53	57.0	445	1	R70754		PE40AB protein compris	8.86e-01
11	53	57.0	446	1	R20200		TGF-alpha-PE40Ab.	8.86e-01
12	53	57.0	446	1	R06993		PE40Ab protein compris	8.86e-01
13	53	57.0	446	1	R06449		TGF-alpha-PE40-Ab mod	8.86e-01
14	53	57.0	446	1	W19869		TGF-57-PE40 encoded by	8.86e-01
15	53	57.0	446	1	R06447		TGF-57-pseudomonas exo	8.86e-01
16	53	57.0	446	1	W19871		TGF-alpha-PE40Ab.	8.86e-01
17	53	57.0	447	1	R95055		II-2-DETA-DGAL4 multidi	8.86e-01
18	53	57.0	452	1	R32454		PE(2-414)-Ma(57-68) hy	8.86e-01
19	53	57.0	452	1	R36806		PE domains I and II fu	8.86e-01
20	53	57.0	460	1	R99581		Heregulin/Pseudomonas	8.86e-01
21	53	57.0	488	1	R91735		Heregulin-PE40 HAR-TX	8.86e-01
22	53	57.0	489	1	W05137		TGF alpha-ETA fusion p	8.86e-01
23	53	57.0	522	1	R04934		Immunotoxin hybrid of	8.86e-01

97 46 49.5 329 1 R46250 Heat-stable carbamylas 1.77e+01
 98 46 49.5 329 1 R46269 Improved Heat-stable c 1.77e+01
 99 46 49.5 329 1 R46249 Heat-stable carbamylas 1.77e+01
 100 46 49.5 329 1 R46266 Improved Heat-stable c 1.77e+01

ALIGNMENTS

RESULT 1
 ID R80618 standard; Protein; 14 AA.
 AC R80618;
 DE 28-FEB-1996 (first entry)
 DT Immunogenic peptide of tumour rejection antigen (MAGE-1).
 KW Tumour rejection antigen; MAGE-1; monoclonal antibody; Mab;
 KW diagnosis; immunoassay; cancer; immunogen; antisera.
 OS Homo sapiens.
 PN W09520974-A1.
 PD 10-AUG-1995.
 PF 05-JAN-1995; U00095.
 PR 01-FEB-1994; US-190411.
 PA (LUDW) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.
 PI Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;
 PI Stockert E, Van der bruggen P;
 WPI: 95-283606/37.
 DT New monoclonal antibody binding specifically to MAGE-1 - useful for
 diagnosis and monitoring of cancer, also new hybridomas, recombinant
 MAGE-1 and immunogenic peptide(s)
 FT Claim 12; Page 20; 33pp; English.
 CC A monoclonal antibody directed against the tumour rejection antigen
 (MAGE-1) can be used to detect MAGE-1 in samples by standard
 CC immunoassay methods for diagnosis and monitoring of cancer etc. The
 CC monoclonal antibody is designated MA454 and is produced by the
 CC hybridoma deposited as ATCC HB11540. The monoclonal antibody is
 CC specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
 CC Peptide fragments of MAGE-1 (See R80618-20) may be useful as
 CC immunogens for production of the monoclonal antibody and antisera.
 SQ Sequence 14 AA;

Query Match 100.0%; Score 93; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.92e-09;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 INFTRQRPSEGS 40
 |||||
 QY 1 INFTRQRPSEGS 14

RESULT 2
 ID R70909 standard; Protein; 309 AA.
 AC R70909;
 DE 09-OCT-1995 (first entry)
 DT Human melanoma antigen MAGE-1.
 DE Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;
 KW HLA-restricted cytotoxic T-lymphocyte activity.
 OS Homo sapiens.
 PN W09504542-A.
 PD 16-FEB-1995.
 PF 02-AUG-1994; U08721.
 PR 06-AUG-1993; US-103623.
 PA (CYTE-) CYTEL CORP.
 PI Fikes JD, Livingston BD, Sette AD, Sidney JC;
 DR WPI: 95-090681/12.
 DR N-PSDB; Q85435.
 PT Human melanoma antigen, MAGE-1, peptide(s) - useful for
 stimulating immune response against melanoma
 PS Example 1; Fig 1; 59pp; English.
 CC Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used
 CC to produce the C-terminal MAGE-1 peptides described in R70915 to
 CC R70969. These peptides are useful for defining epitopes that
 CC engender a HLA-restricted cytotoxic lymphocyte activity against
 CC MAGE-1 antigens. Compsns. containing these peptides can be

CC administered, as a vaccine to patients susceptible to MAGE
 CC associated tumours, e.g. melanomas.
 SQ Sequence 309 AA;

Query Match 100.0%; Score 93; DB 1; Length 335;
 Best Local Similarity 100.0%; Pred. No. 1.92e-09;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 94 INFTRQRPSEGS 107
 |||||
 QY 1 INFTRQRPSEGS 14

RESULT 3
 ID R50092 standard; Protein; 909 AA.
 AC R50092;
 DT 26-OCT-1994 (first entry)
 DE Humanised anti-CEA sfv fragment-human beta-glucuronidase fusion
 DE protein.
 KW Carcinoembryonic antigen; single chain variable region; sfv fragment;
 KW fusion gene; cancer treatment; targetted drug delivery; tumour.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal_peptide
 FT Protein 20..909
 FT /label= fusion.protein
 FT /note= "humanised anti-CEA sfv fragment fused to
 human beta-glucuronidase"
 PN EP-590530-A.
 PD 06-APR-1994.
 PF 24-SEP-1993; 115418.
 PR 02-OCT-1992; DE-233152.
 PA (BEHW) BEHRINGWERKE AG.
 PA Bosslet K, Czech J, Gehrmann M, Seemann G;
 DR WPI: 94-111012/14.
 DR N-PSDB; Q58896.
 PT New fusion protein contg. enzyme for prodrug activation - coupled
 PT to antigen binding component, esp. sfv antibody fragment, partic.
 PT for treatment of tumours
 PS Claim 13; Page 12-15; 35pp; German.
 CC The sequence R50092 comprises a humanised sfv-fragment against CEA
 CC fused to a human beta-glucuronidase. The fusion protein is
 CC useful for targetting beta-glucuronidase to cancer cells expressing
 CC CEA, where the enzyme is able to convert a prodrug into its active
 CC form. Any fusion protein not bound to tumour can be removed by
 CC internalisation via the mannose-6-phosphate and galactose receptors.
 SQ Sequence 909 AA;

Query Match 61.3%; Score 57; DB 1; Length 935;
 Best Local Similarity 63.6%; Pred. No. 1.46e-01;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 893 FTRQRPKSA 903
 |||||
 QY 3 FTRQRPSEGS 13

RESULT 4
 ID P81863 standard; protein; 96 AA.
 AC P81863;
 DT 16-DEC-1990 (first entry)
 DE Sequence encoded by LAV MA L R gene
 KW HIV; HTLV III; AIDS; diagnosis; vaccine; probe; hybridisation.
 OS Lymphadenopathy associated virus MA L.
 PN W08707906-A.
 PD 30-DEC-1987.
 PF 22-JUN-1987; E00326.
 PR 23-JUN-1986; EP-401380.
 PA (INSP) Inst Pasteur.
 PI Alizon M, Sonigo P, Wain-Hobson S, Montagnier L;
 DR WPI: 88-014396/02.
 DR N-PSDB; N80437.

PT New variants of lymphadenopathy associated virus (LAV) -
 PT used for prodn. of DNA, antigens and antibodies used in
 PT diagnosis of AIDS and pre-AIDS

PS Claim 8; Fig 8A-8I; 72pp; English.
 CC LAV EL I (N80436) and LAV MA L (N80437) were isolated from the peripheral
 CC blood lymphocytes of patients. Different AIDS virus isolates concerned
 CC are designated by 3 letters of the patients name. Stable probes including
 CC the DNA sequences can be used for detection of the new LAV viruses or
 CC related viruses or DNA proviruses in eg. biological samples. The proteins
 CC or peptides can be used for detection of antibodies induced in vivo and
 CC present in biological fluids. The DNA can also be used for the expression
 CC of LAV viral antigens for the prodn. of a vaccine against LAV. The
 CC polypeptides can also be used for the prodn. of antibodies for the
 CC detection of proteins related to the LAV viruses, partic. for diagnosis
 CC of AIDS or pre-AIDS.
 SQ Sequence 96 AA;

Query Match 59.1%; Score 55; DB 1; Length 122;
 Best Local Similarity 57.1%; Pred. No. 3.62e-01;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 107 IGITRRRRNGSS 120
 | :||||: :|||
 QY 1 INFTRQRPSEGS 14

RESULT 5

ID R65121 standard; peptide: 9 AA.

AC R65121;
 DT 09-OCT-1995 (first entry)
 DE MAGE 1 immunogenic peptide 66-74.
 KW MAGE 1; immunogenic peptide 66-74; cytotoxic C cells;
 KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
 KW fungal infections; tuberculosis; hepatitis.
 OS Homo sapiens.

PN WO9504817-A.
 PD 16-FEB-1995.
 PF 01-AUG-1994; U08672.
 PR 06-AUG-1993; US-103401.
 PA (CYTE-) CYTEL CORP.
 PI Cells E, Kubo R, Serra H, Tsai V, Wentworth P;
 DR WPI: 95-090895/12.

PT In vitro activation of cytotoxic T cells for selected killing of
 PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
 PT incubating them with antigen presenting cells loaded with
 PT appropriate immunogenic peptide

PS Example 3; Page 35; 53pp; English.
 CC R65109-R65145 are immunogenic peptides, they are used in a new
 CC method for the in vitro activation of cytotoxic T cells (CTC).
 CC This is achieved by incubating the CTCs with antigen presenting
 CC cells loaded with an appropriate immunogenic peptide (e.g. one
 CC of the above peptides). By selecting the peptides used the
 CC following diseases and infections can be treated; cancer, AIDS,
 CC hepatitis, other viral and bacterial infections, malaria and
 CC tuberculosis.
 SQ Sequence 9 AA;

Query Match 57.0%; Score 53; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 8.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 INFTRQR 35
 | :|||||
 QY 1 INFTRQR 7

RESULT 6

ID R12258 standard; protein: 96 AA.

AC R12258;
 DT 20-AUG-1991 (first entry)
 DE HIV-1 strain OII open reading frame (ORF) R protein.
 KW HIV-1; AIDS; retroviruses.
 OS Homo sapiens.

PN US5019510-A.
 PD 28-MAY-1991.
 PF 28-OCT-1987; 113655.
 PR 28-OCT-1987; US-113655.
 PA (INSP) INST PASTEUR.
 PI Main-Hobson S, Huet T, Delaporte E, Brun-Vezinet F;
 DR WPI: 91-177518/24.
 PT Purified human retrovirus - is mutant of HIV-1 having
 PT characteristics of HIV-1 OII, used in diagnosis of HIV infection
 PS Disclosure; fig 4; 23pp; English.
 CC This sequence constitutes the ORF R protein constituent of a new
 CC strain of HIV-1 retrovirus, OII. This mutant retroviral strain is
 CC useful in an assay for diagnosing HIV infection. See also Q11943
 CC (OII nucleotide sequence), R12255-57 and R12259-62 (other HIV OII
 CC constituent proteins).
 SQ Sequence 96 AA;

Query Match 57.0%; Score 53; DB 1; Length 122;
 Best Local Similarity 50.0%; Pred. No. 8.86e-01;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 107 IGITRRRRNGAS 120
 | :||||: :|||
 QY 1 INFTRQRPSEGS 14

RESULT 7

ID R95054 standard; protein: 342 AA.

AC R95054;
 DT 19-AUG-1996 (first entry)
 DE TGF-a-DETA-DGALA multidomain protein.
 KW Nucleic acid transfer system; gene transfer; gene therapy;
 KW cell targeting; multidomain protein; vector; cancer;
 KW exotoxin A; DETA; ompa; signal peptide; GAL4; TGF-a;
 KW transforming growth factor-alpha.
 OS Chimeric synthetic;
 OS Chimeric Homo sapiens;
 OS Chimeric Pseudomonas aeruginosa;
 OS Chimeric Saccharomyces cerevisiae.

FH Key Location/Qualifiers

FT Peptide 1..8
 FT /Label= FLAG_epitope
 FT Peptide 9..12
 FT /Label= Spacer
 FT Domain 13..62
 FT /Label= TGF-a
 FT /note= "amino acids 1-50 of human TGF-a"
 FT Peptide 63..65
 FT /Label= Spacer
 FT Peptide 66..71
 FT /Label= Hexa-histidine
 FT Peptide 72
 FT /Label= Spacer
 FT Domain 73..187
 FT /Label= ETA
 FT /note= "amino acids 252-366 of ETA"
 FT Peptide 188
 FT /Label= Spacer
 FT Domain 189..334
 FT /Label= GAL4
 FT /note= "amino acids 2-147 of yeast GAL4"
 FT Peptide 335..342
 FT /Label= Spacer
 FT /note= "endoplasmic reticulum retention signal"
 PN WO9613599-A1.

PD 09-MAY-1996.

PF 31-OCT-1995; E04270.

PR 01-NOV-1994; EP-810627.

PA (WELS/) WELS W.

PI Fominaya J, Wels W;

DR WPI: 96-239505/24.

DR N-PSDB; T29409.

PT Nucleic acid transfer system for gene therapy, e.g. against cancer

PT - includes toxin translocation domain to target nucleic acid to
 PT specific cell
 PS Claim 7; Page 64-65; 106pp; English.
 CC A multidomain protein (R95054) has a FLAG epitope, a portion
 CC of human transforming growth factor-alpha (TGF-a) that acts as a
 CC ligand domain, a non-cytotoxic portion of Pseudomonas aeruginosa
 CC exotoxin A acting as a translocation domain and the DNA
 CC binding domain of yeast GAL4. It is the product of a fusion
 CC gene (T29410) and can be expressed in E. coli (resulting in
 CC removal of an ompA signal peptide). It is used with an effector
 CC nucleic acid that comprises e.g. a gene to be delivered to
 CC a cell and a cognate structure for the GAL4 DNA binding domain.
 CC This provides a novel means of nucleic acid transfer, suitable
 CC for gene therapy.
 SQ Sequence 342 AA;

Query Match 57.0%; Score 53; DB 1; Length 368;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 119 FTRHRQP 125
 |||:||||
 Qy 3 FTRQRQP 9

RESULT 8
 ID R36807 standard; Protein; 414 AA.
 AC R36807;
 DT 25-AUG-1993 (first entry)
 DE Pseudomonas exotoxin domains I and II encoded by pVC-PEBT.
 DE Vaccine; cytotoxic T lymphocyte; CTL; Influenza A virus;
 KW matrix protein; Ma; Pseudomonas exotoxin; cell recognition domain;
 KW translocation domain; anti-viral agent.
 OS Pseudomonas aeruginosa.
 PN EP-541335-A.
 PD 12-MAY-1993.
 PF 04-NOV-1992; 310067.
 PR 08-NOV-1991; US-792507.
 PA (MERI) MERCK & CO INC.
 PI Donnelly JJ, Friedman A, Howe LA, Liu MA, Marshall MS;
 PI Montgomery DL, Oliff AA, Shi X, Ulmer J;
 DR WPI; 93-154266/19.
 DR N-PSDB; Q41715.
 PT Recombinant DNA encoding bacterial toxin-antigen conjugates - are
 PT useful as vaccines against viral infections, tumours and
 PT parasites
 PS Example 5; Page 30-32; 81pp; English.
 CC Control plasmid pVC-PEBT encodes a T7 promoter-driven gene fusion
 CC consisting of PE amino acids 2-414 followed by termination codons,
 CC instead of by at least part of the Influenza A virus Matrix
 CC protein (as in e.g. Q41714).
 SQ Sequence 414 AA;

Query Match 57.0%; Score 53; DB 1; Length 440;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 299 FTRHRQP 305
 |||:||||
 Qy 3 FTRQRQP 9

RESULT 9
 ID R32455 standard; Protein; 414 AA.
 AC R32455;
 DT 20-JUL-1993 (first entry)
 DE PE amino acids 2-414.
 DE PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein;
 KW T7 polymerase; fusion; hybrid; pVC-PEBT; pVC-PEM1-2.
 OS Synthetic.
 PN EP-532090-A.
 PD 17-MAR-1993.
 PD 02-SEP-1992; 202660.

PR 09-SEP-1991; US-756249.
 PA (MERI) MERCK & CO INC.
 PI Donnelly JJ, Friedman A, Howe LA, Liu MA, Marshall MS;
 PI Montgomery DL, Oliff AA, Shi X, Ulmer J;
 DR WPI; 93-087107/11.
 DR N-PSDB; Q371108.
 PT Bacterial toxin-antigen protein conjugates - to elicit cytotoxic
 PT T-lymphocyte immune response, used for preventing viral
 PT infections, e.g. by influenza virus, HIV and human
 PT papilloma virus
 PS Disclosure; Page 33-35; 85pp; English.
 CC Example 5 describes the construction of pVC-PEBT.
 CC A control plasmid was constructed which encodes a T7 polymerase
 CC driven gene fusion consisting of PE amino acids 2 to 414 followed by
 CC termination codons. pVC-PEM1-2 was digested with SacII and ligated to
 CC remove the M1 sequence. The vector was gel purified and ligated to
 CC an oligonucleotide that builds back PE codon no. 414 followed by
 CC termination signals shown in Q37893. The resulting construction
 CC was named pVC-PEBT (Q371108).
 SQ Sequence 414 AA;

Query Match 57.0%; Score 53; DB 1; Length 440;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 299 FTRHRQP 305
 |||:||||
 Qy 3 FTRQRQP 9

RESULT 10
 ID R07054 standard; Protein; 419 AA.
 AC R07054;
 DT 18-JAN-1991 (first entry)
 DE PE40AB protein comprising a portion of the Pseudomonas exotoxin A.
 DE TGF-alpha-PE40; PE40ab; tumour; epidermal growth factor; EGF;
 KW transforming growth factor-alpha; TGF-alpha.
 OS Pseudomonas sp.
 PN EP-389043-A.
 PD 26-SEP-1990.
 PF 15-MAR-1990; 200613.
 PR 22-MAR-1989; US-327214.
 PA (MERI) MERCK & CO INC.
 PI Riemen MW, Stirdivant SM;
 DR WPI; 90-291988/39.
 DR N-PSDB; Q06127.
 PT Modified PE40 by substitution with other amino acids for cysteine -
 PT improving specificity of targeting agent for tumour cells.
 PS Disclosure; Table 3; 21pp; English.
 CC By replacing cysteine residues at positions 265 and 287 and/or 372
 CC and 379, chemical ambiguities may be eliminated, and targeting
 CC specificity for targeted agents of tumour cells eg. EGF or TGF-alpha
 CC may be improved.
 SQ Sequence 419 AA;

Query Match 57.0%; Score 53; DB 1; Length 445;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 105 FTRHRQP 111
 |||:||||
 Qy 3 FTRQRQP 9

RESULT 11
 ID R20200 standard; Protein; 420 AA.
 AC R20200;
 DT 16-APR-1992 (first entry)
 DE TGF-alpha-PE40AB.
 DE Pseudomonas exotoxin; bladder; mutant; target; receptor binding.
 KW Key Location/Qualifiers
 FT Region 5, 54
 FT /label= TGFalpha1-50

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FT Region 59. 420
FT /label= PE252-613
FT Misc_difference 176
FT /note= "Ser -> Thr"
FT /misc_difference 179
FT /note= "Cys -> Ala"
FT Misc_difference 186
FT /note= "Cys -> Ala"
PN EP-467536-A.
PD 22-JAN-1992. 305582.
PF 20-JUN-1991. 305582.
PR 21-JUN-1990; US-542281.
PR 14-MAR-1991; US-669269.
PA (MERI ) MERCK & CO INC.
PI Ahern J, Heimbrook DC, Oliff AI, Stirdivant SM;
DR WPI; 92-026359/04.
PT Treatment of bladder cancer using hybrid protein - comprising
PT cell targeting agent e.g. EGF that binds to EGF receptor on
PT tumour cells and PE40 cell toxin
PS Disclosure: Page 18-19; 34pp; English.
CC The modified PE40 domains of the hybrid proteins have two or four of
CC the Cys residues (designated Cys265, Cys287, Cys372 and Cys372)
CC substituted with neutral amino acids, e.g. Gly, Ala, or Phe.
CC TGF-alpha-PE40ab (R20199) has Cys265 and Cys287 replaced;
CC TGF-alpha-PE40ab (R20200) has Cys372 and Cys379 replaced; and
CC TGF-alpha-PE40ab (R20201) has all four replaced.
CC The modified hybrid proteins were produced in E.coli transformed
CC with TAC expression vectors. Site specific mutations were introduced
CC to the unmodified TGF-alpha-PE40 gene cloned in pTACTGF57-PE40.
CC The mol. efficiently targets receptors on human bladder tumour cells
CC (the modified PE40 domain has improved receptor binding) and is
CC used for selectively killing bladder tumour cells.
SQ Sequence 420 AA;

Query Match 57.0%; Score 53; DB 1; Length 446;
Best Local Similarity 85.7%; Pred. No. 8.86e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 105 FTRHRQP 111
QY 3 FTRQRP 9

RESULT 12
ID R06993 standard; protein; 420 AA.
AC R06993;
DE PE40ab protein comprising a portion of the Pseudomonas exotoxin A
DE lacking cysteine residues at 372 and 379.
KW TGF-alpha-PE40; PE40ab; tumour; epidermal growth factor; EGF;
KW transforming growth factor-alpha; TGF-alpha.
OS Pseudomonas sp.
PN EP-389043-A.
PD 26-SEP-1990.
PF 15-MAR-1990; 200613.
PR 22-MAR-1989; US-327214.
PA (MERI ) MERCK & CO INC.
PI Riemen NW, Stirdivant SM;
DR WPI; 90-291988/39.
PT Modified PE40 by substitution with other amino acids for cysteine -
PT improving specificity of targeting agent for tumour cells.
PS Disclosure: Table 5; 21pp; English.
CC By replacing cysteine residues at positions 265 and 287 and/or 372
CC and 379, chemical ambiguities may be eliminated, and targeting
CC specificity for targeted agents of tumour cells eg. EGF or TGF-alpha
CC may be improved.
CC See also Q06127.
SQ Sequence 420 AA;

Query Match 57.0%; Score 53; DB 1; Length 446;
Best Local Similarity 85.7%; Pred. No. 8.86e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 105 FTRHRQP 111
QY 3 FTRQRP 9

RESULT 13
ID R06449 standard; protein; 420 AA.
AC R06449;
DE TGF-alpha-PE40-Ab modified pseudomonas exotoxin hybrid protein.
DE Pseudomonas exotoxin-40 (PE40); protein targeting agent;
KW psoriasis treatment; anti-tumour agent; TGF-alpha-PE40-Ab;
FH Key Location/Qualifiers
FT Region 1. 54
FT /label= residues -4 to +50 of TGF-alpha
FT Region 58. 420
FT /label= residues +252 to +613 of PE
FT /note= residues 369, 372 and 379 are modified"
PN EP-383599-A.
PD 22-AUG-1990.
PF 15-FEB-1990; 301639.
PR 17-FEB-1989; US-312540.
PR 03-AUG-1989; US-389092.
PR 21-DEC-1989; US-449187.
PA (MERI ) MERCK & CO INC.
PI Oliff A, Jones DD, Edwards GM;.
DR WPI; 90-255832/34.
PT Modified pseudomonas exotoxin hybrid proteins - has at least 2
PT cysteine residues replaced or deleted to improve binding to
PT receptors.
PS Example; Table 5; 20pp; English.
CC Modified pseudomonas exotoxin (PE40) linked to
CC 5' portion of transforming growth factor (TGF)-alpha as a targeting
CC agent. Three site-specific mutations have been introduced c.f wild-
CC type PE40. The Cys residues at positions 369 and 379 of the
CC exotoxin have been replaced by Ala residues. Ser at position 369
CC has been replaced with Thr. These changes improve receptor binding.
CC The hybrid protein can bind and kill tumour cells or keratinocytes
CC possessing TGF receptors for treatment of psoriasis or warts.
CC See also R06447-R06448 and R06450
SQ Sequence 420 AA;

Query Match 57.0%; Score 53; DB 1; Length 446;
Best Local Similarity 85.7%; Pred. No. 8.86e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 105 FTRHRQP 111
QY 3 FTRQRP 9

RESULT 14
ID W19869 standard; protein; 420 AA.
AC W19869;
DE 19-AUG-1997 (first entry)
DE TGF-57-PE40 encoded by pTAC TGF-57-PE40.
KW Fusion protein; transforming growth factor-alpha; TGF-alpha; PE40;
KW Pseudomonas exotoxin A; PE-A; translocation; enzymatic domain;
KW cytosol; cellular intoxication; targeting domain; PE40ab; PE40ab;
KW targeting-toxin molecule; target specificity; epidermal growth factor;
KW EGF; cytotoxic; cancer.
OS Chimeric - Homo sapiens.
OS Chimeric - Pseudomonas aeruginosa.
FH Key Location/Qualifiers
FT Region 1. 58
FT /label= TGF-alpha
FT Protein 59. 420
FT /label= PE40
FT Misc_difference 143. 145
FT /note= "encoded by GCCTG"
FT Misc_difference 72
FT /note= "Corresponds to Cys265"
FT Misc_difference 94

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FT /note= "Corresponds to Cys287"
 FT Misc_difference 179
 FT /note= "Corresponds to Cys372"
 FT Misc_difference 186
 FT /note= "Corresponds to Cys379"
 PN US5621078-A.
 PD 15-APR-1997.
 PF 22-MAR-1989; 327214.
 PR 22-MAR-1989; US-327214.
 PR 24-JUN-1991; US-708267.
 PR 30-APR-1992; US-879037.
 PR 10-SEP-1993; US-120698.
 PR 21-FEB-1995; US-391259.
 PR (MERI) MERCK & CO INC.
 PI Riemen MW. Stirdivant SM;
 DR WPI; 97-235227/21.
 DR N-PSDB; T72116.
 PT Modified pseudomonas exotoxin 40 polypeptide(s) - for production of
 PT cancer-specific cytotoxic conjugates
 PS Example 1; Column 13-16; 15pp; English.
 CC This sequence represents a fusion protein containing transforming growth
 CC factor (TGF)-alpha and PE40. PE40 comprises residues 252-613 of
 CC Pseudomonas exotoxin A (PE-A) and has a molecular weight of 40 kD.
 CC PE40 retains the translocation and enzymatic domains responsible for
 CC delivery of the protein to the cytosol and cellular intoxication
 CC activity, but lacks the PE-A targeting domain. The invention concerns
 CC modified PE40 polypeptides, PE40aB, which has Ala at positions 265 and
 CC 287, and PE40ab, which has Ala at positions 265, 287, 372 and 379
 CC (numbering according to the native 66kD PE-A sequence). The Cys
 CC residues at positions 265, 287, 372 and 379 were found to interfere
 CC with the construction of "targeting-toxin" molecules by chemical
 CC conjugation methods. Substitution of the Cys residues in these positions
 CC allows conjugates with greater target specificity to be prepared.
 CC Conjugates comprising the modified PE40 peptides and epidermal growth
 CC factor (EGF) or TGF-alpha (see also W19870-72) are cytotoxic and can
 CC be targeted to cancers.
 SQ Sequence 420 AA;

 Query Match 57.0%; Score 53; DB 1; Length 446;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Db 105 FTRHRQP 111
 |||:||||
 QY 3 FTRQRQP 9

 RESULT 15
 ID R06447 standard; protein; 420 AA.
 AC R06447;
 DT 04-JAN-1991 (first entry)
 DE TGF-57-Pseudomonas exotoxin 40 fusion protein.
 KW Pseudomonas exotoxin-40 (PE40); protein targeting agent;
 KW psoriasis treatment; anti-tumour agent;
 FH Key Location/Qualifiers
 FT Region 1..54
 FT /label= residues 14 to +50 of TGF-alpha
 FT Region 58..420
 FT /label= residues +252 to +613 of PE
 PN EP-383599-A.
 PD 22-AUG-1990.
 PF 15-FEB-1990; 301639.
 PR 17-FEB-1989; US-312540.
 PR 03-AUG-1989; US-389092.
 PR 21-DEC-1989; US-449187.
 PR (MERI) MERCK & CO INC.
 PI Oliff A, Jones DD, Edwards GM.
 DR WPI; 90-255832/34.
 DR N-PSDB; Q05666.
 PT Modified pseudomonas exotoxin hybrid proteins - has at least 2
 PT cysteine residues replaced or deleted to improve binding to
 PT receptors.
 PS Example ; Table 2; 20pp; English.

CC Modified pseudomonas exotoxin (PE40) linked to
 CC 5' portion of transforming growth factor (TGF)-alpha as a targeting
 CC agent. The corresponding nucleotide sequence was constructed from
 CC a synthetic oligonucleotide encoding the 5' portion of TGF-alpha
 CC and linked to PE40 and a linker cassette called "cassette 57". The
 CC recombinant plasmid was used to transform E.coli JM109 cells.
 CC The hybrid protein can bind and kill tumour cells or keratinocytes
 CC possessing TGF receptors for treatment of psoriasis or warts.
 CC See also R06448-R06450
 SQ Sequence 420 AA;

 Query Match 57.0%; Score 53; DB 1; Length 446;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Db 105 FTRHRQP 111
 |||:||||
 QY 3 FTRQRQP 9

 RESULT 16
 ID W19871 standard; protein; 420 AA.
 AC W19871;
 DT 19-AUG-1997 (first entry)
 DE TGF-alpha-PE40aB.
 KW Fusion protein; transforming growth factor-alpha; TGF-alpha; PE40;
 KW Pseudomonas exotoxin A; PE-A; translocation; enzymatic domain;
 KW cytosol; cellular intoxication; targeting domain; PE40aB; PE40ab;
 KW targeting-toxin molecule; target specificity; epidermal growth factor;
 KW EGF; cytotoxic; cancer.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Pseudomonas aeruginosa.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Protein 1..58
 FT /label= TGF-alpha
 FT Protein 59..420
 FT /label= PE40aB
 FT Modified site 72
 FT /note= "Corresponds to Cys265"
 FT Misc_difference 94
 FT /note= "Corresponds to Cys287"
 FT Misc_difference 179
 FT /label= Cys372Ala
 FT Misc_difference 186
 FT /label= Cys379Ala
 PN US5621078-A.
 PD 15-APR-1997.
 PF 22-MAR-1989; 327214.
 PR 22-MAR-1989; US-327214.
 PR 24-JUN-1991; US-708267.
 PR 30-APR-1992; US-879037.
 PR 10-SEP-1993; US-120698.
 PR 21-FEB-1995; US-391259.
 PR (MERI) MERCK & CO INC.
 PI Riemen MW. Stirdivant SM;
 DR WPI; 97-235227/21.
 PT Modified Pseudomonas exotoxin 40 polypeptide(s) - for production of
 PT cancer-specific cytotoxic conjugates
 PS Example 2; Column 21-24; 15pp; English.
 CC The sequences given in W19870-72 represent fusion proteins containing
 CC transforming growth factor (TGF)-alpha and modified PE40 proteins.
 CC PE40 comprises residues 252-613 of Pseudomonas exotoxin A (PE-A) and
 CC has a molecular weight of 40 kD. PE40 retains the translocation and
 CC enzymatic domains responsible for delivery of the protein to the cytosol
 CC and cellular intoxication activity, but lacks the PE-A targeting domain.
 CC The modified PE40 proteins are PE40aB, which has Ala at positions 265 and
 CC 287, PE40ab, which has Ala at positions 372 and 379, and PE40ab, which
 CC has Ala at positions 265, 287, 372 and 379 (numbering according to the
 CC native 66kD PE-A sequence). The Cys residues at positions 265, 287, 372
 CC and 379 were found to interfere with the construction of "targeting-
 CC toxin" molecules by chemical conjugation methods. Substitution of the
 CC Cys residues in these positions allows conjugates with greater target

CC specificity to be prepared. The modified PE40 proteins are named
 CC according to which domain the modified Cys residues appear in. Domain A
 CC comprises Cys 265 and 287, and domain B comprises Cys 372 and 379.
 CC An upper case letter (A, B) indicates that Cys is present in these
 CC positions, whereas a lower case letter (a, b) indicates that these
 CC positions have been mutated to Ala. Conjugates comprising the modified
 CC PE40 peptides and epidermal growth factor (EGF) or TGF-alpha are
 CC cytotoxic and can be targeted to cancers.
 SQ Sequence 420 AA;

Query Match 57.0%; Score 53; DB 1; Length 446;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 105 FTRHRQP 111
 |||||
 QY 3 FTRQROP 9

RESULT 17
 ID R95055 standard; Protein; 421 AA.
 AC R95055;
 DT 19-AUG-1996 (first entry)
 DE IL-2-DETA-DGAL4 multidomain protein.
 KW Nucleic acid transfer system; gene transfer; gene therapy;
 KW cell targeting; multidomain protein; vector; cancer;
 KW exotoxin A; DETA; ompA; signal peptide; GAL4; interleukin-2;
 KW IL-2.

OS Chimeric synthetic;
 OS Chimeric Homo sapiens;
 OS Chimeric Pseudomonas aeruginosa;
 OS Chimeric Saccharomyces cerevisiae.

FH Key Location/Qualifiers

FT Peptide 1..8

FT /label= FLAG_epitope

FT Peptide 9..17

FT /label= Spacer

FT Domain 18..150

FT /label= IL-2

FT /note= "amino acids 1-113 of human IL-2

FT Peptide 151

FT /label= Spacer

FT Domain 152..266

FT /label= ETA

FT /note= "amino acids 252-366 of ETA"

FT Peptide 267

FT /label= Spacer

FT Domain 268..413

FT /label= GAL4

FT /note= "amino acids 2-147 of yeast GAL4"

FT Peptide 414..421

FT /label= Spacer

FT /note= "endoplasmic reticulum retention signal"

PN W09613599-A1.

PD 09-MAY-1996.

PF 31-OCT-1995; E04270.

PR 01-NOV-1994; EP-810627.

PA (WELLS) WELLS W.

PI Fominaya J, Wells W;

DR WPI: 96-239505/24.

DR N-PSDB; T29411.

PT Nucleic acid transfer system for gene therapy, e.g. against cancer
 PT - includes toxin translocation domain to target nucleic acid to
 PT specific cell

PS Claim 7; Page 67-69; 106pp; English.

CC A multidomain protein (R95055) has a FLAG epitope, a portion

CC of human interleukin-2 that acts as a ligand domain, a

CC non-cytotoxic portion of Pseudomonas aeruginosa exotoxin A acting

CC as a translocation domain and the DNA binding domain of yeast GAL4.

CC It is the product of a fusion gene (T29411) and can be expressed

CC in E. coli (resulting in removal of an ompA signal peptide). It is

CC used with an effector nucleic acid that comprises e.g. a gene to be

CC delivered to a cell and a cognate structure for the GAL4 DNA binding

CC domain. This provides a novel means of nucleic acid transfer,
 CC suitable for gene therapy.
 SQ Sequence 421 AA;

Query Match 57.0%; Score 53; DB 1; Length 447;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 198 FTRHRQP 204
 |||||
 QY 3 FTRQROP 9

RESULT 18
 ID R32454 standard; Protein; 426 AA.
 AC R32454;
 DT 20-JUL-1993 (first entry)
 DE PE(2-414)-Ma (57-68) hybrid protein.
 KW PE; Pseudomonas exotoxin; influenza A virus; M1; matrix protein;
 KW ompA; leader; signal; fusion; hybrid; BS-PEMa-1; pVC45DR+T;
 KW pVC-ompA-PEMa-1; pVC-PEMa-1; T7 promoter; RBS; ribosome binding site;
 KW initiation sequence; build-back.
 KW Synthetic.
 PN EP-532090-A.
 PD 17-MAR-1993.
 PF 02-SEP-1992; 202660.
 PR 09-SEP-1991; US-756249.
 PA (MERI) MERCK & CO INC.
 PI Donnelly JJ, Friedman A, Hawe LA, Liu MA, Marshall MS;
 PI Montgomery DL, Oliff AI, Shi X, Ulmer J;
 DR WPI: 93-087107/11.
 DR N-PSDB; Q37892.

PT Bacterial toxin-antigen protein conjugates - to elicit cytotoxic
 PT T-lymphocyte immune response, used for preventing viral
 PT infections, e.g. by influenza virus, HIV and human
 PT papilloma: virus
 PS Disclosure; Page 30-31; 85pp; English.
 CC Example 4 describes the subcloning of pEMA from BS-PEMa-1 into
 CC pVC45DF+T. The pEMA insert (Q37890) was prep. by restricting
 CC BS-PEMa-1 with SacI and removing the 3' overhang by treatment with
 CC T4 DNA polymerase, then restricting with ApaI and gel purifying.
 CC pVC45DF+T was restricted with EcoRI and the 5' overhang filled in
 CC with Klenow enzyme treatment. It was subsequently restricted with
 CC ApaI and gel purified. The vector and fragment were ligated together,
 CC and the resulting construction was named pVC-ompA-PEMa-1.
 CC The ompA signal sequence was removed from pVC-ompA-PEMa-1 by
 CC digestion with XbaI and HindIII. An oligonucleotide fragment contg.
 CC the T7 promoter, ribosome binding site, initiation sequence and a
 CC build-back of the 5' end of the PE coding region (Q37891) was
 CC ligated into the vector. The resulting plasmid construct was named
 CC pVC-PEMa-1 and encodes a T7 polymerase-driven gene fusion consisting
 CC of PE amino acids 2 through 414 joined to influenza M1 amino acids
 CC 57 to 68 (Ma) (Q37892).
 SQ Sequence 426 AA;

Query Match 57.0%; Score 53; DB 1; Length 452;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 299 FTRHRQP 305
 |||||
 QY 3 FTRQROP 9

RESULT 19
 ID R36806 standard; Protein; 426 AA.
 AC R36806;
 DT 25-AUG-1993 (first entry)
 DE PE domains I and II fused to influenza A virus Ma.
 KW Vaccine; cytotoxic T lymphocyte; CTL; influenza A virus;
 KW matrix protein; Ma; Pseudomonas exotoxin; cell recognition domain;
 KW translocation domain; anti-viral agent; fusion construct.
 OS Chimeric Pseudomonas aeruginosa.

OS Chimeric Influenza A virus.
 FH Key Location/Qualifiers
 FT Region 2. .414
 FT /note- "PE domains I and II"
 FT Region 415. .426
 FT /note- "amino acids 57-68 of Influenza A Virus
 FT Matrix protein"
 PN EP-541335-A.
 PD 12-MAY-1993.
 PF 04-NOV-1992; 310067.
 PR 08-NOV-1991; US-792507.
 PA (MERI) MERCK & CO INC.
 PI Donnelly JJ, Friedman A, Hawe LA, Liu MA, Marshall MS;
 PI Montgomery DL, Oliff AA, Shi X, Ulmer J;
 DR WPI; 93-154266/19.
 DR N-PSDB; Q41714.
 PT Recombinant DNA encoding bacterial toxin-antigen conjugates - are
 PT useful as vaccines against viral infections, tumours and
 PT parasites
 PS Example 4; Page 25; 81pp; English.
 CC An MI gene fragment (encoding amino acids 57-68 of influenza A virus
 CC matrix protein) was subcloned into BS-PE, a plasmid constructed by
 CC inserting a 1.3kb NruI/SacII fragment of plasmid pVC45-DF+r containing
 CC the domain I and II coding regions of Pseudomonas exotoxin into
 CC pBluescript II SK restricted with HincII and SacII. The PE-derived
 CC portion of the hybrid protein allows internalisation of the protein
 CC by an antigen-presenting cell. The hybrid protein is then processed
 CC and an antigenic segment (i.e. the Influenza A virus matrix protein)
 CC is presented on the cell surface where it elicits an immune response.
 SQ Sequence 426 AA;

Query Match 57.0%; Score 53; DB 1; Length 452;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 299 FTRHRQP 305
 |||:||||
 QY 3 FTRQRP 9

RESULT 20
 ID R99581 standard; protein; 434 AA.
 AC R99581;
 DT 07-NOV-1996 (first entry)
 DE Heregulin/Pseudomonas ligand toxin.
 KW Heregulin; HRG beta2; Pseudomonas; exotoxin; ligand toxin; cancer;
 KW treatment; breast cancer; treatment; selective targeting; erbB3;
 KW erbB4.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1. .8
 FT /label- FLAG peptide.
 FT Region 10. .70
 FT /label- HRG beta2 protein sequence.
 FT Region 71. .434
 FT /label- Pseudomonas PE40 exotoxin sequence.
 PN WO9616176-A1.
 PD 30-MAY-1996.
 PF 17-NOV-1995; AU0767.
 PR 22-NOV-1994; AU-009598.
 PA (CRCB-) CRC BIOPHARMACEUTICAL RES PTY LTD.
 PI Daly RJ, Fiddes RJ;
 DR WPI; 96-268612/27.
 PT Ligand-toxin, partic. useful for treating cancer cells - comprising
 PT a sequence homologous to the EGF-like domain of heregulin beta 2
 PT fused to a toxin
 PS Claim 4; Figure 1; 23pp; English.
 CC The ligand toxin consists of the epidermal growth factor-like domain
 CC of heregulin beta2 (HRG beta2) amino acids 177-237, fused to a
 CC modified Pseudomonas exotoxin (PE40). The HRG beta2-PE40 ligand
 CC toxin was engineered and expressed using the pFlag prokaryotic
 CC expression system. The ligand toxin can be used for treating a
 CC cancer in which there is an overexpression of erbB3 and/or erbB4.

CC It selectively targets such cancer cells with no toxic effects on
 CC nearby benign cells. The ligand toxin can be used in particular for
 CC the treatment of breast cancer.
 SQ Sequence 434 AA;

Query Match 57.0%; Score 53; DB 1; Length 460;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 119 FTRHRQP 125
 |||:||||
 QY 3 FTRQRP 9

RESULT 21
 ID R91735 standard; Protein; 462 AA.
 AC R91735;
 DT 05-JUL-1996 (first entry)
 DE Heregulin-PE40 HAR-TX beta-2 chimeric protein.
 KW HER4/p180erbB4; HER4; receptor tyrosine kinase; HAR-TX beta-2;
 KW epidermal growth factor receptor; cancer; diagnosis; therapy;
 KW amphiregulin; heregulin; toxin; PE40; breast carcinoma.
 OS Chimeric Rattus sp.;
 OS Chimeric Pseudomonas sp.;
 OS Chimeric synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1. .35
 FT /label- Sig_peptide
 FT /note- "amphiregulin leader sequence"
 FT Protein 36. .95
 FT /label- Heregulin
 FT Peptide 96. .98
 FT /label- Linker
 FT Protein 99. .462
 FT /label- PE40
 PN WO9612019-A2.
 PD 25-APR-1996.
 PF 10-OCT-1995; U13524.
 PR 14-OCT-1994; US-323442.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Culouscou J, Hellstrom I, Hellstrom KE, Plowman GD;
 PI Shoyab M, Siegal C;
 DR WPI; 96-222005/22.
 DR N-PSDB; T18534.
 PT DNA encoding receptor tyrosine kinase, HER4 - related to human
 PT epidermal growth factor receptor, used for diagnosis and therapy of
 PT human cancers
 PS Claim 57; Page 156-158; 203pp; English.
 CC Cytotoxic fusion protein HAR-TX beta-2 (R91735) comprises a chimeric
 CC rat heregulin beta-2 ligand and pseudomonas exotoxin PE40, joined to
 CC an amphiregulin leader sequence that facilitates purification. The
 CC fusion protein is generated by expression of the corresponding
 CC chimeric coding sequence (see T18534). The fusion protein
 CC specifically targets cells that express receptor tyrosine kinase
 CC HER4 (see R91733), e.g. prostate carcinoma, bladder carcinoma and
 CC breast carcinoma cells, allowing targeted cancer therapy.
 SQ Sequence 462 AA;

Query Match 57.0%; Score 53; DB 1; Length 488;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 147 FTRHRQP 153
 |||:||||
 QY 3 FTRQRP 9

RESULT 22
 ID W05137 standard; Protein; 463 AA.
 AC W05137;
 DT 29-JAN-1997 (first entry)
 DE TGF alpha-ETA fusion protein.
 KW Single chain antibody; scfv; monoclonal antibody; MAb; TGF;

KW transforming growth factor alpha; receptor; plasmid pSW202-TGF;
 KW cancer; therapy; antitumour; exotoxin A; ETA.
 OS Chimeric Homo sapiens;
 OS Chimeric Pseudomonas aeruginosa;
 OS Chimeric synthetic.

FH Key Location/Qualifiers
 FT Peptide 1. .21
 FT /label= Sig_peptide
 FT /note= "ompA signal peptide"
 FT Peptide 22. .38
 FT /label= Spacer
 FT Protein 39. .278
 FT /label= TGF-alpha
 FT Peptide 279. .289
 FT /label= Spacer
 FT Protein 290. .651
 FT /label= ETA

FT /note= "exotoxin A amino acids 252-613"
 PN EP-739984-A1.
 PD 30-OCT-1996.
 PF 26-APR-1995; 106275.
 PF 26-APR-1995; EP-106275.

PA (SANT-) SAN TUMORFORSCHUNGS GMBH.
 PI Groner B, Schmidt M, Wels W;
 DR WPI: 96-478748/48.
 DR N-PSDB: T42037.

PT Bivalent fusion proteins that bind epidermal growth factor receptor
 or analogues - and comprise at least two different cell surface
 PT binding domain(s), useful for tumour therapy

PS Example 8; Page 23-24; 52pp; English.
 CC TGF alpha-ETA (W05137) comprises human transforming growth
 CC factor (TGF) alpha joined to the Pseudomonas aeruginosa cytotoxin,
 CC exotoxin A (ETA). It is encoded by plasmid pSW202-TGF (see also
 CC T42037) obt'd. by ligating TGF-alpha cDNA into plasmid pSW202-5 (see
 CC also T42036). The construct can be used to produce novel bivalent
 CC fusion proteins (see also W05138-44) in bacterial host cells, for
 CC use as antitumour agents.

SQ Sequence 463 AA;

Query Match 57.0%; Score 53; DB 1; Length 489;

Best Local Similarity 85.7%; Pred. No. 8.86e-01;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 148 FTRHRQP 154

|||||

QY 3 FTRORQP 9

RESULT 23

ID R04934 standard; protein; 496 AA.

AC R04934;

DT 26-SEP-1990 (first entry)

DE Immunotoxin hybrid of human interleukin-2 and Pseudomonas exotoxin.

KE Pseudomonas exotoxin; interleukin-2; P840; diabetes;

KW arthritis; Crohn's disease; autoimmune disease.

OS Synthetic.

PN EP-369316-A.

PD 23-MAY-1990.

PF 9-NOV-1989; 120754.

PF 17-NOV-1988; US-272356; EP-120754.

PA (HOFF) Hoffmann-La Roche.

PI Grace JW;

DR WPI: 90-157493/21.

PT Immuno:toxin contg. natural human IL-2 sequence as

PT N-terminal component -

PT and Pseudomonas exotoxin region, and encoding DNA sequence

PT vectors and transformed cells, for treating auto:immune disease.

PS Disclosure; p; English.

CC Hybrid enzyme is useful in treating autoimmune diseases, type I

CC diabetes, rheumatoid arthritis, Crohn's disease, and in suppressing

CC allograft and organ transplant rejection.

SQ Sequence 496 AA;

Query Match 57.0%; Score 53; DB 1; Length 522;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 181 FTRHRQP 187

|||||

QY 3 FTRORQP 9

RESULT 24

ID R95053 standard; Protein; 530 AA.

AC R95053;

DT 18-AUG-1996 (first entry)

DE scfv(FRP5)-DETA-DGAL4 multidomain protein.

KW Nucleic acid transfer system; gene transfer; gene therapy;

KW cell targeting; multidomain protein; vector; cancer;

KW exotoxin A; DETA; single chain antibody; scfv; GAL4.

OS Chimeric synthetic;

OS Chimeric Mus sp.;

OS Chimeric Pseudomonas aeruginosa;

OS Chimeric Saccharomyces cerevisiae.

FH Key Location/Qualifiers

FT Peptide 1. .8

FT /label= FLAG_epitope

FT Peptide 9. .17

FT /label= Spacer

FT Domain 18. .257

FT /label= Scfv(FRP5)

FT Peptide 258. .260

FT /label= Spacer

FT Domain 261. .375

FT /label= ETA

FT /note= "amino acids 252-366 of exotoxin-A"

FT Peptide 376

FT /label= Spacer

FT Domain 377. .522

FT /label= GAL4

FT /note= "amino acids 2-147 of yeast GAL4"

FT Peptide 523. .530

FT /label= Spacer

FT /note= "endoplasmic reticulum retention peptide"

PN W09613599-A1.

PD 09-MAY-1996.

PF 31-OCT-1995; E04270.

PF 01-NOV-1994; EP-810627.

PA (WELS/) WELS W.

PI Fominaya J, Wels W;

DR WPI: 96-239505/24.

DR N-PSDB: T29409.

PT Nucleic acid transfer system for gene therapy, e.g. against cancer

PT - includes toxin translocation domain to target nucleic acid to

PT specific cell

PS Claim 7; Page 59-61; 106pp; English.

CC A multidomain protein (R95053) has a FLAG epitope, a single

CC chain antibody, scfv, of monoclonal antibody FRP5 (raised

CC against human tumour cell HER2 antigen) that acts as a ligand

CC domain, a non-cytotoxic portion of Pseudomonas aeruginosa

CC exotoxin A acting as a translocation domain and the DNA

CC binding domain of yeast GAL4. It is the product of a fusion

CC gene (T29409) and can be expressed in E. coli (resulting in

CC removal of ompA signal peptide). It is used with an effector

CC nucleic acid that comprises e.g. a gene to be delivered to

CC a cell and a cognate structure for the GAL4 DNA binding domain.

CC This provides a novel means of nucleic acid transfer, suitable

CC for gene therapy.

SQ Sequence 530 AA;

Query Match 57.0%; Score 53; DB 1; Length 556;

Best Local Similarity 85.7%; Pred. No. 8.86e-01;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 307 FTRHRQP 313

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QY      3 FTRQRP 9

RESULT 25
ID R04920 standard; protein; 549 AA.
AC R04920;
DT 02-OCT-1990 (first entry)
DE Immunoprotein PEX46.
KW Soluble T4 protein; immunotoxin; Pseudomona endotoxin A; AIDS; HIV; ARC;
KW angiogenin; fusion protein; PEX46; pEX46.
FH Key Location/Qualifiers
FT Region 2..182
FT /label-AAS 3-183 of T4 protein
FT Region 183..549
FT /label-AAS 253-613 of Pseudomonas exotoxin A (PE40)
PN WO9004414-A.
PD 03-MAY-1990.
PF 18-OCT-1989; U04584.
PR 18-OCT-1988; US-259355.
PA (BIOJ) Biogen Inc.
PI Meade HM, Lobb RR, Gates LL, Winkler G;
DR WPI: 90-163876/21.
PT New immunotoxin contg. soluble T4 protein components and toxin -
PT esp. Pseudomonas endotoxin A, for treating or controlling AIDS
PT and related conditions, and new DNA sequences.
PS Disclosure: 7pp; English.
CC This fusion immunoprotein was produced by constructing a hybrid DNA
CC sequence of a soluble T4 protein and a fragment of Pseudomonas exotoxin A
CC (PE40) in which all binding region of PE was removed and which did not
CC contain the boundary region. The hybrid DNA can then be inserted into an
CC expression vector and used to produce recombinant fusion protein which is
CC useful for preventing or treating AIDS, ARC, and HIV infections. The T4
CC protein is an HIV receptor which binds to the virus or to infected cells
CC carrying the gp120/160 marker antigen, so provides v. specific targeting
CC with minimal damage to non-target cells. Unmodified chain of PEX45 has
CC a Mol. Wt. of 59,658.
SQ Sequence 549 AA;

Query Match 57.0%; Score 53; DB 1; Length 575;
Best Local Similarity 85.7%; Pred. No. 8.86e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 234 FTRQRP 240
QY      3 FTRQRP 9

RESULT 26
ID R04923 standard; protein; 557 AA.
AC R04923;
DT 02-OCT-1990 (first entry)
DE Immunoprotein TANG11.
KW Soluble T4 protein; immunotoxin; Pseudomona endotoxin A; AIDS; HIV; ARC;
KW angiogenin; fusion protein; TANG11.
FH Key Location/Qualifiers
FT Region 1..182
FT /label-AAS 3-183 of T4 protein
FT Region 184..300
FT /label-translocation domain of PE
FT Region 301..340
FT /label-binding domain of PE
FT Region 341..429
FT /label-linker from ADP-ribosylation domain of PE
FT Region 433..559
FT /label-mature angiogenin
PN WO9004414-A.
PD 03-MAY-1990.
PF 18-OCT-1989; U04584.
PR 18-OCT-1988; US-259355.
PA (BIOJ) Biogen Inc.
PI Meade HM, Lobb RR, Gates LL, Winkler G;
DR WPI: 90-163876/21.
PT New immunotoxin contg. soluble T4 protein components and toxin -

esp. Pseudomonas endotoxin A, for treating or controlling AIDS
PT and related conditions, and new DNA sequences.
PS Disclosure: 7pp; English.
CC This fusion immunoprotein was produced by constructing a hybrid DNA
CC sequence of a soluble T4 protein and a fragment of Pseudomonas exotoxin A
CC (PE40) in which all binding region of PE was removed and which did not
CC contain the boundary region. The hybrid DNA can then be inserted into an
CC expression vector and used to produce recombinant fusion protein which is
CC useful for preventing or treating AIDS, ARC, and HIV infections. The T4
CC protein is an HIV receptor which binds to the virus or to infected cells
CC carrying the gp120/160 marker antigen, so provides v. specific targeting
CC with minimal damage to non-target cells. Unmodified chain of PEX45 has
CC a Mol. Wt. of 59,658.
SQ Sequence 549 AA;

Query Match 57.0%; Score 53; DB 1; Length 575;
Best Local Similarity 85.7%; Pred. No. 8.86e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 234 FTRQRP 240
QY      3 FTRQRP 9

RESULT 27
ID R04919 standard; protein; 574 AA.
AC R04919;
DT 02-OCT-1990 (first entry)
DE Immunoprotein PEX45.
KW Soluble T4 protein; immunotoxin; Pseudomona endotoxin A; AIDS; HIV; ARC;
KW angiogenin; fusion protein; PEX45; pEX45.
FH Key Location/Qualifiers
FT Region 2..182
FT /label-AAS 3-183 of T4 protein
FT Region 183..574
FT /label-AAS224-613 of Pseudomonas exotoxin A
PN WO9004414-A.
PD 03-MAY-1990.
PF 18-OCT-1989; U04584.
PR 18-OCT-1988; US-259355.
PA (BIOJ) Biogen Inc.
PI Meade HM, Lobb RR, Gates LL, Winkler G;
DR WPI: 90-163876/21.
PT New immunotoxin contg. soluble T4 protein components and toxin -
PT esp. Pseudomonas endotoxin A, for treating or controlling AIDS
PT and related conditions, and new DNA sequences.
PS Disclosure: 7pp; English.
CC This fusion immunoprotein was produced by constructing a hybrid DNA
CC sequence of a soluble T4 protein and a fragment of Pseudomonas exotoxin A
CC contg. the translocation and ADP-ribosylation domains. The hybrid DNA
CC can then be inserted into an expression vector and used to produce
CC recombinant fusion protein, useful for preventing or treating AIDS,
CC ARC, and HIV infections. The T4 protein is an HIV receptor which binds to
CC the virus or to infected cells carrying the gp120/160 marker antigen, so
CC provides v. specific targeting with minimal damage to non-target cells.
CC The unmodified chain of PEX45 has a Mol. Wt. of 62,491.
SQ Sequence 574 AA;

Query Match 57.0%; Score 53; DB 1; Length 600;
Best Local Similarity 85.7%; Pred. No. 8.86e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 259 FTRQRP 265
QY      3 FTRQRP 9

RESULT 28
ID R04924 standard; protein; 577 AA.
AC R04924;
DT 02-OCT-1990 (first entry)
DE Immunoprotein TANG12.
KW Soluble T4 protein; immunotoxin; Pseudomona endotoxin A; AIDS; HIV; ARC;
KW angiogenin; fusion protein; TANG12.

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FH Key Location/Qualifiers
 FT Region 1. .182
 FT /Label=AA3 3-183 of T4 protein
 FT Region 184. .300
 FT /Label=translocation domain of PE
 FT Region 301. .340
 FT /Label=binding domain of PE
 FT Region 341. .429
 FT /Label=linker from ADP ribosylation domain of PE
 FT Peptide 431. .454
 FT /Label=angiogenin signal sequence
 FT Protein 455. .577
 FT /Label=mature angiogenin
 PN W09004414-A.
 PD 03-MAY-1990.
 PF 18-OCT-1989; U04584.
 PR 18-OCT-1988; US-259355.
 PA (BIOJ) Biogen Inc.
 PI Meade HM, Lobb RR, Gates LL, Winkler G;
 DR WPI; 90-163876/21.
 PT New immunotoxin contg. soluble T4 protein components and toxin -
 PT esp. Pseudomonas endotoxin A, for treating or controlling AIDS
 PT and related conditions, and new DNA sequences.
 PS Disclosure; 7pp; English.
 CC This fusion immunoprotein was produced by constructing a hybrid DNA
 CC sequence of a soluble T4 protein, a fragment of Pseudomonas exotoxin A
 CC including the translocation domain and part of the ADP ribosylation
 CC domain, and the gene for the signal sequence and mature angiogenin.
 CC The hybrid DNA can then be inserted into an expression vector and used
 CC to produce recombinant fusion protein which is useful for preventing or
 CC treating AIDS, ARC, and HIV infections. The T4 protein is an HIV receptor
 CC which binds to the virus or infected cells carrying the gp120/160 marker
 CC antigen, so provides v. specific targeting with minimal damage to
 CC non-target cells.
 SQ Sequence 577 AA;

Query Match 57.0%; Score 53; DB 1; Length 603;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 234 FTRHRQP 240
 |||:||||
 QY 3 FTRQRQP 9

RESULT 29
 ID R40105 standard; Protein; 613 AA.
 AC R40105;
 DT 27-JAN-1994 (first entry)
 DE Pseudomonas exotoxin (S25C).
 KW target site; cytotoxin; PE; diphtheria toxin; DT; immunotoxin;
 KW monoclonal antibody; ligand; cell surface; mutation;
 KW steric unpaired cysteine; s.u.c.
 OS Pseudomonas aeruginosa.
 FH Key Location/Qualifiers
 FT Misc_difference 25
 FT /note= "unpaired cysteine residue replaces Ser"
 FT W09315113-A.
 PN 05-AUG-1993.
 PF 15-JAN-1993; U00358.
 PR 24-JAN-1992; US-825396.
 PA (TANO-) TANOX BIOSYSTEMS INC.
 PI Chang TW;
 DR WPI; 93-258616/32.
 PT Site-specifically mutated cytotoxin(s) with an unpaired cysteine
 PT receptor binding used as immuno:toxins for highly specific
 PT targeting
 PS Claim 3; Page 20-23; 30pp; English.
 CC The new mutated toxin has an unpaired cysteine residue in
 CC or near the cytotoxin's receptor-binding site, and retains the
 CC same receptor-binding ability and cytotoxicity as the native

CC cytotoxins provided they are not conjugated with a binding mol.
 CC The toxins are cross-linked through the free SH group of their
 CC unpaired cysteine residues to binding mols. (including monoclonal
 CC antibodies, fragments and other ligands) to form immunotoxins, and
 CC these immunotoxins do not bind to the cell surface receptors which
 CC are bound by the native cytotoxin. However, when the cross-linker
 CC is cleaved and the binding mol. is released, the cytotoxin regains
 CC its receptor-binding ability and its cytotoxicity.
 SQ Sequence 613 AA;

Query Match 57.0%; Score 53; DB 1; Length 639;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 298 FTRHRQP 304
 |||:||||
 QY 3 FTRQRQP 9

RESULT 30
 ID R40106 standard; Protein; 613 AA.
 AC R40106;
 DT 27-JAN-1994 (first entry)
 DE Pseudomonas exotoxin (S88C).
 KW Pseudomonas exotoxin; PE; diphtheria toxin; DT; immunotoxin;
 KW target site; cytotoxin; unpaired cysteine; receptor; binding site;
 KW monoclonal antibody; ligand; cell surface; mutation;
 KW steric unpaired cysteine; s.u.c.
 OS Pseudomonas aeruginosa.
 FH Key Location/Qualifiers
 FT /note= "unpaired cysteine residue replaces Ser"
 FT W09315113-A.
 PN 05-AUG-1993.
 PF 15-JAN-1993; U00358.
 PR 24-JAN-1992; US-825396.
 PA (TANO-) TANOX BIOSYSTEMS INC.
 PI Chang TW;
 DR WPI; 93-258616/32.

PT Site-specifically mutated cytotoxin(s) with an unpaired cysteine
 PT - such that conjugation of a binding mol. to the Cys blocks
 PT receptor binding used as immuno:toxins for highly specific
 PT targeting
 PS Claim 3; Page 20-23; 30pp; English.
 CC The new mutated toxin has an unpaired cysteine residue in
 CC or near the cytotoxin's receptor-binding site, and retains the
 CC same receptor-binding ability and cytotoxicity as the native
 CC cytotoxins provided they are not conjugated with a binding mol.
 CC The toxins are cross-linked through the free SH group of their
 CC unpaired cysteine residues to binding mols. (including monoclonal
 CC antibodies, fragments and other ligands) to form immunotoxins, and
 CC these immunotoxins do not bind to the cell surface receptors which
 CC are bound by the native cytotoxin. However, when the cross-linker
 CC is cleaved and the binding mol. is released, the cytotoxin regains
 CC its receptor-binding ability and its cytotoxicity.
 SQ Sequence 613 AA;

Query Match 57.0%; Score 53; DB 1; Length 639;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 298 FTRHRQP 304
 |||:||||
 QY 3 FTRQRQP 9

RESULT 31
 ID R40107 standard; Protein; 613 AA.
 AC R40107;
 DT 27-JAN-1994 (first entry)
 DE Pseudomonas exotoxin (S96C).
 KW Pseudomonas exotoxin; PE; diphtheria toxin; DT; immunotoxin;
 KW target site; cytotoxin; unpaired cysteine; receptor; binding site;

KW monoclonal antibody; ligand; cell surface; mutation;
 KW steric unpaired cysteine; s.u.c.
 OS Pseudomonas aeruginosa.
 FH Key Location/Qualifiers

FT Misc_difference 96

FT /note= "unpaired cysteine residue replaces Ser"

PN W09315113-A.

PD 05-AUG-1993.

PF 15-JAN-1993; U00358.

PR 24-JAN-1992; US-825396.

PA (TANO-) TANOX BIOSYSTEMS INC.

PI Chang TW;

DR WPI; 93-258616/32.

PT Site-specifically mutated cytotoxin(s) with an unpaired cysteine

PT - such that conjugation of a binding mol. to the Cys blocks

PT receptor binding used as immuno:toxins for highly specific

PT targetting

PS Claim 3; Page 20-23; 30pp; English.

CC The new mutated toxin has an unpaired cysteine residue in

CC or near the cytotoxin's receptor-binding site, and retains the

CC same receptor-binding ability and cytotoxicity as the native

CC cytotoxins provided they are not conjugated with a binding mol.

CC The toxins are cross-linked through the free SH group of their

CC unpaired cysteine residues to binding mols. (including monoclonal

CC antibodies, fragments and other ligands) to form immunotoxins, and

CC these immunotoxins do not bind to the cell surface receptors which

CC are bound by the native cytotoxin. However, when the cross-linker

CC is cleaved and the binding mol. is released, the cytotoxin regains

CC its receptor-binding ability and its cytotoxicity.

SQ Sequence 613 AA;

Query Match 57.0%; Score 53; DB 1; Length 639;

Best Local Similarity 85.7%; Pred. No. 8.86e-01;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 298 FTRHRQP 304

3 FTRQRQP 9

RESULT 32

ID R40113 standard; Protein; 613 AA.

AC R40113;

DT 27-JAN-1994 (first entry)

DE Pseudomonas exotoxin (S245C).

KW target site; cytotoxin; PE; diphtheria toxin; DT; immunotoxin;

KW monoclonal antibody; ligand; cell surface; mutation;

KW steric unpaired cysteine; s.u.c.

OS Pseudomonas aeruginosa.

FH Key Location/Qualifiers

FT Misc_difference 245

FT /note= "unpaired cysteine residue replaces Ser"

PN W09315113-A.

PD 05-AUG-1993.

PF 15-JAN-1993; U00358.

PR 24-JAN-1992; US-825396.

PA (TANO-) TANOX BIOSYSTEMS INC.

PI Chang TW;

DR WPI; 93-258616/32.

PT Site-specifically mutated cytotoxin(s) with an unpaired cysteine

PT - such that conjugation of a binding mol. to the Cys blocks

PT receptor binding used as immuno:toxins for highly specific

PT targetting

PS Claim 3; Page 20-23; 30pp; English.

CC The new mutated toxin has an unpaired cysteine residue in

CC or near the cytotoxin's receptor-binding site, and retains the

CC same receptor-binding ability and cytotoxicity as the native

CC cytotoxins provided they are not conjugated with a binding mol.

CC The toxins are cross-linked through the free SH group of their

CC unpaired cysteine residues to binding mols. (including monoclonal

CC antibodies, fragments and other ligands) to form immunotoxins, and

CC these immunotoxins do not bind to the cell surface receptors which

CC are bound by the native cytotoxin. However, when the cross-linker

CC is cleaved and the binding mol. is released, the cytotoxin regains

CC its receptor-binding ability and its cytotoxicity.

SQ Sequence 613 AA;

Query Match 57.0%; Score 53; DB 1; Length 639;

Best Local Similarity 85.7%; Pred. No. 8.86e-01;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 298 FTRHRQP 304

3 FTRQRQP 9

RESULT 33

ID R40110 standard; Protein; 613 AA.

AC R40110;

DT 27-JAN-1994 (first entry)

DE Pseudomonas exotoxin (S188C).

KW target site; cytotoxin; PE; diphtheria toxin; DT; immunotoxin;

KW monoclonal antibody; ligand; cell surface; mutation;

KW steric unpaired cysteine; s.u.c.

OS Pseudomonas aeruginosa.

FH Key Location/Qualifiers

FT Misc_difference 188

FT /note= "unpaired cysteine residue replaces Ser"

PN W09315113-A.

PD 05-AUG-1993.

PF 15-JAN-1993; US-825396.

PR 24-JAN-1992; US-825396.

PA (TANO-) TANOX BIOSYSTEMS INC.

PI Chang TW;

DR WPI; 93-258616/32.

PT Site-specifically mutated cytotoxin(s) with an unpaired cysteine

PT - such that conjugation of a binding mol. to the Cys blocks

PT receptor binding used as immuno:toxins for highly specific

PT targetting

PS Claim 3; Page 20-23; 30pp; English.

CC The new mutated toxin has an unpaired cysteine residue in

CC or near the cytotoxin's receptor-binding site, and retains the

CC same receptor-binding ability and cytotoxicity as the native

CC cytotoxins provided they are not conjugated with a binding mol.

CC The toxins are cross-linked through the free SH group of their

CC unpaired cysteine residues to binding mols. (including monoclonal

CC antibodies, fragments and other ligands) to form immunotoxins, and

CC these immunotoxins do not bind to the cell surface receptors which

CC are bound by the native cytotoxin. However, when the cross-linker

CC is cleaved and the binding mol. is released, the cytotoxin regains

CC its receptor-binding ability and its cytotoxicity.

SQ Sequence 613 AA;

Query Match 57.0%; Score 53; DB 1; Length 639;

Best Local Similarity 85.7%; Pred. No. 8.86e-01;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 298 FTRHRQP 304

3 FTRQRQP 9

RESULT 34

ID R40108 standard; Protein; 613 AA.

AC R40108;

DT 27-JAN-1994 (first entry)

DE Pseudomonas exotoxin (S158C).

KW target site; cytotoxin; PE; diphtheria toxin; DT; immunotoxin;

KW monoclonal antibody; ligand; cell surface; mutation;

KW steric unpaired cysteine; s.u.c.

OS Pseudomonas aeruginosa.

FH Key Location/Qualifiers

FT Misc_difference 158

FT /note= "unpaired cysteine residue replaces Ser"
 PN W09315113-A.
 PD 05-AUG-1993.
 PF 15-JAN-1993; U00358.
 PR 24-JAN-1992; US-825396.
 PA (TANO-) TANOX BIOSYSTEMS INC.
 PI Chang TW;
 DR WPI; 93-258616/32.
 PT Site-specifically mutated cytotoxin(s) with an unpaired cysteine
 PT - such that conjugation of a binding mol. to the Cys blocks
 PT receptor binding used as immuno:toxins for highly specific
 PT targeting
 PS Claim 3; Page 20-23; 30pp; English.
 CC The new mutated toxin has an unpaired cysteine residue in
 CC or near the cytotoxin's receptor-binding site, and retains the
 CC same receptor-binding ability and cytotoxicity as the native
 CC cytotoxins provided they are not conjugated with a binding mol.
 CC The toxins are cross-linked through the free SH group of their
 CC unpaired cysteine residues to binding mols. (including monoclonal
 CC antibodies, fragments and other ligands) to form immunotoxins, and
 CC these immunotoxins do not bind to the cell surface receptors which
 CC are bound by the native cytotoxin. However, when the cross-linker
 CC is cleaved and the binding mol. is released, the cytotoxin regains
 CC its receptor-binding ability and its cytotoxicity.
 SQ Sequence 613 AA;

Query Match 57.0%; Score 53; DB 1; Length 639;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 298 FTRHRQP 304
 |||:||||
 QY 3 FTRQRP 9

RESULT 35
 ID R40109 standard; Protein; 613 AA.
 AC R40109;
 DT 27-JAN-1994 (first entry)
 DE Pseudomonas exotoxin (R182C).
 KW Pseudomonas exotoxin; PE; diphtheria toxin; DT; immunotoxin;
 KW target site; cytotoxin; unpaired cysteine; receptor; binding site;
 KW monoclonal antibody; ligand; cell surface; mutation;
 KW steric unpaired cysteine; S.U.C.
 OS Pseudomonas aeruginosa.
 FH Key Location/Qualifiers
 FT Misc_difference 182
 FT /note= "unpaired cysteine residue replaces Arg"
 PN W09315113-A.
 PD 05-AUG-1993.
 PF 15-JAN-1993; U00358.
 PR 24-JAN-1992; US-825396.
 PA (TANO-) TANOX BIOSYSTEMS INC.
 PI Chang TW;
 DR WPI; 93-258616/32.
 PT Site-specifically mutated cytotoxin(s) with an unpaired cysteine
 PT - such that conjugation of a binding mol. to the Cys blocks
 PT receptor binding used as immuno:toxins for highly specific
 PT targeting
 PS Claim 3; Page 20-23; 30pp; English.
 CC The new mutated toxin has an unpaired cysteine residue in
 CC or near the cytotoxin's receptor-binding site, and retains the
 CC same receptor-binding ability and cytotoxicity as the native
 CC cytotoxins provided they are not conjugated with a binding mol.
 CC The toxins are cross-linked through the free SH group of their
 CC unpaired cysteine residues to binding mols. (including monoclonal
 CC antibodies, fragments and other ligands) to form immunotoxins, and
 CC these immunotoxins do not bind to the cell surface receptors which
 CC are bound by the native cytotoxin. However, when the cross-linker
 CC is cleaved and the binding mol. is released, the cytotoxin regains
 CC its receptor-binding ability and its cytotoxicity.
 SQ Sequence 613 AA;

Query Match 57.0%; Score 53; DB 1; Length 639;
 Best Local Similarity 85.7%; Pred. No. 8.86e-01;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 298 FTRHRQP 304
 |||:||||
 QY 3 FTRQRP 9

Search completed: Tue Apr 7 08:39:14 1998
 Job time : 10 secs.

MUSEAH
(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Apr 7 08:38:32 1998; MasPar time 4.81 Seconds
Tabular output not generated.
124.671 Million cell updates/sec

Title: >US-08-190-411A-2
Description: (1-14) from 5541104.pgp
Perfect Score: 93
Sequence: 1 INFRQRPSEGSS 14

Scoring table: PAM 150
Gap 15

Searched: 195121 seqs, 42852602 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: pir55
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 22.202; Variance 34.214; scale 0.649

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	93	100.0	280	2	JC2358	TOIG of: jc2358 check 6.37e-08
2	60	64.5	114	2	MADLEHQLQ	This is a DE line. 4.18e-01
3	58	62.4	172	2	I40349	TOIG of: i40349 check 9.87e-01
4	57	61.3	317	2	I38661	A:Accession: PH1297 1.51e+00
5	57	61.3	317	2	JC2359	A:Accession: PH1298 1.51e+00
6	57	61.3	651	2	A26581	A:Title: Mucopolysacch 1.51e+00
7	56	60.2	648	2	A29577	C:Superfamily: beta-gl 2.30e+00
8	56	60.2	648	2	I49692	TOIG of: i49692 check 2.30e+00
9	56	60.2	648	2	A32576	TOIG of: a32576 check 2.30e+00
10	56	60.2	648	2	B32576	TOIG of: b32576 check 2.30e+00
11	55	59.1	96	2	S54380	TOIG of: s54380 check 3.49e+00
12	55	59.1	1703	2	S15047	A:Accession: S16820 3.49e+00
13	54	58.1	186	2	S46450	This is a DE line. 5.27e+00
14	54	58.1	355	2	S60396	A:CROSS-references: EM 5.27e+00
15	54	58.1	373	2	A69158	A:Accession: A69158 5.27e+00
16	53	57.0	167	2	B53293	A:Accession: B53293 7.93e+00
17	53	57.0	188	1	THE	A:Title: The complete 7.93e+00
18	53	57.0	271	2	F69442	A:Accession: F69442 7.93e+00
19	53	57.0	638	2	A30347	A:Accession: A30347 7.93e+00
20	50	53.8	317	2	S24721	A:Accession: S24721 2.63e+01
21	50	53.8	317	2	S24747	A:Accession: S24747 2.63e+01
22	50	53.8	317	2	S24732	A:Accession: S24732 2.63e+01
23	50	53.8	330	2	S10256	A:Accession: S10256 2.63e+01

24	50	53.8	330	2	B60816	TOIG of: b60816 check 2.63e+01
25	50	53.8	410	2	A48585	TOIG of: a48585 check 2.63e+01
26	50	53.8	793	1	SURFCA	TOIG of: surfca check 2.63e+01
27	50	53.8	889	2	A41259	TOIG of: a41259 check 2.63e+01
28	49	52.7	102	1	DING	A:Accession: D26306 3.89e+01
29	49	52.7	102	1	DING	A:Accession: B26306 3.89e+01
30	49	52.7	128	1	NRYY	A:Accession: A00824 3.89e+01
31	49	52.7	130	2	S03523	TOIG of: s03523 check 3.89e+01
32	49	52.7	237	2	A48912	TOIG of: a48912 check 3.89e+01
33	49	52.7	314	2	I68889	A:Accession: PH1294 3.89e+01
34	49	52.7	343	2	S74937	A:Accession: S74937 3.89e+01
35	49	52.7	349	2	A28658	A:Accession: A28658 3.89e+01
36	49	52.7	364	1	AL	A:Accession: A93972 3.89e+01
37	49	52.7	494	2	A47059	TOIG of: a47059 check 3.89e+01
38	49	52.7	542	2	J01524	TOIG of: j01524 check 3.89e+01
39	49	52.7	648	2	A25047	A:Accession: A25047 3.89e+01
40	49	52.7	933	2	S53523	F:316-933/Domain: form 3.89e+01
41	48	51.6	94	1	R3PJ19	TOIG of: r3pj19 check 5.71e+01
42	48	51.6	162	2	S75317	A:Accession: S75317 5.71e+01
43	48	51.6	165	2	G64568	A:Authors: Hayes, W.S. 5.71e+01
44	48	51.6	179	1	E	A:Accession: A01107 5.71e+01
45	48	51.6	220	2	S35789	TOIG of: s35789 check 5.71e+01
46	48	51.6	272	2	C32058	A:Accession: C32058 5.71e+01
47	48	51.6	518	2	S42387	TOIG of: s42387 check 5.71e+01
48	48	51.6	551	3	S03667	TOIG of: s03667 check 5.71e+01
49	48	51.6	552	1	WJFFEN	A:Accession: A93354 5.71e+01
50	48	51.6	559	2	I49444	TOIG of: i49444 check 5.71e+01
51	48	51.6	584	2	B25682	TOIG of: b25682 check 5.71e+01
52	48	51.6	3573	2	S23070	F:561-843/Domain: lacy 5.71e+01
53	47	50.5	159	2	A48428	TOIG of: a48428 check 8.36e+01
54	47	50.5	162	2	S76806	A:Accession: S76806 8.36e+01
55	47	50.5	178	2	JC2022	A:Accession: JC2022 8.36e+01
56	47	50.5	199	2	D69901	A:Status: preliminary; 8.36e+01
57	47	50.5	231	1	RDNCUF	This is a DE line. 8.36e+01
58	47	50.5	288	2	H64647	A:Authors: Hayes, W.S. 8.36e+01
59	47	50.5	292	1	A40650	A:Experimental source: 8.36e+01
60	47	50.5	297	2	G69892	A:Status: preliminary; 8.36e+01
61	47	50.5	305	2	S22313	TOIG of: s22313 check 8.36e+01
62	47	50.5	317	2	A40498	TOIG of: a40498 check 8.36e+01
63	47	50.5	321	2	S22822	TOIG of: s22822 check 8.36e+01
64	47	50.5	321	2	A48136	TOIG of: a48136 check 8.36e+01
65	47	50.5	322	2	A23677	A:Accession: A23677 8.36e+01
66	47	50.5	322	2	I52910	TOIG of: i52910 check 8.36e+01
67	47	50.5	322	2	I58195	TOIG of: i58195 check 8.36e+01
68	47	50.5	324	2	J02292	This is a DE line. 8.36e+01
69	47	50.5	324	2	I39382	A:Accession: I39382 8.36e+01
70	47	50.5	324	2	A55971	A:Accession: A55971 8.36e+01
71	47	50.5	348	2	A49594	A:CROSS-references: GB 8.36e+01
72	47	50.5	364	2	PS0015	TOIG of: ps0015 check 8.36e+01
73	47	50.5	397	2	S64841	TOIG of: s64841 check 8.36e+01
74	47	50.5	459	2	S03116	R:Lee, K.L.; Makkijje, 8.36e+01
75	47	50.5	460	2	B45353	TOIG of: b45353 check 8.36e+01
76	47	50.5	506	2	D69963	A:Experimental source: 8.36e+01
77	47	50.5	517	2	S20248	TOIG of: s20248 check 8.36e+01
78	47	50.5	527	2	S13763	TOIG of: s13763 check 8.36e+01
79	47	50.5	602	2	J00215	TOIG of: j00215 check 8.36e+01
80	47	50.5	608	2	J00227	TOIG of: j00227 check 8.36e+01
81	47	50.5	630	2	I00228	TOIG of: i00228 check 8.36e+01
82	47	50.5	631	2	I56997	TOIG of: i56997 check 8.36e+01
83	47	50.5	958	2	A47179	TOIG of: a47179 check 8.36e+01
84	47	50.5	984	1	GLYCEROL-3	A:Title: The complete. 8.36e+01
85	47	50.5	1060	2	S54779	A:CROSS-references: EM 8.36e+01
86	47	50.5	1359	2	S49883	A:Accession: A28406 8.36e+01
87	46	49.5	152	1	NHRT	A:Accession: A91313 1.22e+02
88	46	49.5	301	1	E	A:Title: The complete 1.22e+02
89	46	49.5	303	2	A38274	TOIG of: a38274 check 1.22e+02
90	46	49.5	320	1	D49349	A:CROSS-references: EM 1.22e+02
91	46	49.5	328	2	S64306	TOIG of: s64306 check 1.22e+02
92	46	49.5	406	2	S17712	TOIG of: s17712 check 1.22e+02
93	46	49.5	425	1	KRXL2A	F:1-16/Region: coil 1A 1.22e+02
94	46	49.5	428	2	S07916	A:Accession: S07916 1.22e+02
95	46	49.5	492	2	S71112	TOIG of: s71112 check 1.22e+02
96	46	49.5	492	2	S07124	TOIG of: s07124 check 1.22e+02

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97 46 49.5 504 2 S46752 TOIG of: s46752 check 1.22e+02
98 46 49.5 831 3 JX0359 TOIG of: jx0359 check 1.22e+02
99 46 49.5 1204 2 S62506 TOIG of: s62506 check 1.22e+02
100 46 49.5 1507 2 B47328 TOIG of: b47328 check 1.22e+02

ALIGNMENTS
RESULT 1
ID JC2358 STANDARD; PRT; 280 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: jc2358 check: 467 from: 1 to: 280.
XX
CC TOIG of: jc2358 check: 467 from: 1 to: 280
CC
CC >P1:JC2358
CC tumor-associated antigen , MAGE-1 - human
CC C:Species: Homo sapiens (man)
CC C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Mar-19
96
CC C:Accession: JC2358
CC R:Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
CC Biochem. Biophys. Res. Commun. 202, 549-555, 1994.
CC A:Title: Cloning and analysis of MAGE-1-related genes.
CC A:Reference number: JC2358
CC A:Accession: JC2358
CC A:Molecule type: mRNA
CC A:Residues: 1-280 <DIN>
CC A:Experimental source: melanoma cell line DM150
CC C:Genetics:
CC A:Gene: MAGE
CC F:161-169/Region: HLA-A1 binding #status predicted
SQ SEQUENCE 280 AA; 30932 MW; 426797 CN;

Query Match 100.0%; Score 93; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 6.37e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 68 INFTRQRPSEGS 81
QY 1 INFTRQRPSEGS 14
|||||
|||||

RESULT 2
ID MADELHQLQTLISLTVGLGVKAELEAALLDYRDDLDIWKSHGYPVADLDQVTVDKLLMYTMDAATAD
STANDARD; PRT; 114 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE This is a DE line.
XX
SQ SEQUENCE 114 AA; 12387 MW; 67681 CN;

Query Match 64.5%; Score 60; DB 2; Length 114;
Best Local Similarity 72.7%; Pred. No. 4.18e-01;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 87 FTRQRPQDOS 97
QY 3 FTRQRPSEGS 13
|||||
|||||

RESULT 3
ID I40349 STANDARD; PRT; 172 AA.
XX
AC xxxxxx
XX
```

```
DT 01-JAN-1900
XX
DE TOIG of: i40349 check: 9523 from: 1 to: 172.
XX
CC TOIG of: i40349 check: 9523 from: 1 to: 172
CC
CC >F1:I40349
CC ribosomal protein L10 - Brucella abortus (fragment)
CC C:Species: Brucella abortus
CC C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-19
96
CC C:Accession: I40349
CC R:Oliveira, S.C.; Zhu, Y.; Splitter, G.A.
CC Gene 140, 137-138, 1994
CC A:Title: Sequences of the rplJL operon containing the L10 and L7/L12 gene
s from Brucella abortus.
CC A:Reference number: I40348; MUID:94171071
CC A:Accession: I40349
CC A>Status: preliminary; translated from GB/EMBL/DBJ
CC A:Molecule type: DNA
CC A:Residues: 1-172 <RES>
CC A:Cross-references: GB:L23505; NID:g387910; PID:g387911
CC C:Genetics:
CC A:Gene: rplJ
SQ SEQUENCE 172 AA; 18441 MW; 149510 CN;

Query Match 62.4%; Score 58; DB 2; Length 172;
Best Local Similarity 60.0%; Pred. No. 9.87e-01;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 13 VKFVROROPG 22
QY 1 INFTRQRPSP 10
::: |||||

RESULT 4
ID I38661 STANDARD; PRT; 317 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A:Accession: PH1297.
XX
CC A:Accession: PH1297
CC A:Molecule type: DNA
CC A:Residues: 169-177 <TRA>
CC C:Genetics:
CC A:Gene: GDB:MAGE4
CC A:Cross-references: GDB:331119
CC A:Map position: Xq28-Xq28
CC A:Introns: #status absent
SQ SEQUENCE 317 AA; 34899 MW; 528124 CN;

Query Match 61.3%; Score 57; DB 2; Length 317;
Best Local Similarity 71.4%; Pred. No. 1.51e+00;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 76 ISFTCWQRPNEGSS 89
QY 1 INFTRQRPSEGS 14
|||||
|||||

RESULT 5
ID JC2359 STANDARD; PRT; 317 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A:Accession: PH1298.
XX
CC A:Accession: PH1298
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CC A: Molecule type: DNA
CC A: Residues: 169-177 <TRA>
CC R: Fenton, R.G.
CC submitted to the EMBL Data Library, June 1994
CC A: Reference number: G07128
CC A: Accession: G01446
CC A: Status: preliminary; translated from GB/EMBL/DBJ
CC A: Molecule type: mRNA
CC A: Residues: 1-317 <FEN>
CC A: Cross-references: EMBL:U01340; NID:g499123; PID:g499124
CC C: Genetics;
CC A: Gene: MAGE-X2
CC F: 169-177/Region: HLA-A1 binding #status predicted
SQ SEQUENCE 317 AA: 34928 MW: 530585 CN;

01-JAN-1900	
DT	
XX	
XX	TOIG of: i49692 check: 9973 from: 1 to: 648.
DE	
XX	
XX	TOIG of: i49692 check: 9973 from: 1 to: 648
CC	
CC	
CC	>p1;i49692

```

97
CC C:Species: Mus musculus (house mouse)
CC C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Feb-19
CC
CC C:Accession: I49692
CC C:Runkelstein, B.; Leary, S.L.; Stein, J.C.; Catterall, J.F.
CC C:Mol. Cell. Biol. 8, 1160-1168, 1988
CC C:A>Title: Genomic organization and sequence of the Gus-sa allele of the m
CC C: urine beta-glucuronidase gene.
CC C:A:Reference number: I49692; MUID:88216590
CC C:A:Accession: I49692
CC C:A>Status: preliminary; translated from GB/EMBL/DBJ
CC C:A:Molecule type: mRNA
CC C:A:Residues: 1-648 <RES>
CC C:A:Cross-references: GB:M19279; NID:g193524; PID:g309257
CC C:A:Superfamily: beta-glucuronidase
CC C:SEQUENCE 648 AA; 74192 MW; 2302638 CN;

Query Match 60.2%; Score 56; DB 2; Length 648;
Best Local Similarity 100.0%; Pred. No. 2.30e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 605 FTRORQP 611
|||||||
Qy 3 FTRORQP 9

```

ID A32576 STANDARD; PRT; 648 AA.
 XX
 XX
 AC xxxxxx
 XX
 XX
 DT 01-JAN-1900
 XX
 XX
 DE TOIG of: a32576 check: 9124 from: 1 to: 648.

```

CC      1016  GR: A32576  CHECK: 3124  FROM: 1  CO: 040
CC
CC      >P1:A32576
CC      beta-glucuronidase (EC 3.2.1.31) B - mouse
CC      C:Species: Mus musculus (house mouse)
CC      C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 31-Oct-19
CC      97
CC      C:Accession: A32576
CC      R:Wawrzyniak, C.J.; Gallagher, P.M.; D'Amore, M.A.; Carter, J.E.; Lund, S
CC      D.; Rinchik, E.M.; Ganschow, R.E.
CC      Mol. Cell. Biol. 9, 4074-4078, 1989
CC      A:Title: DNA determinants of structural and regulatory variation within t
CC      he murine beta-glucuronidase gene complex.
CC      A:Reference number: A32576; MUID:89384641
CC      A:Accession: A32576
CC

```

```
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 1-648 <WAW>
CC A:Cross-references: GB:M28540; GB:M27816; NID:g193718; PID:g193719
CC C:Superfamily: beta-glucuronidase
CC C:Keywords: glycosidase; hydrolase
SQ SEQUENCE 648 AA; 74195 MW; 2298575 CN;

Query Match 60.2%; Score 56; DB 2; Length 648;
Best Local Similarity 100.0%; Pred. No. 2.30e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 605 FTRORQP 611
|||||
QY 3 FTRORQP 9

RESULT 10
ID B32576 STANDARD; PRT; 648 AA.
XX
AC xxxxxx
DT 01-JAN-1900
DE
TOIG of: b32576 check: 8794 from: 1 to: 648.
XX
TOIG of: b32576 check: 8794 from: 1 to: 648
CC
>P1:B32576
CC beta-glucuronidase (EC 3.2.1.31) H - mouse
CC C:Species: Mus musculus (house mouse)
CC C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 08-Sep-19
97
CC C:Accession: B32576
CC R:Wawryniak, C.J.; Gallagher, P.M.; D'Amore, M.A.; Carter, J.E.; Lund, S
.d.; Rinchik, E.M.; Ganschow, R.E.
CC Mol. Cell. Biol. 9, 4074-4078, 1989
CC A:Title: DNA determinants of structural and regulatory variation within t
he murine beta-glucuronidase gene complex
CC A:Reference number: A32576; MUID:89384641
CC A:Accession: B32576
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 1-648 <WAW>
CC A:Cross-references: GB:M28541; NID:g193720; PID:g193721; GB:M27816
CC C:Superfamily: beta-glucuronidase
CC C:Keywords: glycosidase; hydrolase
SQ SEQUENCE 648 AA; 74207 MW; 2297966 CN;

Query Match 60.2%; Score 56; DB 2; Length 648;
Best Local Similarity 100.0%; Pred. No. 2.30e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 605 FTRORQP 611
|||||
QY 3 FTRORQP 9

RESULT 11
ID S54380 STANDARD; PRT; 96 AA.
XX
AC xxxxxx
DT 01-JAN-1900
DE
TOIG of: s54380 check: 8538 from: 1 to: 96.
XX
TOIG of: s54380 check: 8538 from: 1 to: 96
CC
>P1:S54380
CC vpr protein - human immunodeficiency virus type 1
CC C:Species: human immunodeficiency virus type 1, HIV-1
CC C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 08-Sep-19
```

```
97
CC C:Accession: S54380
CC R:Theodore, T.; Buckler-White, A.J.
CC submitted to the EMBL Data Library, July 1989
CC A:Reference number: S54377
CC A:Accession: S54380
CC A:Status: preliminary
CC A:Molecule type: genomic RNA
CC A:Residues: 1-96 <THE>
CC A:Cross-references: EMBL:M2639; NID:g329377; PID:g329383
CC C:Superfamily: AIDS vpr protein
SQ SEQUENCE 96 AA; 11380 MW; 42519 CN;

Query Match 59.1%; Score 55; DB 2; Length 96;
Best Local Similarity 57.1%; Pred. No. 3.49e+00;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRQRARRNGSS 94
|:||||:|
QY 1 INFTRQRPSEGS 14

RESULT 12
ID S15047 STANDARD; PRT; 1703 AA.
XX
AC xxxxxx
DT 01-JAN-1900
DE
XX A:Accession: S16820.
CC A:Accession: S16820
CC A:Molecule type: DNA
CC A:Residues: 1-1703 <YOS>
CC A:Cross-references: EMBL:X57837; NID:g4499; PID:g4500
CC R:Cheret, G.; Sor, F.
CC submitted to the Protein Sequence Database, July 1996
CC A:Reference number: S67169
CC A:Accession: S67192
CC A:Molecule type: DNA
CC A:Residues: 1-1703 <CHE>
CC A:Cross-references: EMBL:Z75198; NID:g1420643; PID:e252424; PID:g1420644;
MIPS:YOR290c
CC A:Experimental source: strain S288C
CC R:Czilepluch, C.; Jauniaux, J.C.; Kordes, E.; Poirey, R.; Pujol, A.; Tobia
sch, E.
CC submitted to the Protein Sequence Database, July 1996
CC A:Reference number: S67194
CC A:Accession: S67194
CC A:Molecule type: DNA
CC A:Residues: 1-308 <CZI>
CC A:Cross-references: EMBL:Z75198; MIPS:YOR290c
CC A:Experimental source: strain S288C
CC R:Cheret, G.; Bernardi, A.; Sor, F.
CC Yeast 12, 1059-1064, 1996
CC A:Title: DNA sequence analysis of the VP1-SNF2 region on chromosome XV o
f Saccharomyces cerevisiae.
CC A:Reference number: S72039
CC A:Accession: S72058
CC A:Status: nucleic acid sequence not shown; translation not shown
CC A:Molecule type: DNA
CC A:Residues: 1-1703 <CHW>
CC A:Cross-references: EMBL:X89633
CC A:Note: the nucleotide sequence was submitted to the EMBL Data Library, J
une 1995
CC C:Genetics:
CC A:Gene: SGD:SNF2; GAM1
CC A:Cross-references: MIPS:YOR290c; SGD:S0005816
CC A:Map position: 15R
CC C:Superfamily: unassigned bromodomain proteins; bromodomain homology
CC C:Keywords: nucleus; transcription regulation
CC F:1576-1631/Domain: bromodomain homology <BRO>
SQ SEQUENCE 1703 AA; 194050 MW; 14055514 CN;
```



```
Query Match      59.1%; Score 55; DB 2; Length 1703;
Best Local Similarity 50.0%; Pred. No. 3.49e+00;
Matches      5; Conservative      5; Mismatches      0; Indels      0; Gaps      0;

Db 299 EFARROPTD 308
   :|:|:|:|:|:|:
QY 2 NFTRQRPSE 11

RESULT 13
ID S46450 STANDARD; PRT; 186 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX This is a DE line.
XX
SQ SEQUENCE 186 AA; 20952 MW; 191295 CN;

Query Match      58.1%; Score 54; DB 2; Length 186;
Best Local Similarity 63.6%; Pred. No. 5.27e+00;
Matches      7; Conservative      2; Mismatches      2; Indels      0; Gaps      0;

Db 159 FTROHQPODPS 169
   :|:|:|:|:|:|:
QY 3 FTROHQPSEGS 13

-RESULT 14
ID S60396 STANDARD; PRT; 355 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A;Cross-references: EMBL:U23084; NID:g1050853; PID:g1050856.
XX
CC A;Cross-references: EMBL:U23084; NID:g1050853; PID:g1050856
CC A;Note: the nucleotide sequence was submitted to the EMBL Data Library, M
arch 1995
CC R;Maurer, C.T.C.; Urbanus, J.H.M.; Planta, R.J.
CC submitted to the Protein Sequence Database, April 1996
CC A;Reference number: S63286
CC A;Accession: S63280
CC A;Molecule type: DNA
CC A;Residues: 1-355 <MAW>
CC A;Cross-references: EMBL:Z71580; NID:g1302399; PID:e239733; PID:g1302400;
CC MIPS:YNLJ304w
CC A;Experimental source: strain S288C
CC C;Genetics:
CC A;Map position: 14L
SQ SEQUENCE 355 AA; 40678 MW; 624416 CN;

Query Match      58.1%; Score 54; DB 2; Length 355;
Best Local Similarity 87.5%; Pred. No. 5.27e+00;
Matches      7; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

Db 321 FNETRQ 328
   :|:|:|:|:|:|:
QY 1 INFTRQ 8

RESULT 15
ID A69158 STANDARD; PRT; 373 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A;Accession: A69158.
XX
```

```
CC A;Accession: A69158
CC A;Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A;Molecule type: DNA
CC A;Residues: 1-373 <MTH>
CC A;Cross-references: GB:AE000666
CC A;Experimental source: strain Delta H
CC C;Genetics:
CC A;Gene: MTH444
SQ SEQUENCE 373 AA; 42263 MW; 688580 CN;

Query Match      58.1%; Score 54; DB 2; Length 373;
Best Local Similarity 60.0%; Pred. No. 5.27e+00;
Matches      6; Conservative      4; Mismatches      0; Indels      0; Gaps      0;

Db 277 IKFTRDRDPA 286
   :|:|:|:|:|:|:
QY 1 INFTRQ 10

RESULT 16
ID B53293 STANDARD; PRT; 167 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A;Accession: B53293.
XX
CC A;Accession: B53293
CC A;Status: preliminary
CC A;Molecule type: DNA
CC A;Residues: 1-167 <DOL>
CC A;Cross-references: GB:L19521
CC C;Genetics:
CC A;Start codon: GTT
SQ SEQUENCE 167 AA; 18772 MW; 146186 CN;

Query Match      57.0%; Score 53; DB 2; Length 167;
Best Local Similarity 50.0%; Pred. No. 7.93e+00;
Matches      5; Conservative      5; Mismatches      0; Indels      0; Gaps      0;

Db 74 VNYARQ 83
   :|:|:|:|:|:|:
QY 1 INFTRQ 10

RESULT 17
ID THE INITIATION OF TRANSCRIPTION; THE COMPLEX ALSO REGULATES TRP REPRESSOR
BIOSYNTHESIS BY BINDING TO ITS REGULATORY REGION STANDARD; PRT; 205
AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A;Title: The complete genome sequence of Escherichia coli K-12.
XX
CC A;Title: The complete genome sequence of Escherichia coli K-12.
CC A;Reference number: A64720; MUID:97426617
CC A;Accession: H65254
CC A;Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A;Molecule type: DNA
CC A;Residues: 1-108 <BLAT>
CC A;Cross-references: GB:AE000509; GB:U00096; NID:g2367383; PID:g1790854; U
WGP:b4393
CC A;Experimental source: strain K-12, substrain MG1655
CC C;Genetics:
CC A;Gene: trpR
CC A;Map position: 100 min
CC C;Function:
CC A;Description: an aporepressor; when complexed with L-tryptophan it binds
```

the operator region of the trp operon and prevents
SQ SEQUENCE 205 AA; 23624 MW; 206628 CN;

Query Match 57.0%; Score 53; DB 1; Length 188;
Best Local Similarity 53.8%; Pred. No. 7.93e+00;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 10 ILYTRPREPRESS 22
I :|| I:| I:|

QY 1 INFTRQRPSEGS 13

RESULT 18
ID F69442 STANDARD; PRT; 271 AA.

XX

AC xxxxxx

XX 01-JAN-1900

XX A;Accession: F69442.

XX A;Accession: F69442

CC A;Status: preliminary; nucleic acid sequence not shown; translation not shown
CC A;Molecule type: DNA
CC A;Residues: 1-271 <KLE>
CC A;Cross-references: GB:AE000782; TIGR:AF1543
SQ SEQUENCE 271 AA; 31009 MW; 390830 CN;

Query Match 57.0%; Score 53; DB 2; Length 271;
Best Local Similarity 41.7%; Pred. No. 7.93e+00;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 11 DFVRHRQNEGG 22

I :|| I:| I:|

QY 2 NFTRQRPSEGS 13

RESULT 19
ID A30347 STANDARD; PRT; 638 AA.

XX

AC xxxxxx

XX 01-JAN-1900

XX A;Accession: A30347.

XX A;Accession: A30347

CC A;Status: preliminary

CC A;Molecule type: DNA

CC A;Residues: 1-638 <GRA>

CC C;Keywords: exotoxin

SQ SEQUENCE 638 AA; 69308 MW; 1915001 CN;

Query Match 57.0%; Score 53; DB 2; Length 638;
Best Local Similarity 85.7%; Pred. No. 7.93e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 297 FTRHRQP 303

|||||

QY 3 FTRQRP 9

RESULT 20
ID S24721 STANDARD; PRT; 317 AA.

XX

AC xxxxxx

XX 01-JAN-1900

XX A;Accession: S24721.

XX A;Accession: S24721

CC A;Status: nucleic acid sequence not shown; translation not shown
CC A;Molecule type: DNA
CC A;Residues: 1-317 <ZHO>
CC A;Cross-references: EMBL:X64851; NID:g44848; PID:g44849
CC A;Experimental source: strain FA19
CC A;Note: the nucleotide sequence was submitted to the EMBL Data Library, M arch 1992

CC C;Genetics:

CC A;Gene: fbp

CC C;Superfamily: sfuA protein

CC C;Keywords: iron binding

SQ SEQUENCE 317 AA; 34244 MW; 507109 CN;

Query Match 53.8%; Score 50; DB 2; Length 317;
Best Local Similarity 50.0%; Pred. No. 2.63e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 227 LNFVRHRDPG 236

:|| I:| I:|

QY 1 INFTRQRP 10

RESULT 21
ID S24747 STANDARD; PRT; 317 AA.

XX

AC xxxxxx

XX 01-JAN-1900

XX A;Accession: S24747.

XX A;Accession: S24747

CC A;Status: nucleic acid sequence not shown; translation not shown

CC A;Molecule type: DNA

CC A;Residues: 1-317 <ZHO>

CC A;Cross-references: EMBL:X64852; NID:g45244; PID:g45245

CC A;Experimental source: strain S3446

CC A;Note: the nucleotide sequence was submitted to the EMBL Data Library, M arch 1992

CC C;Genetics:

CC A;Gene: fbp

CC C;Superfamily: sfuA protein

CC C;Keywords: iron binding

SQ SEQUENCE 317 AA; 34246 MW; 505589 CN;

Query Match 53.8%; Score 50; DB 2; Length 317;
Best Local Similarity 50.0%; Pred. No. 2.63e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 227 LNFVRHRDPG 236

:|| I:| I:|

QY 1 INFTRQRP 10

RESULT 22
ID S24732 STANDARD; PRT; 317 AA.

XX

AC xxxxxx

XX 01-JAN-1900

XX A;Accession: S24732.

XX A;Accession: S24732

CC A;Status: nucleic acid sequence not shown; translation not shown

CC A;Molecule type: DNA

CC A;Residues: 1-317 <ZHO>

CC A;Cross-references: EMBL:X64853; NID:g45051; PID:g45052

CC A;Experimental source: strain HF130

CC A;Note: the nucleotide sequence was submitted to the EMBL Data Library, M arch 1992

CC A;Accession: S24725

CC A;Status: nucleic acid sequence not shown; translation not shown

CC A;Molecule type: DNA
CC A;Residues: 1-317 <ZH2>
CC A;Cross-references: EMBL:X64858; NID:g45013; PID:g45014
CC A;Experimental source: strain 44/46
CC A;Note: the nucleotide sequence was submitted to the EMBL Data Library, M arch 1992
CC A;Accession: S24729
CC A;Status: nucleic acid sequence not shown; translation not shown
CC A;Molecule type: DNA
CC A;Residues: 1-317 <ZH3>
CC A;Cross-references: EMBL:X64857; NID:g45045; PID:g45046
CC A;Experimental source: strain HF116
CC A;Note: the nucleotide sequence was submitted to the EMBL Data Library, M arch 1992
CC A;Accession: S24735
CC A;Status: nucleic acid sequence not shown; translation not shown
CC A;Molecule type: DNA
CC A;Residues: 1-317 <ZH4>
CC A;Cross-references: EMBL:X64856; NID:g45057; PID:g45058
CC A;Experimental source: strain HF46
CC A;Note: the nucleotide sequence was submitted to the EMBL Data Library, M arch 1992
CC A;Accession: S24738
CC A;Status: nucleic acid sequence not shown; translation not shown
CC A;Molecule type: DNA
CC A;Residues: 1-317 <ZH5>
CC A;Cross-references: EMBL:X64859; NID:g45101; PID:g45102
CC A;Experimental source: strain M470
CC A;Note: the nucleotide sequence was submitted to the EMBL Data Library, M arch 1992
CC A;Accession: S24740
CC A;Status: nucleic acid sequence not shown; translation not shown
CC A;Molecule type: DNA
CC A;Residues: 1-317 <ZH6>
CC A;Cross-references: EMBL:X64855; NID:g45157; PID:g45158
CC A;Experimental source: strain N94II
CC A;Note: the nucleotide sequence was submitted to the EMBL Data Library, M arch 1992
CC A;Accession: S24744
CC A;Status: nucleic acid sequence not shown; translation not shown
CC A;Molecule type: DNA
CC A;Residues: 1-317 <ZH7>
CC A;Cross-references: EMBL:X64854; NID:g45173; PID:g45174
CC A;Experimental source: strain P63
CC A;Note: the nucleotide sequence was submitted to the EMBL Data Library, M arch 1992
CC C;Genetics:
CC A;Gene: fbp
CC C;Superfamily: sfuA protein
CC C;Keywords: iron binding
CC C;Species: Neisseria meningitidis
SQ SEQUENCE 317 AA; 34232 MW; 507979 CN;

Query Match 53.8%; Score 50; DB 2; Length 317;
Best Local Similarity 50.0%; Pred. No. 2.63e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 227 LNFVHRDPG 236
::: |::|:
QY 1 INTRQRQPS 10

RESULT 23
ID S10256 STANDARD; PRT; 330 AA.

XX AC
XX xxxxxx
DT 01-JAN-1900

DE A;Accession: S10256.

XX A;Accession: S10256

CC A;Molecule type: DNA

CC A;Residues: 1-330 <BER>

CC A;Cross-references: EMBL:X51901; NID:g44857; PID:g44858
CC R;Morse, S.A.; Mietzner, T.A.; Bolen, G.; LeFaou, A.; Schoolnik, G.
CC Antonie Van Leeuwenhoek 53, 465-469, 1987
CC A;Title: Characterization of the major iron-regulated protein of Neisseria gonorrhoeae and Neisseria meningitidis.
CC A;Reference number: A60816
CC A;Accession: A60816
CC A;Molecule type: protein
CC A;Residues: 23-69 <MOR>
CC R;Mietzner, T.A.; Bolen, G.; Schoolnik, G.K.; Morse, S.A.
CC J. Exp. Med. 165, 1041-1057, 1987
CC A;Title: Purification and characterization of the major iron-regulated protein expressed by pathogenic Neisseriae.
CC A;Reference number: A46544
CC A;Accession: A46544
CC A;Status: preliminary
CC A;Molecule type: protein
CC A;Residues: 23-69 <MIE>
CC C;Genetics:
CC A;Gene: fbp
CC C;Superfamily: sfuA protein
CC C;Keywords: iron binding
CC C;F;1-22/Domain: signal sequence #status experimental <SIG>
CC F;23-330/Product: iron-binding protein #status experimental <MAT>
SQ SEQUENCE 330 AA; 35769 MW; 546828 CN;
Query Match 53.8%; Score 50; DB 2; Length 330;
Best Local Similarity 50.0%; Pred. No. 2.63e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Db 235 LNFVHRDPG 244
::: |::|:
QY 1 INTRQRQPS 10
RESULT 24
ID B60816 STANDARD; PRT; 330 AA.
XX AC
XX xxxxxx
DT 01-JAN-1900
DE TOIG of: b60816 check: 1589 from: 1 to: 330.
XX TOIG of: b60816 check: 1589 from: 1 to: 330
CC TOIG of: b60816 check: 1589 from: 1 to: 330
CC >P1:B60816
CC major iron-regulated protein - Neisseria meningitidis
CC N;Alternate names: iron-binding protein; MIRP
CC C;Species: Neisseria meningitidis
CC C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Sep-1997
CC C;Accession: S10978; B60816
CC R;Berish, S.A.; Kapczynski, D.R.; Morse, S.A.
CC Nucleic Acids Res 18, 4596, 1990
CC A;Title: Nucleotide sequence of the fbp gene from Neisseria meningitidis.
CC A;Reference number: S10978
CC A;Accession: S10978
CC A;Molecule type: DNA
CC A;Residues: 1-330 <BER>
CC A;Cross-references: EMBL:X53467; NID:g45037; PID:g45038
CC R;Morse, S.A.; Mietzner, T.A.; Bolen, G.; LeFaou, A.; Schoolnik, G.
CC Antonie Van Leeuwenhoek 53, 465-469, 1987
CC A;Title: Characterization of the major iron-regulated protein of Neisseria gonorrhoeae and Neisseria meningitidis.
CC A;Reference number: A60816
CC A;Accession: B60816
CC A;Molecule type: protein
CC A;Residues: 23-69 <MOR>
CC C;Genetics:
CC A;Gene: fbp
CC C;Superfamily: sfuA protein
CC C;Keywords: iron binding

```
CC F:23-330/Product: major iron-regulated protein #status experimental <MAT>
SQ SEQUENCE 330 AA; 35741 MW; 544204 CN;

Query Match 53.8%; Score 50; DB 2; Length 330;
Best Local Similarity 50.0%; Pred. No. 2.63e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 235 LNFVHRDPG 244
QY 1 INFTRQRPQS 10
||| |||:|:|
||| |||:|:|

RESULT 25
ID A48585 STANDARD; PRT; 410 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: a48585 check: 4186 from: 1 to: 410.
XX
CC TOIG of: a48585 check: 4186 from: 1 to: 410
CC
CC >P1:A48585
CC transcription factor DP-1 - human
CC C:Species: Homo sapiens (man)
CC C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 10-Sep-19
97
CC C:Accession: A48585
CC R:Helin, K.; Wu, C.L.; Fattaey, A.R.; Lees, J.A.; Dynlacht, B.D.; Ngwu, C
.; Harlow, E.
CC Genes Dev. 7, 1850-1861, 1993
CC A:Title: Heterodimerization of the transcription factors E2F-1 and DP-1 l
eads to cooperative trans-activation.
CC A:Reference number: A48585
CC A:Accession: A48585
CC A:Status: preliminary; nucleic acid sequence not shown
CC A:Molecule type: mRNA
CC A:Residues: 1-410 <HEL>
CC A:Cross-references: GB:L23959; NID:g414316; PID:g414317
CC C:Keywords: DNA binding; transcription factor
SQ SEQUENCE 410 AA; 45070 MW; 833309 CN;

Query Match 53.8%; Score 50; DB 2; Length 410;
Best Local Similarity 46.2%; Pred. No. 2.63e+01;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 87 HFASQNPDSPP 99
QY 2 NFTRQRPSEGS 14
||| |||:|:|
||| |||:|:|

RESULT 26
ID SURFCA STANDARD; PRT; 793 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: surfca check: 4832 from: 1 to: 793.
XX
CC TOIG of: surfca check: 4832 from: 1 to: 793
CC
CC >P1:SURFCA
CC ATP-dependent Clp proteinase (EC 3.4.21.-) chain A homolog - Rhodopsuom
onas blastica
CC C:Species: Rhodopsuomonas blastica
CC C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 28-Feb-19
97
CC C:Accession: S04667
CC R:Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
CC J. Mol. Biol. 179, 185-214, 1984
CC A:Title: Rhodopsuomonas blastica atp operon. Nucleotide sequence and tr
```

```
anscription.
CC A:Reference number: S04666; MUID:85058188
CC A:Accession: S04667
CC A:Molecule type: DNA
CC A:Residues: 1-793 <TYB>
CC C:Superfamily: ATP-dependent Clp proteinase chain A
CC C:Keywords: ATP; hydrolase; nucleotide binding; P-loop; serine proteinase
F:244-253/Region: nucleotide-binding motif A (P-loop)
CC F:311-315/Region: nucleotide-binding motif B
CC F:525-533/Region: nucleotide-binding motif A (P-loop)
CC F:590-594/Region: nucleotide-binding motif B
SQ SEQUENCE 793 AA; 86890 MW; 3017877 CN;

Query Match 53.8%; Score 50; DB 1; Length 793;
Best Local Similarity 35.7%; Pred. No. 2.63e+01;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 647 IGFGRRRTGEDTA 660
QY 1 INFTRQRPSEGS 14
||| |||:|:|
||| |||:|:|

RESULT 27
ID A41259 STANDARD; PRT; 889 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: a41259 check: 4909 from: 1 to: 889.
XX
CC TOIG of: a41259 check: 4909 from: 1 to: 889
CC
CC >P1:A41259
CC potassium transport protein TRK2, low-affinity - yeast (Saccharomyces cer
evisiae)
CC N:Alternate names: protein YKR050w
CC C:Species: Saccharomyces cerevisiae
CC C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 05-Dec-19
97
CC C:Accession: A41259; S38124; S17489
CC R:KO, C.H.; Gaber, R.F.
CC Mol. Cell. Biol. 11, 4266-4273, 1991
CC A:Title: TRK1 and TRK2 encode structurally related K(+) transporters in S
accharomyces cerevisiae.
CC A:Reference number: A41259; MUID:91304419
CC A:Accession: A41259
CC A:Molecule type: DNA
CC A:Residues: 1-889 <KOC>
CC A:Cross-references: GB:M65215; NID:g173032; PID:g173033
CC R:Visiers, S.; Urrestarazu, L.A.; Jauniaux, J.C.
CC submitted to the Protein Sequence Database, March 1994
CC A:Reference number: S38118
CC A:Accession: S38124
CC A:Molecule type: DNA
CC A:Residues: 1-889 <VIS>
CC A:Cross-references: EMBL:28275; NID:g486502; PID:g486503; MIPS:YKR050w
CC A:Experimental source: strain S288C
CC C:Genetics:
CC A:Gene: SGD:TRK2
CC A:Cross-references: SGD:S0001758
CC A:Map position: 11R
CC C:Superfamily: potassium transport protein TRK1
CC C:Keywords: ion transport; potassium transport; transmembrane protein
F:53-73/Domain: transmembrane #status predicted <TM01>
CC F:80-101/Domain: transmembrane #status predicted <TM02>
CC F:109-131/Domain: transmembrane #status predicted <TM03>
CC F:465-481/Domain: transmembrane #status predicted <TM04>
CC F:500-521/Domain: transmembrane #status predicted <TM05>
CC F:525-545/Domain: transmembrane #status predicted <TM06>
CC F:549-569/Domain: transmembrane #status predicted <TM07>
CC F:585-605/Domain: transmembrane #status predicted <TM08>
CC F:609-630/Domain: transmembrane #status predicted <TM09>
```

CC F:658-662/Domain: transmembrane #status predicted <TM10>
CC F:744-764/Domain: transmembrane #status predicted <TM11>
CC F:777-797/Domain: transmembrane #status predicted <TM12>
SQ SEQUENCE 889 AA; 101085 MW; 4294395 CN;

Query Match 53.8%; Score 50; DB 2; Length 889;
Best Local Similarity 60.0%; Pred. No. 2.63e+01;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 233 NFSSKRPSPD 242
II: ||||:
QY 2 NFTRQRPSE 11

RESULT 28
ID DING EGG-LAYING HORMONE, THAT CONTROL THE PHYSIOLOGICAL PROCESSES OF EGG-L
AYING. STANDARD; PRT; 132 AA.

XX
AC xxxxxx

XX
DT 01-JAN-1900

XX
DE A:Accession: D26306.

XX
CC A:Accession: D26306

CC A:Molecule type: protein

CC A:Residues: 117-152;156-173 <NA2>

CC C:Comment: Atrial gland peptides A and B initiate egg-laying by stimulati
ng bag cell neurons to release other peptides, incl
SQ SEQUENCE 132 AA; 15099 MW; 109782 CN;

Query Match 52.7%; Score 49; DB 1; Length 102;
Best Local Similarity 41.7%; Pred. No. 3.89e+01;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 72 ILYAREPREPES 83
I::I::I::I::

QY 1 INFTRQRPSEG 12

RESULT 29
ID DING EGG-LAYING HORMONE, THAT CONTROL THE PHYSIOLOGICAL PROCESSES OF EGG-L
AYING. STANDARD; PRT; 132 AA.

XX
AC xxxxxx

XX
DT 01-JAN-1900

XX
DE A:Accession: B26306.

XX
CC A:Accession: B26306

CC A:Molecule type: protein

CC A:Residues: 117-152;156-173 <NA2>

CC C:Comment: Atrial gland peptides A and B initiate egg-laying by stimulati
ng bag cell neurons to release other peptides, incl
SQ SEQUENCE 132 AA; 15099 MW; 109782 CN;

Query Match 52.7%; Score 49; DB 1; Length 102;
Best Local Similarity 41.7%; Pred. No. 3.89e+01;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 72 ILYAREPREPES 83
I::I::I::I::

QY 1 INFTRQRPSEG 12

RESULT 30
ID NRYV STANDARD; PRT; 128 AA.

XX
AC xxxxxx

XX
DT 01-JAN-1900

XX

DE A:Accession: A00824.
XX
CC A:Accession: A00824
CC A:Molecule type: protein
CC A:Residues: 1-128 <BEI>
CC C:Comment: The capybara is a rodent belonging to the same superfamily as
the guinea pig.
CC C:Superfamily: pancreatic ribonuclease
CC C:Keywords: hydrolase; nucleic acid digestion; pancreas
CC F:12,41,119/Active Site: His, Lys, His #status predicted
CC F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
SQ SEQUENCE 128 AA; 14345 MW; 92128 CN;

Query Match 52.7%; Score 49; DB 1; Length 128;
Best Local Similarity 57.1%; Pred. No. 3.89e+01;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 6 MKFQRQHVDSGSS 19
::||: ||||

QY 1 INFTRQRPSEGSS 14

RESULT 31
ID S03523 STANDARD; PRT; 130 AA.

XX
AC xxxxxx

XX
DT 01-JAN-1900

XX
DE TOIG of: s03523 check: 7915 from: 1 to: 130.

XX
CC TOIG of: s03523 check: 7915 from: 1 to: 130

CC
CC >F1:S03523

CC T-cell receptor alpha chain precursor V-J region (HD-Mar) - human (fragme
nt)

CC C:Species: Homo sapiens (man)

CC C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Sep-19

97

CC C:Accession: S03523

CC R:Luria, S.; Gross, G.; Horowitz, M.; Givol, D.

CC EMBO J. 6, 3307-3312, 1987

CC A:Title: Promoter and enhancer elements in the rearranged alpha chain gen
e of the human T cell receptor.

CC A:Reference number: S03523; MUID:88111516

CC A:Accession: S03523

CC A:Molecule type: DNA

CC A:Residues: 1-130 <LUR>

CC A:Cross-references: EMBL:X06192; NID:g36908; PID:g296677

CC A:Note: this sequence was determined from the differentiated gene

CC C:Genetics:

CC A:Introns: 15/1

CC C:Superfamily: immunoglobulin V region; immunoglobulin homology

CC C:Keywords: T-cell receptor

CC F:1-18/Domain: signal sequence #status predicted <SIG>

CC F:19-110/Product: T-cell receptor alpha chain V region HD-Mar #status pre
dicted <MAT>

CC F:114-130/Domain: J region (J-alpha-3) #status experimental <JRE>

SQ SEQUENCE 130 AA; 14687 MW; 94561 CN;

Query Match 52.7%; Score 49; DB 2; Length 130;

Best Local Similarity 41.7%; Pred. No. 3.89e+01;

Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 94 FIRDQSPDSAT 105
I::I::I::I::

QY 3 FTRQRPSEGSS 14

RESULT 32

ID A48912 STANDARD; PRT; 237 AA.

XX
AC xxxxxx

```
XX 01-JAN-1900
DT
DE
DE
DE
XX TOIG of: a48912 check: 632 from: 1 to: 237.
XX
CC TOIG of: a48912 check: 632 from: 1 to: 237
CC
CC >P1:A48912
CC leucine zipper protein Nrl, retina-specific - mouse
CC C:Species: Mus musculus (house mouse)
CC C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-19
CC 97
CC C:Accession: A48912
CC R:Farjo, O.; Jackson, A.U.; Xu, J.; Gryzenia, M.; Skolnick, C.; Agarwal,
CC N.: Swaroop, A.
CC Genomics 18, 216-222, 1993
CC A:Title: Molecular characterization of the murine neural retina leucine z
CC ipper gene, Nrl.
CC A:Reference number: A48912
CC A:Accession: A48912
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 1-237 <FAR>
CC A:Cross-references: GB:L14935; NID:g388916; PID:g388917
CC C:Genetics:
CC A:Gene: Nrl
CC C:Superfamily: maf transforming protein; maf homology
CC C:Keywords: DNA binding; leucine zipper; retina
CC F:133-222/Domain: maf homology <MAF>
CC SEQUENCE 237 AA; 26083 MW; 238917 CN;

Query Match 52.7%; Score 49; DB 2; Length 237;
Best Local Similarity 50.0%; Pred. No. 3.89e+01;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 19 MKFEIKREPSEGRS 32
QY 1 INFTRQRPSEGS 14
:::|:|||||

RESULT 33
ID I6889 STANDARD; PRT; 314 AA.
XX
XX
XX
XX 01-JAN-1900.
XX
XX A:Accession: PH1294.
XX
XX A:Accession: PH1294
XX A:Molecule type: DNA
XX A:Residues: 168-176 <TRA>
XX C:Genetics:
XX A:Gene: GDB:MAGEA2; MAGE2
XX A:Cross-references: GDB:273684
XX A:Map position: Xq28-Xq28
XX SEQUENCE 314 AA; 35054 MW; 525196 CN;

Query Match 52.7%; Score 49; DB 2; Length 314;
Best Local Similarity 64.3%; Pred. No. 3.89e+01;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 75 INYTLWROSDEGSS 88
QY 1 INFTRQRPSEGS 14
||:|:|||||

RESULT 34
ID -S74937 STANDARD; PRT; 343 AA.
XX
XX
XX
XX 01-JAN-1900
DT
DT
DT
DT
XX A:Accession: S74937.
XX
XX A:Accession: S74937
XX A:Status: preliminary
XX A:Molecule type: DNA
XX A:Residues: 1-343 <KAN>
XX A:Cross-references: EMBL:D90902; NID:g1652027; PID:d1017710; PID:g1652052
XX A:Note: the nucleotide sequence was submitted to the EMBL Data Library, J
XX une 1996
XX SEQUENCE 343 AA; 37956 MW; 575559 CN;

Query Match 52.7%; Score 49; DB 2; Length 343;
Best Local Similarity 87.5%; Pred. No. 3.89e+01;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 315 RORQPSTG 322
QY 5 RORQPSEG 12
|||||||

RESULT 35
ID A28658 STANDARD; PRT; 349 AA.
XX
XX
XX
XX 01-JAN-1900
XX
XX A:Accession: A28658.
XX
XX A:Accession: A28658
XX A:Molecule type: DNA
XX A:Residues: 1-349 <STA>
XX A:Cross-references: GB:J03196; NID:gl49174; PID:gl49175
XX C:Keywords: hydrolase
XX SEQUENCE 349 AA; 37801 MW; 607988 CN;

Query Match 52.7%; Score 49; DB 2; Length 349;
Best Local Similarity 50.0%; Pred. No. 3.89e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 298 VSINRQRPQA 307
QY 1 INFTRQRPQS 10
:::|:|||||

Search completed: Tue Apr 7 08:38:47 1998
Job time : 15 secs.
```

WQSEFH

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:37:29 1998; MasPar time 2.36 Seconds

Tabular output not generated.

Title: >US-08-190-411A-2
Description: (1-14) from 5541104.ppe
Perfect Score: 93
Sequence: 1 INFTROPSEGSS 14

Scoring table: PAM 150
Gap 15

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 25.257; Variance 27.960; scale 0.903

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	%	ID	Description	Pred. No.
1	93	100.0	309	1	MAG1_HUMAN	MELANOMA-ASSOCIATED AN
2	58	62.4	172	1	RL10_BRUAB	50S RIBOSOMAL PROTEIN
3	57	61.3	317	1	MAG4_HUMAN	MELANOMA-ASSOCIATED AN
4	57	61.3	651	1	BGLR_HUMAN	BETA-GLUCURONIDASE PRE
5	56	60.2	648	1	BGLR_MOUSE	BETA-GLUCURONIDASE PRE
6	55	59.1	96	1	VPR_HV122	VPR PROTEIN (R ORF PRO
7	55	59.1	96	1	VPR_HV122	VPR PROTEIN (R ORF PRO
8	55	59.1	1703	1	SNF2_YEAST	TRANSCRIPTION REGULATO
9	54	58.1	355	1	Y44_YEAST	HYPOTHETICAL 40.7 KD G
10	53	57.0	96	1	VPR_HV10Y	VPR PROTEIN (R ORF PRO
11	53	57.0	96	1	VPR_HV10Y	VPR PROTEIN (R ORF PRO
12	53	57.0	96	1	VPR_HV10Y	VPR PROTEIN (R ORF PRO
13	53	57.0	511	1	ACH5_CAEEL	ACETYLCHOLINE RECEPTOR
14	53	57.0	638	1	TOXA_PSEAE	EXOTOXIN A PRECURSOR (
15	51	54.8	331	1	SRA9_CAEEL	SRA-9 PROTEIN.
16	50	53.8	96	1	VPR_HV10Y	VPR PROTEIN (R ORF PRO
17	50	53.8	330	1	FBP_NEIGO	MAJOR FERRIC IRON BIND
18	50	53.8	730	1	FBP_NEIME	MAJOR FERRIC IRON BIND
19	50	53.8	93	1	CLPA_HOBLA	CLPA HOMOLOG PROTEIN.
20	50	53.8	889	1	TRK2_YEAST	POTASSIUM TRANSPORT PR
21	49	52.7	96	1	VPR_HV10Y	VPR PROTEIN (R ORF PRO
22	49	52.7	128	1	RNP_HVDHY	RIBONUCLEASE PANCREATI
23	49	52.7	155	1	RS7_MYCSM	30S RIBOSOMAL PROTEIN

97 45 48.4 1017 1 MCM6_YEAST MINICHROMOSOME MAINTEN 6.29e+01
 98 45 48.4 1226 1 YMAL_CABEL PROBABLE INTEGRIN ALPH 6.29e+01
 99 45 48.4 3344 1 POLG_PRSVH GENOME POLYPROTEIN (CO 6.29e+01
 100 45 48.4 5217 1 HTSL_COCCA HC-TOXIN SYNTHETASE (E 6.29e+01

ALIGNMENTS

```

RESULT 1
ID MAG1_HUMAN STANDARD; PRT; 309 AA.
AC P43355; 000346;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 1 (MAGE-1 ANTIGEN) (ANTIGEN M22-E).
GN MAGE1 OR MAGE1 OR MAGE1A.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 92086861.
RA VAN DER BRUGGEN P., TRAVERSARI C., CHOMEZ P., LURQUIN C., DE PLAEN E.,
RA VAN DEN EYNDE B., KNUTH A., BOON T.;
RL SCIENCE 254:1643-1647(1991).
RN [2]
RX MEDLINE; 94311935.
RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
RN [3]
RX MEDLINE; 94157413.
RA GAUGIER B., VAN DEN EYNDE B., VAN DER BRUGGEN P., ROMERO P.,
RA GAFORIO J.J., DE PLAEN E., LETHE B., BRASSEUR F., BOON T.;
RL J. EXP. MED. 179:921-930(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS
CC CYTOLYTIC T LYMPHOCYTES.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES. NEVER EXPRESSED IN KIDNEY TUMORS, LEUKEMIAS AND
CC LYMPHOMAS.
CC -!- POLYMORPHISM: THE VARIANT AT POSITION 32 LIKELY REPRESENTS A
CC POLYMORPHISM OF THE MAGE-1 GENE.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
DR EMBL; M77481; G416115; -
DR EMBL; U82672; G2078527; -
DR MIM; 300016; -
DR KW ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.
FT VARIANT 32 32 T -> A.
FT DOMAIN 33 36 POLY-SER.
FT MUTAGEN 163 163 D->A: ABOLISHES HLA-A1 BINDING.
FT MUTAGEN 169 169 Y->A: ABOLISHES HLA-A1 BINDING.
FT CONFLICT 72 72 R -> Q (IN REF. 3).
SQ SEQUENCE 309 AA; 34342 MW; E5CB1300 CRC32;

```

Query Match 100.0%; Score 93; DB 1; Length 309;
 Best Local Similarity 100.0%; Pred.No. 4.59e-11;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 68 INFTRQRPSEGS 81
 QY 1 INFTRQRPSEGS 14

```

RESULT 2
ID RL10_BRUAB STANDARD; PRT; 172 AA.
AC P41107;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE 50S RIBOSOMAL PROTEIN L10.
GN RPLJ.
OS BRUCELLA ABORTUS.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC UNCERTAIN.
RN [1]
RX STRAIN-19;
RX MEDLINE; 94171071.
RA OLIVEIRA S.C., ZHU Y., SPLITTER G.A.;
RL GENE 140:137-138(1994).
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR EMBL; L23505; G387911; -
DR PROSITE; PS01109; RIBOSOMAL_L10; 1.
KW RIBOSOMAL PROTEIN.
SQ SEQUENCE 172 AA; 18459 MW; 196B1070 CRC32;

```

Query Match 62.4%; Score 58; DB 1; Length 172;
 Best Local Similarity 60.0%; Pred. No. 1.04e-01;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 13 VKFVRQROPQ 22
 QY 1 INFTRQROPQ 10

```

RESULT 3
ID MAG4_HUMAN STANDARD; PRT; 317 AA.
AC P43358;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 4 (MAGE-4 ANTIGEN) (MAGE-X2) (MAGE-41).
GN MAGE4 OR MAGE4.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
RN [2]
RX SEQUENCE FROM N.A.
RC TISSUE-SKIN;
RX MEDLINE; 94311935.
RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
RN [3]
RX SEQUENCE FROM N.A.
RX MEDLINE; 95369706.
RA IMAI Y., SHICHIO S., YAMADA A., KATAYAMA T., YANO H., ITOH K.;
RL GENE 160:287-290(1995).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY WITH
CC MAGE-1.

```


DR EMBL; U10687; G533515; -.
 DR DR EMBL; U10688; G533517; -.
 DR DR EMBL; U10340; G499124; -.
 DR EMBL; D32077; G1125018; -.
 KW ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.
 FT DOMAIN 41 44 POLY-SER.
 FT VARIANT 173 173 T -> A.
 FT CONFLICT 307 307 E -> Q (IN REF. 2).
 SQ SEQUENCE 317 AA; 34929 MW; 3CE38AF9 CRC32;

Query Match 61.3%; Score 57; DB 1; Length 317;
 Best Local Similarity 71.4%; Pred. No. 1.77e-01;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 76 ISFTCWPQNEGSS 89
 QY 1 INFTQRPSEGS 14

RESULT 4
 ID BGLR HUMAN STANDARD; PRT; 651 AA.
 AC P08236;
 DT 01-AUG-1988 (REL. 08, CREATED)
 DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1).
 GN GUSB.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87118233.
 RA OSHIMA A., KYLE J.W., MILLER R.D., HOFFMANN J.W., POWELL P.P.,
 RA GRUBB J.H., SLY W.S., TROPAK M., GUISE K.S., GRAVEL R.A.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 84:685-689(1987).
 RN [2]
 RP SEQUENCE OF 1-70 FROM N.A.
 RX MEDLINE; 92009900.
 RA SHIPLEY J.M., MILLER R.D., WU B.M., GRUBB J.H., CHRISTENSEN S.G.,
 RA KYLE J.W., SLY W.S.;
 RL GENOMICS 10:1009-1018(1991).
 RN [3]
 RP SEQUENCE OF 23-32 AND 160-175.
 RC TISSUE-PLACENTA;
 RX MEDLINE; 92162201.
 RA TANAKA J., GASA S., SAKURADA K., MIYAZAKI T., KASAI M., MAKITA A.;
 RL BIOL. CHEM. HOPPE-SEYLER 373:57-62(1992).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE; 96185449.
 RA JAIN S., DRENDEL W.B., CHEN Z.W., MATHEWS F.S., SLY W.S., GRUBB J.H.;
 RL NAT. STRUCT. BIOL. 3:375-381(1996).
 RN [5]
 RP VARIANT MPS-VII TRP-216.
 RX MEDLINE; 94154730.
 RA VERVOORT R., LISSENS W., LIEBAERS I.;
 RL HUM. MUTAT. 2:443-445(1993).
 RN [6]
 RP VARIANTS MPS-VII VAL-354 AND TRP-611.
 RX MEDLINE; 94154731.
 RA WU B.M., SLY W.S.;
 RL HUM. MUTAT. 2:446-457(1993).
 RN [7]
 RP VARIANTS MPS-VII CYS-382 AND VAL-619.
 RX MEDLINE; 91090114.
 RA TOMATSU S., FUKUDA S., SUKAGAWA K., IKEDO Y., YAMADA S., YAMADA Y.,
 RA SASAKI T., OKAMOTO H., KUWAHARA T., YAMAGUCHI S., KIMAN T.,
 RA SHINTAKU H., ISSHIKI G., ORII T.;
 RL AM. J. HUM. GENET. 48:89-96(1991).
 RN [8]
 RP VARIANT MPS-VII CYS-627.
 RX MEDLINE; 93190983.

RA SHIPLEY J.M., KLINKENBERG M., WU B.M., BACHINSKY D.R., GRUBB J.H.,
 RA SLY W.S.;
 RL AM. J. HUM. GENET. 52:517-526(1993).
 CC -1- FUNCTION: BETA-GLUCURONIDASE PLAYS AN IMPORTANT ROLE IN THE
 CC DEGRADATION OF DERMATAN AND KERATAN SULFATES.
 CC -1- CATALYTIC ACTIVITY: A BETA-D-GLUCURONOSIDE + H(2)O = AN
 CC ALCOHOL + D-GLUCURONATE.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: LYSOSOMAL.
 CC -1- PM: GLYCOSYLATED WITH 3 TO 4 N-LINKED OLIGOSACCHARIDE CHAINS.
 CC -1- DISEASE: DEFECTS IN GUSB ARE THE CAUSE OF MUCOPOLYSACCHARIDOSIS
 CC TYPE VII (MPS-VII) (ALSO KNOWN AS SLY SYNDROME).
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
 DR EMBL; M15182; G183233; -.
 DR EMBL; M65002; G183707; -.
 DR PIR; A26581; A26581.
 DR PDB; 1BHG; 17-SEP-97.
 DR MIN; 253220; -.
 DR PROSITE; PS00719; GLYCOSYL HYDROL F2_1; 1.
 DR PROSITE; PS00608; GLYCOSYL HYDROL F2_2; 1.
 KW HYDROLASE; GLYCOSIDASE; LYSOSOME; GLYCOPROTEIN; SIGNAL;
 KW MUCOPOLYSACCHARIDOSIS; DISEASE MUTATION; 3D-STRUCTURE.
 FT SIGNAL 1 22
 FT CHAIN 23 651 BETA-GLUCURONIDASE.
 FT ACT_SITE 451 451 PROTON DONOR.
 FT CARBOHYD 173 173
 FT CARBOHYD 272 272 POTENTIAL.
 FT CARBOHYD 420 420
 FT CARBOHYD 631 631 POTENTIAL.
 FT VARIANT 216 216 R -> W (IN MPS-VII).
 FT VARIANT 354 354 A -> V (IN MPS-VII).
 FT VARIANT 382 382 R -> C (IN MPS-VII).
 FT VARIANT 611 611 R -> W (IN MPS-VII).
 FT VARIANT 619 619 A -> V (IN MPS-VII).
 FT VARIANT 627 627 W -> C (IN MPS-VII).
 SQ SEQUENCE 651 AA; 74715 MW; F0E4C8D6 CRC32;

Query Match 61.3%; Score 57; DB 1; Length 651;
 Best Local Similarity 63.6%; Pred. No. 1.77e-01;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 609 FTQRPQKSA 619
 QY 3 FTQRPQSEGS 13

RESULT 5
 ID BGLR MOUSE STANDARD; PRT; 648 AA.
 AC P12265;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31).
 GN GUSB OR GUS.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88085188.
 RA GALLAGHER P.M., D'AMORE M.A., LUND S.D., ELLIOTT R.W., PAZIK J.,
 RA ROHMAN C., KORFHAGEN T.R., GANSCHOW R.E.;
 RL GENOMICS 1:145-152(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88284700.
 RA GALLAGHER P.M., D'AMORE M.A., LUND S.D., GANSCHOW R.E.;
 RL GENOMICS 2:215-219(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89062453.
 RA D'AMORE M.A., GALLAGHER P.M., KORFHAGEN T.R., GANSCHOW R.E.;
 RL BIOCHEMISTRY 27:7131-7140(1988).

[4]
RN SEQUENCE FROM N.A.
RX MEDLINE: 89384641.
RA WARZNIAK C.J., GALLAGHER P.M., D'AMORE M.A., CARTER J.E.,
RA LUND S.D., RINCHIK E.M., GANSCHOW R.E.;
RL MOL. CELL. BIOL. 9:4074-4078(1989).
CC -!- FUNCTION: BETA-GLUCURONIDASE PLAYS AN IMPORTANT ROLE IN THE
CC DEGRADATION OF DERMATAN AND KERATAN SULFATES.
CC -!- CATALYTIC ACTIVITY: A BETA-D-GLUCURONOSIDE + H(2)O = AN
CC ALCOHOL + D-GLUCURONATE.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: LYSOSOMAL.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
DR EMBL: J03047; G309256; -.
DR EMBL: J02836; G387180; -.
DR EMBL: M63836; G193723; -.
DR PIR: A28954; A28954.
DR PIR: A29977; A29977.
DR MGD: MGI:95874; GUS-S.
DR PROSITE: PS00719; GLYCOSYL HYDROL_F2_1; 1.
DR PROSITE: PS00608; GLYCOSYL HYDROL_F2_2; 1.
KW HYDROLASE; GLYCOSIDASE; LYSOSOME; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 22
FT CHAIN 23 648 BETA-GLUCURONIDASE.
FT ACT_SITE 447 447 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 172 172 POTENTIAL.
FT CARBOHYD 416 416 POTENTIAL.
FT CARBOHYD 591 591 POTENTIAL.
FT CARBOHYD 627 627 POTENTIAL.
FT CONFLICT 320 320 V -> I (IN REF. 4).
SQ SEQUENCE 648 AA; 74239 MW; 13A10D2B CRC32;

Query Match 60.2%; Score 56; DB 1; Length 648;
Best Local Similarity 100.0%; Pred. No. 3.00e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 605 FTRQRP 611
QY 3 FTRQRP 9
|||||

RESULT 6
ID VPR_HV122 STANDARD; PRT; 96 AA.
AC P12519;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RA THEODORE T., BUCKLER-WHITE A.;
RL SUBMITTED (NOV-1988) TO THE HIV DATA BANK.
DR EMBL: M22639; G329383; -.
DR DR HIV; M22639; VPR\$226.
KW AIDS.
SQ SEQUENCE 96 AA; 11380 MW; B28C76BE CRC32;

Query Match 59.1%; Score 55; DB 1; Length 96;
Best Local Similarity 57.1%; Pred. No. 5.07e-01;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGSS 94
QY 1 INFTRQRPSEGS 14
|:|||||:||||

RESULT 7
ID VPR_HV1MA STANDARD; PRT; 96 AA.
AC P05955;

DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MAL ISOLATE) (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86245056.
RA ALIZON M., WAIN-HOBSON S., MONTAGNIER L., SONIGO P.;
RL CELL 46:63-74(1986).
DR EMBL: K03456; G328024; -.
DR EMBL: X04415; G60232; -.
DR EMBL: A07116; G492875; -.
KW HIV; K03456; VPR\$MAL.
SQ SEQUENCE 96 AA; 11343 MW; 4AA5A84E CRC32;

Query Match 59.1%; Score 55; DB 1; Length 96;
Best Local Similarity 57.1%; Pred. No. 5.07e-01;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGSS 94
QY 1 INFTRQRPSEGS 14
|:|||||:||||

RESULT 8
ID SNF2_YEAST STANDARD; PRT; 1703 AA.
AC P22082;
DT 01-AUG-1991 (REL. 19, CREATED)
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE TRANSCRIPTORY REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2)
DE (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION
DE FACTOR TYE3).
GN SNF2 OR SWI2 OR GAM1 OR TYE3 OR RIC1 OR YOR290C.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMICETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RX MEDLINE: 91187857
RA LAURENT B.C., TREITEL M.A., CARLSON M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 88:2687-2691(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AH22;
RX MEDLINE: 91360076.
RA YOSHIMOTO H., YAMASHITA I.;
RL MOL. GEN. GENET. 228:270-280(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-X2180-1B;
RX MEDLINE: 95332261.
RA KODAKI T., HOSAKA K., NIKAWA J., YAMASHITA S.;
RL J. BIOCHEM. 117:362-368(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RX MEDLINE: 97051594.
RA CHERET G., BERNARDI A., SOR F.J.;
RL YEAST 12:1059-1064(1996).
RN [5]
RP SEQUENCE OF 1-309 FROM N.A.
RC STRAIN-S288C / FY1679;
RX MEDLINE: 97298310.
RA POIREY R., CZIEPLUCH C., TOBIASCH E., PUJOL A., KORDES E.,
RA JAUNIAUX J.-C.;
RL YEAST 13:479-482(1997).
RN [6]

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Db 321 FNFRQ 328
:|||||
Qy 1 INFTRQ 8

RESULT 10
ID VPR_HV10Y STANDARD; PRT; 96 AA.
AC P20891;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (OVI ISOLATE) (HIV-1).
OC VIRIDAE: SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
[1]
RN RN SEQUENCE FROM N.A.
RP RP MEDLINE; 90148544.
RX RA HUET T., DAZZA M.C., BRUN-VEZINET F., ROELANTS G.E., WAIN-HOBSON S.;
EL AIDS 3:707-715(1989).
CC -1- THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE
CC INDIVIDUAL.
EMBL; M26727; G328446; -.
DR HIV; M26727; VPR\$OVI.
KW AIDS.
SQ SEQUENCE 96 AA; 11494 MW; 4C01E21D CRC32;

Query Match 57.0%; Score 53; DB 1; Length 96;
Best Local Similarity 50.0%; Pred. No. 1.41e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0

Db 81 IGITRQ 94
:|||||
Qy 1 INFTRQ 14

RESULT 11
ID VPR_HV1JR STANDARD; PRT; 96 AA.
AC P20883;
DT 01-FEB-1991 (REL. 17, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (JRCF ISOLATE) (HIV-1).
OC VIRIDAE: SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
[1]
RN RN SEQUENCE FROM N.A.
RP RA KOYANAGI S., CHEN I.S.Y.;
RL SUBMITTED (DEC-1988) TO THE HIV DATA BANK.
DR DR EMBL; M38429; G327817; -.
DR DR HIV; M38429; VPR\$JRCF.
KW AIDS.
SQ SEQUENCE 96 AA; 11419 MW; 1DC76121 CRC32;

Query Match 57.0%; Score 53; DB 1; Length 96;
Best Local Similarity 50.0%; Pred. No. 1.41e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0

Db 81 IGITRQ 94
:|||||
Qy 1 INFTRQ 14

RESULT 12
ID VPR_HV1RH STANDARD; PRT; 96 AA.
AC P05934;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)

DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RE/HAT ISOLATE) (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]

RP SEQUENCE FROM N.A.
RA STARCICH B.R., HAHN B.H., SHAW G.M., MCNEELY P.D., MODROW S.,
RA WOLF H., PARKS E.S., PARKS W.P., JOSEPHS S.F., GALLO R.C.,
RA WONG-STAAL F.;
RL SUBMITTED (XXX-1987) TO THE HIV DATA BANK.
DR ENBL; M17451; G328571; -.
DR HIV; M17451; VPRSF.
KW AIDS.

SQ SEQUENCE 96 AA; 11338 MW; B2F633A3 CRC32;
Query Match 57.0%; Score 53; DB 1; Length 96;
Best Local Similarity 50.0%; Pred. No. 1.41e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGAS 94
I :|||:: :||
QY 1 INFTRQRPSEGS 14

RESULT 13
ID ACH5-CAEEL STANDARD; PRT; 511 AA.
AC Q23022; Q17408; P91265; O02559;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ACETYLCHOLINE RECEPTOR LIKE PROTEIN, ALPHA-TYPE SUBUNIT UNC-38
DE PRECURSOR.
GN UNC-38 OR F21F3.5.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA FLEMING J.T., SOUIRE M.D., BARNES T.M., TORNOE C., MATSUDA K.,
RA SULSTON J.E., BARNARD E.A., SATTLELE D.B., LEWIS J.A.;
RL SUBMITTED (DSC-1996) TO ENBL/GENBANK/DDBJ DATA BANKS.
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA GEISEL C., KRAMER J., ELLIOTT G.;
RL SUBMITTED (FEB-1997) TO ENBL/GENBANK/DDBJ DATA BANKS.
CC -1- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR ENBL; X98600; E285245; -.
DR ENBL; X98599; E285244; -.
DR ENBL; U88175; G1825663; -.
DR WORPEP; F21F3.5; CE09535.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN;
KW TRANSMEMBRANE; SIGNAL.
FT SIGNAL 1 16
FT CHAIN 17 511
FT POTENTIAL.
FT ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
FT ALPHA-TYPE SUBUNIT UNC-38.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT TRANSMEM 261
FT TRANSMEM 282
FT TRANSMEM 291
FT TRANSMEM 311
FT TRANSMEM 324
FT TRANSMEM 344
FT DOMAIN 345
FT DOMAIN 346
FT CYTOPLASMIC (POTENTIAL).
FT POTENTIAL.
FT POTENTIAL.
FT BY SIMILARITY.
FT DISULFID 151
FT DISULFID 165
FT DISULFID 238
FT CARBOHYD 124
FT CARBOHYD 124
FT CARBOHYD 202
FT CARBOHYD 202
FT CONFLICT 248
FT CONFLICT 248
T -> TKHEKLSLKNKLPQNFARIEKYI (IN
REF. 2).

SQ SEQUENCE 511 AA; 59454 MW; E3009E18 CRC32;
Query Match 57.0%; Score 53; DB 1; Length 511;
Best Local Similarity 35.7%; Pred. No. 1.41e+00;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 36 VNYNRHRPSTSPN 49
I :|||:: :||
QY 1 INFTRQRPSEGS 14

RESULT 14
ID TOXA_PSEAE STANDARD; PRT; 638 AA.
AC P11439;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE EXOTOXIN A PRECURSOR (NAD-DEPENDENT ADP-RIBOSYLTRANSFERASE
DE (EC 2.4.2.-)).
GN ETA.
OS PSEUDOMONAS AERUGINOSA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC PSEUDOMONADACEAE.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-53.
RX MEDLINE; 84194063.
RA GRAY G.L., SMITH D.H., BALDRIDGE J.S., HARKINS R.N., VASIL M.L.,
RA CHEN E.Y., HEYNEKER H.L.;
RL PROC. NATL. ACAD. SCI. U.S.A. 81:2645-2649(1984).
RN [2]
RP ACTIVE SITE.
RX MEDLINE; 87250491.
RA CARROLL S.F., COLLIER R.J.;
RL J. BIOL. CHEM. 262:8707-8711(1987).
RN [3]
RP DOMAINS.
RX MEDLINE; 90375493.
RA CHAUDHARY V.K., JINNO Y., GALO M.G., FITZGERALD D., PASTAN I.;
RL J. BIOL. CHEM. 265:16306-16310(1990).
RN [4]
RP DOMAINS.
RX MEDLINE; 91006124.
RA BOURDENET S., VACHERON M.-J., GUINAND M., MICHEL G., ARMINJON F.;
RL EUR. J. BIOCHEM. 192:379-385(1990).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 424-638.
RX MEDLINE; 96016159.
RA LI M., DYDA F., BENHAR I., PASTAN I., DAVIES D.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 92:9308-9312(1995).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 424-638.
RX MEDLINE; 96293446.
RA LI M., DYDA F., BENHAR I., PASTAN I., DAVIES D.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:6902-6906(1996).
CC -1- FUNCTION: THIS TOXIN IS AN NAD-DEPENDENT ADP-RIBOSYLTRANSFERASE.
CC IT CATALYZES THE TRANSFER OF THE ADP RIBOSYL MOIETY OF OXIDIZED
CC NAD ONTO ELONGATION FACTOR 2 (EF-2) THUS ARRESTING PROTEIN
CC SYNTHESIS.
CC -1- PTM: THE 8 CYSTEINES PARTICIPATE IN INTRACHAIN DISULFIDE BONDS.
CC -1- SIMILARITY: REGIONAL SEQUENCE SIMILARITY AT THE ACTIVE SITE
CC WITH DIPHTHERIA TOXIN (DT).
DR ENBL; K01397; G151216; -.
DR PIR; A30347; A30347.
DR PDB; 1AER; 10-JUN-96.
DR PDB; 1DMA; 15-SEP-95.
KW TOXIN; SIGNAL; TRANSFERASE; GLYCOSYLTRANSFERASE; NAD; 3D-STRUCTURE.
FT SIGNAL 1 25
FT CHAIN 26 638
FT DOMAIN 26 277
FT EXOTOXIN A.
FT IA (REQUIRED FOR TARGET CELL
FT RECOGNITION).
FT II (REQUIRED FOR TRANSLLOCATION IN TARGET
FT CELL CYTOPLASM).
FT DOMAIN 278 389
FT DOMAIN 390 429
FT IB.

FT DOMAIN 430 638 III (REQUIRED FOR ADP-RIBOSYL ACTIVITY).
FT ACT_SITE 465 465 INTERACT WITH NAD.
FT ACT_SITE 578 578
SQ SEQUENCE 638 AA; 69309 MW; 33D9876A CRC32;

Query Match 57.0%; Score 53; DB 1; Length 638;
Best Local Similarity 85.7%; Pred. No. 1.41e+00;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 297 FTRHRQP 303
|:|:|:|:
QY 3 FTRORQP 9

RESULT 15
ID SRA9_CABEL STANDARD; PRT; 331 AA.
AC Q09212;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE SRA-9 PROTEIN
GN SRA-9 OR AH6.14.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA JASSAL B.;
RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE SRA FAMILY OF C.ELEGANS RECEPTOR-LIKE PROTEINS.

DR EMBL; 248009; G643104; -.
DR WORMPEP; AH6.14; CE01455.
KW TRANSMEMBRANE; MULTIGENE FAMILY.
FT TRANSMEM 26 46 POTENTIAL.
FT TRANSMEM 104 124 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 189 209 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
FT TRANSMEM 275 295 POTENTIAL.
SQ SEQUENCE 331 AA; 38284 MW; E9D38381 CRC32;

Query Match 54.8%; Score 51; DB 1; Length 331;
Best Local Similarity 54.8%; Pred. No. 3.83e+00;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 310 IEFTKQSQE 320
|:|:|:|:
QY 1 INFTRORQSE 11

RESULT 16
ID VPR_HVIEL STANDARD; PRT; 96 AA.
AC P05956;
DT 01-NOV-1988 (REL. 09, CREATED)
DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE VPR PROTEIN (R ORF PROTEIN).
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE) (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86245056.
RA ALIZON M., WAIN-ROBSON S., MONTAGNIER L., SONIGO P.;
RL CELL 46:63-74(1986).
DR EMBL; K03454; G326681; -.
DR EMBL; A07108; G492867; -.
DR HIV; K03454; VPRSELI.
KW AIDS.
SQ SEQUENCE 96 AA; 11306 MW; FE489F84 CRC32;

Query Match 53.8%; Score 50; DB 1; Length 96;
Best Local Similarity 50.0%; Pred. No. 6.23e+00;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 81 IGIIRQRARNGSS 94
|:|:|:|:
QY 1 INFTRORQSEGS 14

RESULT 17
ID FBP_NEIGO STANDARD; PRT; 330 AA.
AC P17259;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE MAJOR FERRIC IRON BINDING PROTEIN PRECURSOR (FBP) (MAJOR IRON-REGULATED PROTEIN) (MIRP).
GN FBP.
OS NEISSERIA GONORRHOEA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC NEISSERIACEAE.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-F62;
RX MEDLINE; 90237747.
RA BERISH S.A., MIETZNER T.A., MAYER L.W., GENCO C.A., HOLLOWAY B.P., MORSE S.A.;
RL J. EXP. MED. 171:1535-1546(1990).
RN [2]
RP SEQUENCE OF 23-69.
RX MEDLINE; 87168188.
RA MIETZNER T.A., BOLAN G., SCHOOLNIK G.K., MORSE S.A.;
RL J. EXP. MED. 165:1041-1057(1987).
CC -!- FUNCTION: THIS PROTEIN MAY BE A CENTRAL COMPONENT IN THE IRON-ACQUISITION SYSTEM.
CC -!- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -!- INDUCTION: UNDER IRON-DEFICIENCY.
CC -!- IRON CO-PURIFIES WITH FBP AND IS BOUND BY THE PROTEIN AS A FERRIC ION AT AN APPROXIMATE MOLAR RATIO OF 1:1.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING PROTEIN FAMILY 1.
CC EMBL; X51901; G44858; -.
DR PIR; S10256; S10256; -.
DR PROSITE; PS01037; SBP_BACTERIAL_1; 1.
KW TRANSPORT; IRON TRANSPORT; PERIPLASMIC; SIGNAL.
FT SIGNAL 1 22
FT CHAIN 23 330 FERRIC IRON BINDING PROTEIN.
SQ SEQUENCE 330 AA; 35769 MW; F18F3562 CRC32;

Query Match 53.8%; Score 50; DB 1; Length 330;
Best Local Similarity 50.0%; Pred. No. 6.23e+00;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 235 LNFVHRDPG 244
|:|:|:|:
QY 1 INFTRORPS 10

RESULT 18
ID FBP_NEIME STANDARD; PRT; 330 AA.
AC P17940;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE MAJOR FERRIC IRON BINDING PROTEIN PRECURSOR (FBP) (MAJOR IRON-REGULATED PROTEIN) (MIRP).
GN FBP.
OS NEISSERIA MENINGITIDIS.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC NEISSERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.


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Db 81 IGVTRRRRANGAS 94
QY 1 INFTRQPSGSS 14

RESULT 22
ID RNP_HYDHY STANDARD; PRT; 128 AA.
AC P00677;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE A).
GN RNASE1 OR RNS1.
OS HYDROCHORUS HYDROCHAEIS (CAPVBARA) (CARPINCHO).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 87036770.
RA BEINTEMA J.J., NEUTEBOOM B.;
RL J. MOL. EVOL. 19:145-152(1983).
CC -!- CATALYTIC ACTIVITY: ENDONUCLEOTIC CLEAVAGE TO 3'-PHOSPHOMONO-
NUCLEOTIDES AND 3'-PHOSPHOLIGONUCLEOTIDES ENDING IN C-P OR U-P
WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: PANCREAS.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR; A00824; NRY.
DR HSSP; P00656; 1SRN.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW HYDROLASE; NUCLEASE; ENDONUCLEASE.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
SQ SEQUENCE 128 AA; 14345 MW; 23DF27D CRC32;

Query Match 52.7%; Score 49; DB 1; Length 128;
Best Local Similarity 57.1%; Pred. No. 1.01e+01;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 6 MKFQRQHVDSGSS 19
QY 1 INFTRQPSGSS 14

RESULT 23
ID RS7_MYCSM STANDARD; PRT; 155 AA.
AC P41193;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE 30S RIBOSOMAL PROTEIN S7.
GN RPSG.
OS MYCOBACTERIUM SMEGMATIS.
OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-LR222;
RX MEDLINE; 95014056.
RA KENNEY T.J., CHURCHWARD G.;
RL J. BACTERIOL. 176:6153-6156(1994).
CC -!- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
DE EMBL; L34681; G511652; -.
DR PROSITE; PS00052; RIBOSOMAL_S7; 1.
KW RIBOSOMAL PROTEIN; RNA-BINDING.
FT INIT_MET 0 0 BY SIMILARITY.

SQ SEQUENCE 155 AA; 17497 MW; 0409A286 CRC32;

Query Match 52.7%; Score 49; DB 1; Length 155;
Best Local Similarity 62.5%; Pred. No. 1.01e+01;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 104 VNFQRQR 111
QY 1 INFTRQPSGSS 8

RESULT 24
ID NRL_MOUSE STANDARD; PRT; 237 AA.
AC P54846;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE NEURAL RETINA-SPECIFIC LEUCINE ZIPPER PROTEIN (NRL).
GN NRL.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C; TISSUE-RETINA;
RX MEDLINE; 94116986.
RA FARJO Q., JACKSON A.U., XU J., GRZYENIA M., SKOLNICK C.,
AGARWAL N., SWAROOP A.;
RL GENOMICS 18:216-222(1993).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- TISSUE SPECIFICITY: NEURAL RETINA.
CC -!- SIMILARITY: TO OTHER BZIP PROTEINS.
DE EMBL; L14935; G388917; -.
DR TRANSFAC; T01438; -.
DR MGD; MGI:102567; NRL.
KW TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN.
FT DNA_BIND 159 185 BASIC MOTIF.
FT DOMAIN 187 208 LEUCINE-ZIPPER.
SQ SEQUENCE 237 AA; 26083 MW; 8125334E CRC32;

Query Match 52.7%; Score 49; DB 1; Length 237;
Best Local Similarity 50.0%; Pred. No. 1.01e+01;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 19 MKFEIKRPSGSS 32
QY 1 INFTRQPSGSS 14

RESULT 25
ID MAG2_HUMAN STANDARD; PRT; 314 AA.
AC P43356;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 2 (MAGE-2 ANTIGEN).
GN MAGE2 OR MAGE2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94102805.
RA DE SMET C., LURQUIN C., VAN DER BRUGGEN P., DE PLAEN E., BRASSEUR F.,
BOON T.;
RL IMMUNOGENETICS 39:121-129(1994).
RN [2]
RP MUTAGENESIS.
RX TISSUE-BLOOD;
RX MEDLINE; 94157413.
RA GAUGLER B., VAN DER EYNDE B., VAN DER BRUGGEN P., ROMERO P.,
GAFORIO J.J., DE PLAEN E., LETHE B., BRASSEUR F., BOON T.;
J. EXP. MED. 179:921-930(1994).
RL
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CC -1- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
 CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
 CC PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS
 CC CYTOLYTIC T LYMPHOCYTES.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
 CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 CC FOR TESTES.
 CC -1- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY (90%)
 CC WITH MAGE-12.
 DR EMBL; L18920; G436181; -.
 DR ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
 KW DOMAIN 40 43 POLY-SER.
 FT MUTAGEN 170 170 V-2D: IMPROVES ABILITY TO BIND TO HLA-A1.
 SQ SEQUENCE 314 AA; 35055 MW; E101F41E CRC32;

Query Match 52.7%; Score 49; DB 1; Length 314;
 Best Local Similarity 64.3%; Pred. No. 1.01e+01;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 75 INTLWQSDGSS 88
 : : : : :
 QY 1 INFTRQPSGSS 14

RESULT 26
 ID NREB_KLEPN STANDARD; PRT; 349 AA.
 AC P10045;
 DT 01-MAR-1989 (REL. 10, CREATED)
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE NITRILASE, BROMOXNYL-SPECIFIC (EC 3.5.5.1).
 GN BAX.
 OS KLEBSIELLA PNEUMONIAE.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88198177.
 RA STALKER D.M., MALYJ L.D., MCBRIDE K.E.;
 RL J. BIOL. CHEM. 263:6310-6314(1988).
 CC -1- FUNCTION: SPECIFIC FOR THE HERBICIDE BROMOXNYL.
 CC -1- CATALYTIC ACTIVITY: A NITRILE + H(2)O = A CARBOXYLATE + NH(3).
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- EXPRESSION OF THIS BACTERIAL NITRILASE IN TRANSGENIC PLANTS
 CC RESULTS IN HIGH LEVELS OF RESISTANCE TO THE HERBICIDE BROMOXNYL.
 CC -1- SIMILARITY: TO OTHER NITRILASES.
 DR EMBL; J03196; G149175; -.
 DR PIR; A28658; A28658.
 DR PROSITE; PS00920; NITRIL_CHT_1; 1.
 DR PROSITE; PS00921; NITRIL_CHT_2; 1.
 KW HYDROLASE; HERBICIDE RESISTANCE.
 FT ACT_SITE 161 161 BY SIMILARITY.
 SQ SEQUENCE 349 AA; 37801 MW; 5FEE4AFA CRC32;

Query Match 52.7%; Score 49; DB 1; Length 349;
 Best Local Similarity 50.0%; Pred. No. 1.01e+01;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 298 VSINRORQPA 307
 : : : : :
 QY 1 INFTRQPS 10

RESULT 27
 ID SCRB_STAXY STANDARD; PRT; 494 AA.
 AC Q05936;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
 DE SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26) (SUCRASE) (INVERTASE).
 GN SCRB
 OS STAPHYLOCOCCUS XYLOSUS.

OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93139055.
 RA BRUECKNER R., WAGNER E., GOETZ F.;
 RL J. BACTERIOL. 175:851-857(1993).
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
 CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
 DR EMBL; X67744; E264853; -.
 DR PIR; A47059; A47059.
 DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
 KW HYDROLASE; GLYCOSIDASE.
 FT ACT_SITE 48 48 BY SIMILARITY.
 SQ SEQUENCE 494 AA; 57371 MW; 8F97236A CRC32;

Query Match 52.7%; Score 49; DB 1; Length 494;
 Best Local Similarity 63.6%; Pred. No. 1.01e+01;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 358 KFTROLHPYEG 368
 : : : : :
 QY 2 NFTRQRPSEG 12

RESULT 28
 ID MET7_NEUCR STANDARD; PRT; 542 AA.
 AC P38675;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE CYSTATIONINE GAMMA-SYNTHASE (EC 4.2.99.9) (O-SUCCINYLMOMOSERINE
 DE (THIOL)-LYASE).
 GN MET-7.
 OS NEUROSPORA CRASSA.
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; PYRENOMYCETES; SORDARIALES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92175534.
 RA CRAWFORD J.M., GEEVER R.F., ASCH D.K., CASE M.E.;
 RL GENE 111:265-266(1992).
 CC -1- CATALYTIC ACTIVITY: O-SUCCINYLM-L-HOMOSERINE + L-CYSTEINE =
 CC CYSTATIONINE + SUCCINATE (CAN ALSO USE HYDROGEN SULFIDE AND
 CC METHANETHIOL AS SUBSTRATES).
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: SECOND STEP IN METHIONINE BIOSYNTHESIS.
 CC -1- SUBUNIT: MET-3 AND MET-7 ARE REQUIRED TO FORM A FUNCTIONAL
 CC CYSTATIONINE GAMMA-SYNTHASE.
 CC -1- SIMILARITY: STRONG. TO YEAST YJRI30C AND YML082W.
 DR EMBL; M64066; -: NOT_ANNOTATED_CDS.
 DR PIR; JQ1524; JQ1524.
 KW METHIONINE BIOSYNTHESIS; LYASE; PYRIDOXAL PHOSPHATE.
 FT BINDING 350 350 PYRIDOXAL PHOSPHATE (POTENTIAL).
 SQ SEQUENCE 542 AA; 60196 MW; A23C9D9D CRC32;

Query Match 52.7%; Score 49; DB 1; Length 542;
 Best Local Similarity 36.4%; Pred. No. 1.01e+01;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 13 VDFTRSRAPAD 23
 : : : : :
 QY 1 INFTRQRPSE 11

RESULT 29
 ID BGLR_RAT STANDARD; PRT; 648 AA.
 AC P06760;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31).
 GN GUS.
 OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=PREPUTIAL GLAND;
 RM MEDLINE; 87016933.
 RA NISHIMURA Y., ROSENFELD M.G., KREIBICH G., GUBLER U., SABATINI D.D.,
 RA ADESNIK M., ANDY R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 83:7292-7296(1986).
 [2]
 RN SEQUENCE OF 14-648 FROM N.A.
 RP TISSUE=LIVER;
 RC MEDLINE; 88183378.
 RX POWELL P., KYLE J.W., MILLER R.D., PANTANO J., GRUBB J.H., SLY W.S.;
 RL BIOCHEM. J. 250:547-555(1988).
 CC -|- FUNCTION: BETA-GLUCURONIDASE PLAYS AN IMPORTANT ROLE IN THE
 CC DEGRADATION OF DERMATAN AND KERATAN SULFATES.
 CC -|- CATALYTIC ACTIVITY: A BETA-D-GLUCURONOSIDE + H(2)O = AN
 CC ALCOHOL + D-GLUCURONATE.
 CC -|- SUBUNIT: HOMOTETRAMER.
 CC -|- SUBCELLULAR LOCATION: LYSOSOMAL.
 CC -|- PTM: UNDERGOES A POSTTRANSCRIPTIONAL PROTEOLYTIC CLEAVAGE NEAR ITS
 CC C-TERMINAL END, WHICH REDUCES ITS SIZE BY APPROXIMATELY 3 KD. THE
 CC SITE OF THIS CLEAVAGE HAS AS YET NOT BEEN DETERMINED.
 CC -|- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
 DR EMBL; M13962; G204330; -;
 DR EMBL; Y00717; G758260; -;
 DR PIR; A25047; A25047.
 DR PIR; S00345; S00345.
 DR PROSITE; PS00719; GLYCOSYL-HYDROL_F2.1; 1.
 DR PROSITE; PS00608; GLYCOSYL-HYDROL_F2.2; 1.
 KW HYDROLASE; GLYCOSIDASE; LYSOSOME; GLYCOPROTEIN; SIGNAL.
 FT SIGNAL 1 22
 FT CHAIN 23 648 BETA-GLUCURONIDASE.
 FT ACT_SITE 447 447 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 172 172 POTENTIAL.
 FT CARBOHYD 416 416 POTENTIAL.
 FT CARBOHYD 591 591 POTENTIAL.
 FT CARBOHYD 627 627 POTENTIAL.
 FT CARBOHYD 14 14 Q -> E (IN REF. 2).
 FT CONFLICT 21 21 V -> L (IN REF. 2).
 FT CONFLICT 487 487 M -> L (IN REF. 2).
 FT CONFLICT 487 487 M -> L (IN REF. 2).
 SQ SEQUENCE 648 AA; 74793 MW; AF91C615 CRC32;

Query Match 52.78; Score 49; DB 1; Length 648;
 Best Local Similarity 85.78; Pred. No. 1.01e+01;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 605 FTRQRP 611
 QY 3 FTRQRP 9

RESULT 30
 ID ERG7-RAT STANDARD; PRT; 733 AA.
 AC P48450;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE LANOSTEROL SYNTHASE (EC 5.4.99.7) (OXIDOSQUALENE--LANOSTEROL CYCLASE)
 DE (2,3-EPOXY-SQUALENE--LANOSTEROL CYCLASE) (OSC).
 GN OSC OR LSS.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
 RX MEDLINE; 95253156.
 RA KUSANO M., SHIBUYA M., SANKAWA U., EBIZUKA Y.;
 RL BIOL. PHARM. BULL. 18:195-197(1995).
 CC -|- FUNCTION: CATALYZES THE CYCLIZATION OF (S)-2,3 OXIDOSQUALENE TO
 CC LANOSTEROL, A REACTION THAT FORMS THE STEROL NUCLEUS.

CC -|- CATALYTIC ACTIVITY: (S)-2,3-EPOXY-SQUALENE = LANOSTEROL.
 CC -|- PATHWAY: INITIAL STEP IN CHOLESTEROL, STEROID HORMONES AND VITAMIN
 CC D BIOSYNTHESIS.
 CC -|- SIMILARITY: BELONGS TO THE FAMILY OF TERPENE CYCLASES/MUTASES.
 DR EMBL; D45252; G639865; -;
 DR PROSITE; PS01074; TERPENE-SYNTHASES; 1.
 KW ISOMERASE; STEROID BIOSYNTHESIS.
 SQ SEQUENCE 733 AA; 83305 MW; 6ED7B647 CRC32;

Query Match 52.78; Score 49; DB 1; Length 733;
 Best Local Similarity 38.58; Pred. No. 1.01e+01;
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 565 LDFCRKKORADGS 577
 QY 1 INFTRQRPSEGS 13

RESULT 31
 ID RT19_PETHY STANDARD; PRT; 94 AA.
 AC P27527;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE MITOCHONDRIAL RIBOSOMAL PROTEIN S19.
 GN RPS19.
 OS PETUNIA HYBRIDA (PETUNIA).
 OC MITOCHONDRIUM.
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
 OC SOLANALES; SOLANACEAE.
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE; 91252215.
 RA CONKLIN P.L., HANSON M.R.;
 RL NUCLEIC ACIDS RES. 19:2701-2705(1991).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=3704;
 RX MEDLINE; 93306753.
 RA SUTTON C.A., CONKLIN P.L., PRUITT K.D., CALFEE A.J., COBB A.G.,
 RA HANSON M.R.;
 RL CURR. GENET. 23:472-476(1993).
 CC -|- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -|- POSITIONS 39, 46, 55 AND 74 ARE MODIFIED BY RNA EDITING.
 CC -|- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR EMBL; X67028; G14164; ALT_SEQ.
 DR EMBL; X67027; G14200; ALT_SEQ.
 DR EMBL; X57283; G13340; ALT_SEQ.
 DR PIR; S29745; R3PJ19.
 DR PROSITE; PS00323; RIBOSOMAL_S19; 1.
 DR RIBOSOMAL PROTEIN; MITOCHONDRIUM; RNA EDITING.
 KW SEQUENCE 94 AA; 11222 MW; A4BE044C CRC32;

Query Match 51.68; Score 48; DB 1; Length 94;
 Best Local Similarity 60.08; Pred. No. 1.61e+01;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 72 FAFTRKRKPS 81
 QY 1 INFTRQRP 10

RESULT 32
 ID VPR_HVIMN STANDARD; PRT; 96 AA.
 AC P05950;
 DT 01-NOV-1988 (REL. 09, CREATED)
 DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
 DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
 DE VPR PROTEIN (R ORF PROTEIN).
 GN VPR.
 OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MN ISOLATE) (HIV-1).
 OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
 OC LENTIVIRINAE.

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RN SEQUENCE FROM N.A.
RP MEDLINE; 88219542.
RA GURGO C., GUO H.-G., FRANCHINI G., ALDOVINI A., COLLALTI E.,
RA FARRELL K., WONG-STRAAL F., GALLO R.C., REITZ M.S. JR.;
RL VIROLOGY 164:531-536(1988).
CC -!- THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS PATIENT IN 1984.
DR EMBL; M17449; G328035; -
DR HIV; M17449; VPR8MN.
KW AIDS.
SQ SEQUENCE 96 AA; 11344 MW; D7BD031F CRC32;

Query Match          51.6%; Score 48; DB 1; Length 96;
Best Local Similarity 42.9%; Pred. No. 1.61e+01;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 81 IGIHQRRRANGAS 94
QY 1 INFTRQRPSEGS 14

RESULT 33
ID PHCA-STNY3 STANDARD; PRT; 162 AA.
AC Q54715;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE C-PHYCOCYANIN ALPHA CHAIN.
GN CP4 OR SL11578.
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
OC CYANOBACTERIA (BLUE-GREEN ALGAE); CHROCOCCALES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96074307.
RA PLANK T., TOOLE C., ANDERSON L.K.;
RL J. BACTERIOL. 177:6798-6803(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
RA TABATA S.;
RL DNA RES. 3:109-136(1996).
RN [3]
RP SEQUENCE OF 1-19.
RX MEDLINE; 97443974.
RA SAZUKA T., OHARA O.;
RL ELECTROPHORESIS 18:1252-1258(1997).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
CC FROM THE PHYCOBILIPROTEIN COMPLEX.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
DR EMBL; U34930; G1008533; -
DR EMBL; D90904; G1652308; -
KW PHYCOBILISOME; ELECTRON TRANSPORT; PHOTOSYNTHESIS; BILE PIGMENT.
FT BINDING 84
FT BINDING 84 PHYCOCYANOBILIN CHROMOPHORE.
SQ SEQUENCE 162 AA; 17586 MW; 8B79A803 CRC32;

Query Match          51.6%; Score 48; DB 1; Length 162;
Best Local Similarity 50.0%; Pred. No. 1.61e+01;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 26 IAFGRLOANAG 37
QY 1 INFTRQRPSEGS 12

RESULT 34
ID US02_HSVBS STANDARD; PRT; 220 AA.
AC Q08099;

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DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE PROTEIN US2 HOMOLOG.
OS BOVINE HERPESVIRUS TYPE 1.2 (STRAIN ST').
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94167875.
RA LEUNG-TACK P., AUDONNET J.F., RIVIERE M.;
RL VIROLOGY 199:409-421(1994).
CC -!- SIMILARITY: BELONGS TO THE HERPES VIRUSES US2 FAMILY.
DR EMBL; 223068; G312193; -
SQ SEQUENCE 220 AA; 23156 MW; 624A8A07 CRC32;

Query Match          51.6%; Score 48; DB 1; Length 220;
Best Local Similarity 55.8%; Pred. No. 1.61e+01;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 87 LARHROPAP 95
QY 3 FTRQRPSE 11

RESULT 35
ID MCBC-ECOLI STANDARD; PRT; 272 AA.
AC P23185;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 32, LAST ANNOTATION UPDATE)
DE MICROCIN B17 PROCESSING PROTEIN MCBC.
GN MCBC.
OS ESCHERICHIA COLI.
OC PLASMID PHCCB17.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89123111.
RA GENILLOUD O., MORENO F., KOLTER R.;
RL J. BACTERIOL. 171:1126-1135(1989).
CC -!- FUNCTION: NECESSARY TO PROCESS THE INACTIVE MICROCIN B17 (MCBA)
CC PRECURSOR INTO THE ACTIVE PEPTIDE.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -!- SIMILARITY: TO R LEGUMINOSARUM TFXB WHICH IS INVOLVED IN THE
CC PROCESSING OF TRIFOLITOXIN.
DR EMBL; M24253; G522292; -
DR PIR; C32058; C32058.
KW ANTIBIOTIC; PLASMID.
SQ SEQUENCE 272 AA; 30753 MW; E33FD69E CRC32;

Query Match          51.6%; Score 48; DB 1; Length 272;
Best Local Similarity 66.7%; Pred. No. 1.61e+01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 77 NTSRERLPS 85
QY 2 NTRQRPQS 10

Search completed: Tue Apr 7 08:37:41 1998
Job time : 12 secs.

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MORPH
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Apr 7 08:38:00 1998; MasPar time 6.41 Seconds
Tabular output not generated. 91.928 Million cell updates/sec

Title: >US-08-190-411A-2
Description: (1-14) from 5541104.pep
Perfect Score: 93
Sequence: 1 INFTRQRPSEGS 14

Scoring table: PAM 150
Gap 15

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: spiremb15
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 24.243; Variance 28.092; scale 0.863

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	61	65.6	188	9	Q51968 HYPOTHETICAL 20.8 KD P	3.11e-02
2	60	64.5	184	9	Q41197 ORF14	5.36e-02
3	58	62.4	651	4	O18935 BETA-GLUCURONIDASE (EC	1.56e-01
4	57	61.3	317	2	Q14798 MAGE-4 PROTEIN.	2.65e-01
5	57	61.3	512	3	P92039 ACETYLCHOLINE RECEPTOR	4.46e-01
6	56	60.2	96	11	Q79672 VPR PROTEIN.	4.46e-01
7	56	60.2	648	10	O61601 BETA-GLUCURONIDASE STR	4.46e-01
8	56	60.2	648	10	O64473 BETA-GLUCURONIDASE PRE	4.46e-01
9	56	60.2	648	10	O64474 BETA-GLUCURONIDASE PRE	4.46e-01
10	55	59.1	96	11	Q79254 VPR PROTEIN.	7.47e-01
11	55	59.1	311	3	Q23096 W1A8.5	7.47e-01
12	55	59.1	650	1	Q01377 SULFUR CONTROLLER-2.	7.47e-01
13	54	58.1	186	8	Q40394 NGORF14 PROTEIN.	1.24e+00
14	54	58.1	373	9	O26544 SENSORY TRANSDUCTION'H	1.24e+00
15	53	57.0	96	11	O36206 VPR PROTEIN.	2.06e+00
16	53	57.0	96	11	O42054 VPR PROTEIN.	2.06e+00
17	53	57.0	96	11	Q79246 VPR PROTEIN.	2.06e+00
18	53	57.0	96	11	Q79284 VPR PROTEIN.	2.06e+00
19	53	57.0	96	11	O36203 VPR PROTEIN.	2.06e+00
20	53	57.0	96	11	O36205 VPR PROTEIN.	2.06e+00

VPR PROTEIN. 2.06e+00
VPR PROTEIN. 2.06e+00
VPR PROTEIN. 2.06e+00
VPR PROTEIN. 2.06e+00
VPR PROTEIN. 2.06e+00
VPR PROTEIN. 2.06e+00
VPR PROTEIN. 2.06e+00
FOUR ORFS, THREE COMPL 2.06e+00
HISTONE RNA HAIRPIN-BI 2.06e+00
HYPOTHETICAL 31.0 KD P 2.06e+00
STEM-LOOP BINDING PROT 2.06e+00
C05C8.4 PROTEIN. 2.06e+00
VPR PROTEIN. 3.38e+00
HOMOLOGUE OF HSV-1 G1. 3.38e+00
GI GENE PRECURSOR. 3.38e+00
PEPTIDE/HISTIDINE TRAN 3.38e+00
HYPOTHETICAL 65.2 KD P 5.52e+00
VPR PROTEIN (FRAGMENT) 8.94e+00
NUP98-HOX9 FUSION PRO 8.94e+00
HYPOTHETICAL 20.1 KD P 8.94e+00
HOMODOMAIN PROTEIN HO 8.94e+00
HYPOHETICAL 35.9 KD P 8.94e+00
PERIPLASMIC IRON-BINDI 8.94e+00
PERIPLASMIC IRON-BINDI 8.94e+00
PERIPLASMIC IRON-BINDI 8.94e+00
SIMILAR TO TRANSFERRIN 8.94e+00
E2F-RELATED TRANSCRIPT 8.94e+00
TAXADIENE SYNTHASE. 8.94e+00
VPR PROTEIN (FRAGMENT) 1.44e+01
VPR PROTEIN (FRAGMENT) 1.44e+01
VPR PROTEIN. 1.44e+01
HYPOTHETICAL 38.0 KD P 1.44e+01
ASP-RICH. 1.44e+01
BIOTIN CARBOXYLASE SUB 1.44e+01
SH3 BINDING PROTEIN 3B 1.44e+01
SH3 BINDING PROTEIN 2. 1.44e+01
SH3 BINDING PROTEIN. 1.44e+01
F16A11.1. 1.44e+01
OXIDOSUALENE CYCLASE. 1.44e+01
METHYLENETETRAHYDROL 1.44e+01
VPR PROTEIN. 2.30e+01
VPR PROTEIN. 2.30e+01
VPR PROTEIN. 2.30e+01
VPR PROTEIN. 2.30e+01
C18MC, COMPLETE SEQUE 2.30e+01
CNTRL 2, CLONE 19, ACC 2.30e+01
VPR PROTEIN. 2.30e+01
CNTRL 2, CLONE 18, ACC 2.30e+01
VPR PROTEIN. 2.30e+01
ISOLATE NY5, COMPLETE 2.30e+01
K08H2.7. 2.30e+01
PURINE-BINDING CHEMOTA 2.30e+01
US2 PROTEIN. 2.30e+01
EXTRACELLULAR MATRIX P 2.30e+01
VIRAL POLYMERASE, COAT 2.30e+01
TYROSINE KINASE (FRAGM 2.30e+01
POLYPROTEIN. 2.30e+01
5'-TERMINAL REGION OF 3.64e+01
DNA FOR ORFS AND PPRI 3.64e+01
SENSOR REGULATOR. 3.64e+01
ROUS SARCOMA VIRUS TRA 3.64e+01
Y-BOX BINDING PROTEIN. 3.64e+01
CO-CHAPERONE-CURVED DN 3.64e+01
MYB-1B. 3.64e+01
MRNP PARTICLE MAJOR PR 3.64e+01
SIMILAR TO DBPB/YB-1 O 3.64e+01
CCAAT-BINDING PROTEIN 3.64e+01
GLYCOPROTEIN G1. 3.64e+01
CHROMOSOME XII READING 3.64e+01
BETA-TRANSDUCIN. 3.64e+01
HYPOTHETICAL 56.9 KD P 3.64e+01

94 47 50.5 658 3 Q09946 HYPOTHETICAL 75.1 KD P 3.64e+01
95 47 50.5 958 8 Q40554 PNLA-35. 3.64e+01
96 47 50.5 977 3 Q94678 VALS GENE (FRAGMENT). 3.64e+01
97 47 50.5 1048 9 Q05884 HYPOTHETICAL 110.2 KD 3.64e+01
98 47 50.5 1142 11 P89462 RIBONUCLEOTIDE REDUCTA 3.64e+01
99 47 50.5 1180 2 Q32625 MYELOBLAST KIAA0229 (F 3.64e+01
100 47 50.5 1937 9 Q30482 PKS MODULE 4. 3.64e+01

ALIGNMENTS

RESULT 1
ID Q51968 PRELIMINARY; PRT; 188 AA.
AC Q51968;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 20.8 KD PROTEIN.
OS AGROBACTERIUM RHIZOGONES.
OG PLASMID PRI1724.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC RHIZOBIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF03-01724;
RX MEDLINE; 94227335.
RA TANAKA N., IKEDA T., OKA A.;
RL BIOSCI. BIOTECHNOL. BIOCHEM. 58:548-551(1994).
RN [2]
RP REVISIONS.
RC STRAIN-MAFF03-01724;
RA TANAKA N.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RL EMBL; AB006689; D1023202;
KW HYPOTHETICAL PROTEIN; PLASMID.
SQ SEQUENCE 188 AA; 20769 MW; 7FF52496 CRC32;

Query Match 65.6%; Score 61; DB 9; Length 188;
Best Local Similarity 72.7%; Pred. No. 3.11e-02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 161 FTRQRPDQS 171
QY 3 FTRQRPSEGS 13
RESULT 2
ID Q44197 PRELIMINARY; PRT; 184 AA.
AC Q44197;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE ORF14.
OS AGROBACTERIUM RHIZOGONES.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC RHIZOBIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91352070.
RA HANSEN G., LARRIBE M., VAUBERT D., TEMPE J., BIERMANN B.J.,
RA MONTOYA A.L., CHILTON M.D., BREVET J.;
RL PROC. NATL. ACAD. SCI. U.S.A. 88:7763-7767(1991).
DR EMBL; M60490; G142251; -;
SQ SEQUENCE 184 AA; 20254 MW; 73F2711C CRC32;

Query Match 64.5%; Score 60; DB 9; Length 184;
Best Local Similarity 72.7%; Pred. No. 5.36e-02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 157 FTRQRPDQS 167
QY 3 FTRQRPSEGS 13

RESULT 3
ID O18835 PRELIMINARY; PRT; 651 AA.
AC O18835;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE BETA-GLUCURONIDASE (EC 3.2.1.31).
GN GUSB.
OS CANIS FAMILIARIS (DOG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; CARNIVORA.
RN [1]
RP SEQUENCE FROM N.A.
RA RAY J., BOUVET A.B., DESANTO C., FYFE J.C., WU D., WOLFE J.H.,
RA AGUIRRE G.D., PATTERSON D.F., HASKINS M.E., HENTHORN P.S.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF019759; G2425091; -;
DR PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
DR PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
KW HYDROLASE; GLYCOSIDASE.
SQ SEQUENCE 651 AA; 74433 MW; 6CA3E409 CRC32;

Query Match 62.4%; Score 58; DB 4; Length 651;
Best Local Similarity 63.6%; Pred. No. 1.56e-01;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 608 FTRQRPKAAA 618
QY 3 FTRQRPSEGS 13

RESULT 4
ID Q14798 PRELIMINARY; PRT; 317 AA.
AC Q14798;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE MAGE-4 PROTEIN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95369706.
RA IMAI Y., SHICHIGO S., YAMADA A., KATAYAMA T., YANO H., ITOH K.;
RL GENE 160:287-290(1995).
DR EMBL; D32075; G1125014; -;
SQ SEQUENCE 317 AA; 35044 MW; 982B1AC9 CRC32;

Query Match 61.3%; Score 57; DB 2; Length 317;
Best Local Similarity 71.4%; Pred. No. 2.85e-01;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 76 ISFTCWQPNEGSS 89
QY 1 INFTRQPFSEGS 14

RESULT 5
ID P92039 PRELIMINARY; PRT; 512 AA.
AC P92039;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE ACETYLCHOLINE RECEPTOR ALPHA SUBUNIT PRECURSOR.
GN ACHR.
OS HAEMONCHUS CONTORTUS.
OC EUKARYOTA; METAZOA; ACCELOMATES; NEMATODA; SECERNENTEA; SPIRURIDA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97237560.
RA HOEKSTRA R., VISSER A., WILEY L., WEISS A., SANGSTER N., ROOS M.;

SQ SEQUENCE 648 AA; 74207 MW; 408B6BC7 CRC32;

Query Match 60.2%; Score 56; DB 10; Length 648;
Best Local Similarity 100.0%; Pred. No. 4.46e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 605 FTRORQP 611
|||||
QY 3 FTRORQP 9

RESULT 10
ID Q79254 PRELIMINARY; PRT; 96 AA.
AC Q79254;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 3499, HOMOSEXUAL, GERMAN;
RA KUIKEN L., CORNELISSEN E., ZORGRAGER F., HARTMAN S., GIBBS J.,
RA GUDSMIT J.;
RL J. GEN. VIROL. 0:0-0(1996).
DR EMBL; Z68558; E218342; -.
SQ SEQUENCE 96 AA; 11252 MW; 48376E02 CRC32;

Query Match 59.1%; Score 55; DB 11; Length 96;
Best Local Similarity 57.1%; Pred. No. 7.47e-01;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRQRARNSS 94
|:|||||:
QY 1 INFTRQRPSEGS 14

RESULT 11
ID Q23096 PRELIMINARY; PRT; 311 AA.
AC Q23096;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE W01A8.5.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACCELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RA WILKINSON J.;
RL SUBMITTED (APR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
RA COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
RA FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
RA LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B.,
RA O'CALLAGHAN M., PARSONS J., PERCY C., RIEKEN L., ROOPRA A.,
RA SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E.,
RA STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M.,
RA VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
RL NATURE 368:32-38(1994).
DR EMBL; Z71267; E237025; -.
SQ SEQUENCE 311 AA; 35099 MW; CDF5715F CRC32;

Query Match 59.1%; Score 55; DB 3; Length 311;
Best Local Similarity 57.1%; Pred. No. 7.47e-01;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 298 INFTRDNPSTSSN 311
|||||:
QY 1 INFTRQRPSEGS 14

RESULT 12
ID Q01277 PRELIMINARY; PRT; 650 AA.
AC Q01277;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE SULFUR CONTROLLER-2.
GN SCON-2.
OS NEUROSPORA CRASSA.
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; PYRENOMYCETES; SORDARIALES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WILD-TYPE 74-OR23-1A;
RX MEDLINE; 95241499.
RA KUMAR A., PAIETTA J.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 92:3343-3347(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WILD-TYPE 74-OR23-1A;
RX MEDLINE; 90377210.
RA PAIETTA J.V.;
RL MOL. CELL. BIOL. 10:5207-5214(1990).
DR EMBL; U17251; G806758; -.
DR PROSITE; PS00678; G-BETA_REPEATS; 2.
KW REPEAT.

Query Match 59.1%; Score 55; DB 1; Length 650;
Best Local Similarity 53.8%; Pred. No. 7.47e-01;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 196 NYTRORQLAKGPP 208
|:|||||:
QY 2 NFTRQRPSEGS 14

RESULT 13
ID Q40394 PRELIMINARY; PRT; 186 AA.
AC Q40394;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE NGORF14 PROTEIN.
GN NGORF14.
OS NICOTIANA GLAUCA (GLAUCAUS TOBACCO) (TREE TOBACCO).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC SOLANALES; SOLANACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94301302.
RA AOKI S., KAWAKA A., SEKINE M., ICHIKAWA T., FUJITA T.,
RA SHINYO A., SYONO K.;
RL MOL. GEN. GENET. 243:706-710(1994).
DR EMBL; D16559; G1113089; -.
SQ SEQUENCE 186 AA; 20952 MW; 540A964C CRC32;

Query Match 58.1%; Score 54; DB 8; Length 186;
Best Local Similarity 63.6%; Pred. No. 1.24e+00;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 159 FTRQHQPDPS 169
|||||:
QY 3 FTRQRPSEGS 13

RESULT 14
ID Q26544 PRELIMINARY; PRT; 373 AA.

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AC O26544;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE SENSORY TRANSDUCTION HISTIDINE KINASE.
GN MTH444.
OS METHANOBACTERIUM THERMOAUTOTROPHICUM.
OS ARCHAEBACTERIA; EURYARCHAEOTA; METHANOBACTERIALES;
OC METHANOBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RA SMITH D.R.; DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
RA ALBREDE T., BASHIRADEH R., BLAKELY D., COOK R., GILBERT K.,
RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTIER B., QIU D.,
RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R., JIWANI N.,
RA CARUSO A., BUSH D., SAFER H., FAWELL D., PRABHAKAR S., MCDUGALL S.,
RA SHMER G., GOYAL A., PIETROVSKI S., CHURCH G.M., DANIELS C.J.,
RA MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
RL J. BACTERIOL. 179:7135-7155(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RA SMITH D.R.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF000828; G2621510; -
SQ SEQUENCE 373 AA; 42263 MW; A636962D CRC32;

Query Match 58.1%; Score 54; DB 9; Length 373;
Best Local Similarity 60.0%; Pred. No. 1.24e+00;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 277 IKFTRDRDPA 286
Qy 1 INFTRQPS 10
|:||||:|:|

RESULT 15
ID O36206 PRELIMINARY; PRT; 96 AA.
AC O36206;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OS VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RA SONG J., WANG B., GE Y.C., DWYER D., DOWTON D., CUNNINGHAM A.,
RA SAKSANA N.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF000318; G2333859; -
SQ SEQUENCE 96 AA; 11323 MW; 3AFB9942 CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRRARGAS 94
Qy 1 INFTRQPS 14
|:||||:|:|

RESULT 16
ID O42054 PRELIMINARY; PRT; 96 AA.
AC O42054;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OS VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RA SONG J., WANG B., GE Y.C., DWYER D., DOWTON D., CUNNINGHAM A.,
RA SAKSANA N.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF000318; G2333859; -
SQ SEQUENCE 96 AA; 11323 MW; 3AFB9942 CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRRARGAS 94
Qy 1 INFTRQPS 14
|:||||:|:|

RESULT 17
ID Q79246 PRELIMINARY; PRT; 96 AA.
AC Q79246;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OS VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 0709, HOMOSEXUAL, DUTCH;
RA KUIKEN L., CORNELISSEN E., ZORGRADGER F., HARTMAN S., GIBBS J.,
RA GOUDSMIT J.;
RL J. GEN. VIROL. 0:0-0(1996).
DR EMBL; Z68551; E218426; -
SQ SEQUENCE 96 AA; 11488 MW; 21D0C46C CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRRARGAS 94
Qy 1 INFTRQPS 14
|:||||:|:|

RESULT 18
ID Q79284 PRELIMINARY; PRT; 96 AA.
AC Q79284;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OS VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 0070, IV DRUG USER, DUTCH;
RA KUIKEN L., CORNELISSEN E., ZORGRADGER F., HARTMAN S., GIBBS J.,
RA GOUDSMIT J.;
RL J. GEN. VIROL. 0:0-0(1996).
DR EMBL; Z68585; E218358; -
SQ SEQUENCE 96 AA; 11327 MW; E04768CA CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RA SONG J., WANG B., GE Y.C., DWYER D., DOWTON D., CUNNINGHAM A.,
RA SAKSANA N.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF000321; G2393865; -
DR EMBL; AF000320; G2393863; -
SQ SEQUENCE 96 AA; 11351 MW; 66A4027D CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRRARGAS 94
Qy 1 INFTRQPS 14
|:||||:|:|

RESULT 17
ID Q79246 PRELIMINARY; PRT; 96 AA.
AC Q79246;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OS VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 0709, HOMOSEXUAL, DUTCH;
RA KUIKEN L., CORNELISSEN E., ZORGRADGER F., HARTMAN S., GIBBS J.,
RA GOUDSMIT J.;
RL J. GEN. VIROL. 0:0-0(1996).
DR EMBL; Z68551; E218426; -
SQ SEQUENCE 96 AA; 11488 MW; 21D0C46C CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRRARGAS 94
Qy 1 INFTRQPS 14
|:||||:|:|

RESULT 18
ID Q79284 PRELIMINARY; PRT; 96 AA.
AC Q79284;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OS VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 0070, IV DRUG USER, DUTCH;
RA KUIKEN L., CORNELISSEN E., ZORGRADGER F., HARTMAN S., GIBBS J.,
RA GOUDSMIT J.;
RL J. GEN. VIROL. 0:0-0(1996).
DR EMBL; Z68585; E218358; -
SQ SEQUENCE 96 AA; 11327 MW; E04768CA CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Db 81 IGITRRARRNGAS 94
QY 1 INFTRQPSGSS 14

RESULT 19
ID O36203 PRELIMINARY; PRT; 96 AA.
AC O36203;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RA SONG J., WANG B., GE Y.C., DWYER D., DOWTON D., CUNNINGHAM A.,
RA SAKSENA N.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF000315; G3393853; -.
SQ SEQUENCE 96 AA; 11349 MW; C0013AFA CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGAS 94
QY 1 INFTRQPSGSS 14

RESULT 20
ID O36205 PRELIMINARY; PRT; 96 AA.
AC O36205;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RA SONG J., WANG B., GE Y.C., DWYER D., DOWTON D., CUNNINGHAM A.,
RA SAKSENA N.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF000317; G3393857; -.
SQ SEQUENCE 96 AA; 11367 MW; 0840C3DA CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGAS 94
QY 1 INFTRQPSGSS 14

RESULT 21
ID O75757 PRELIMINARY; PRT; 96 AA.
AC O75757;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.

RN SEQUENCE FROM N.A.
RP STRAIN-JREL; TISSUE-BRAIN;
RA KOYANAGI Y., MILES S., MITSUYASU R.T., MERRILL J.E., VINTERS H.V.,
RA CHEN I.S.;
RL SCIENCE 236:819-822(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-JREL; TISSUE-BRAIN;
RX MEDLINE; 91043044.
RA O'BRIEN W.A., KOYANAGI Y., NAMAZIE A., ZHAO J.Q., DIAGNE A.,
RA IDLER K., ZACK J.A., CHEN I.S.;
RL NATURE 348:69-73(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-JREL; TISSUE-BRAIN;
RX MEDLINE; 92092169.
RA PANG S., VINTERS H.V., AKASHI T., O'BRIEN W.A., CHEN I.S.;
RL J. ACQUIR. IMMUNE DEFIC. SYNDR. 4:1082-1092(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-JREL; TISSUE-BRAIN;
RA PANG S., VINTERS H.V., AKASHI T., O'BRIEN W.A., CHEN I.S.,
RA KOYANAGI Y., NAMAZIE A., ZHAO J., DIAGNE A., IDLER K.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U63632; G1465784; -.
SQ SEQUENCE 96 AA; 11377 MW; 50CD3483 CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGAS 94
QY 1 INFTRQPSGSS 14

RESULT 22
ID O79282 PRELIMINARY; PRT; 96 AA.
AC O79282;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 3057, IV DRUG USER, DUTCH;
RA KUIKEN L., CORNELISSEN E., ZORGRAGER F., HARTMAN S., GIBBS J.,
RA GOUDSMIT J.;
RL J. GEN. VIROL. 0:0-0(1996).
DR EMBL: Z68584; E218438; -.
SQ SEQUENCE 96 AA; 11369 MW; 4C351F74 CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGAS 94
QY 1 INFTRQPSGSS 14

RESULT 23
ID Q89516 PRELIMINARY; PRT; 96 AA.
AC Q89516;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE VPR PROTEIN.

GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT LW;
RA WANG B., CHUN GE Y.C., PALASANTHIRAN P., XIANG S.H., ZIEGLER J.,
RA RANDLE C., DOWTON D., CUNNINGHAM A., SAKSENA N.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT LW;
RA BLOUIN C.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
SQ SEQUENCE 96 AA; 11323 MW; 36B8DAC9 CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGAS 94
| :||||: :|:
QY 1 INFTRQPSGSS 14

RESULT 24
ID Q79234 PRELIMINARY; PRT; 96 AA.
AC Q79234;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 0140, HOMOSEXUAL, DUTCH;
RA KUIKEN L., CORNELISSEN E., ZORGRAGER F., HARTMAN S., GIBBS J.,
RA GOUDSMIT J.;
RL J. GEN. VIROL. 0:0-0(1996).
DR EMBL; 268540; E218330; -.
SQ SEQUENCE 96 AA; 11338 MW; E5898B92 CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGAS 94
| :||||: :|:
QY 1 INFTRQPSGSS 14

RESULT 25
ID Q79247 PRELIMINARY; PRT; 96 AA.
AC Q79247;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 1145, HOMOSEXUAL, DUTCH;
RA KUIKEN L., CORNELISSEN E., ZORGRAGER F., HARTMAN S., GIBBS J.,
RA GOUDSMIT J.;
RL J. GEN. VIROL. 0:0-0(1996).
DR EMBL; 268552; E218337; -.

SQ SEQUENCE 96 AA; 11323 MW; 250A3402 CRC32;
Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGAS 94
| :||||: :|:
QY 1 INFTRQPSGSS 14

RESULT 26
ID Q79244 PRELIMINARY; PRT; 96 AA.
AC Q79244;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT 0617, HOMOSEXUAL, DUTCH;
RA KUIKEN L., CORNELISSEN E., ZORGRAGER F., HARTMAN S., GIBBS J.,
RA GOUDSMIT J.;
RL J. GEN. VIROL. 0:0-0(1996).
DR EMBL; 268549; E218425; -.
SQ SEQUENCE 96 AA; 11378 MW; D20333D8 CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGTS 94
| :||||: :|:
QY 1 INFTRQPSGSS 14

RESULT 27
ID Q74809 PRELIMINARY; PRT; 96 AA.
AC Q74809;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE VPR PROTEIN.
GN VPR.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-D31;
RX MEDLINE; 93090480.
RA KREUTZ R., DIETRICH U., KUHNEL H., NIESELT-STUWE K., EIGEN M.,
RA RUBSAMEN-WAIGMANN H.;
RL AIDS RES. HUM. RETROVIRUSES 8:1619-1629(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-D31;
RA BRYANT B.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U43096; G1171168; -.
SQ SEQUENCE 96 AA; 11386 MW; C2597A11 CRC32;

Query Match 57.0%; Score 53; DB 11; Length 96;
Best Local Similarity 50.0%; Pred. No. 2.06e+00;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 81 IGITRRARRNGAS 94
| :||||: :|:
QY 1 INFTRQPSGSS 14

QY 3 FTQRQPSGSS 14

Search completed: Tue Apr 7 08:38:14 1998
Job time : 14 secs.

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:41:04 1998; MasPar time 2.35 Seconds

Tabular output not generated. 86.413 Million cell updates/sec

Title: >US-08-190-411A-3
 Description: (1-12) from 5541104.pep
 Perfect Score: 82
 Sequence: 1 LFRVITKKVAD 12

Scoring table: PAM 150
 Gap 15

Searched: 111725 seqs, 16919825 residues

Post-processing: Minimum Match 0%
 Listing first 100 summaries

Database: a-geneseq30
 l:a-geneseq1

Statistics: Mean 19.964; Variance 25.854; scale 0.772

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	82	100.0	38	1 R80619	Immunogenic peptide of	1.60e-08
2	82	100.0	335	1 R70909	Human melanoma antigen	1.60e-08
3	65	79.3	36	1 R47325	HLA-A3 MAGE 1 antigen	3.04e-04
4	58	70.7	35	1 R47324	HLA-A3 MAGE 1 antigen	1.37e-02
5	58	70.7	35	1 R65120	MAGE 1 immunogenic pep	1.37e-02
6	58	70.7	35	1 R49228	HLA-A11 MAGE 1 antigen	1.37e-02
7	58	70.7	36	1 R65125	MAGE 1 immunogenic pep	1.37e-02
8	58	70.7	36	1 R49230	HLA-A11 MAGE 1 antigen	1.37e-02
9	48	58.5	604	1 W11578	Bacillus licheniformis	2.22e+00
10	47	57.3	335	1 R67916	(1-3)-beta-D-glucan se	3.59e+00
11	47	57.3	748	1 R98227	Rat neuronal protein k	3.59e+00
12	46	56.1	166	1 P91891	Part of the sequence o	5.77e+00
13	46	56.1	356	1 P81996	Sequence encoded by no	5.77e+00
14	46	56.1	569	1 W07702	Mouse ETS2 repressor f	5.77e+00
15	46	56.1	574	1 W07700	Human ETS2 repressor f	5.77e+00
16	46	56.1	754	1 R90617	Sulfolobus solfataricu	5.77e+00
17	45	54.9	185	1 R60900	Borrelia VSDA antigen	9.22e+00
18	45	54.9	199	1 R62793	Borrelia KL11 antigen	9.22e+00
19	45	54.9	199	1 R60908	Borrelia PBI antigen v	9.22e+00
20	45	54.9	200	1 R62786	Borrelia VSDA antigen	9.22e+00
21	45	54.9	201	1 R62784	Borrelia M57 antigen v	9.22e+00
22	45	54.9	203	1 R60904	Borrelia IP90 antigen	9.22e+00
23	45	54.9	203	1 R62792	Borrelia B1TS antigen	9.22e+00

Borrelia IP90 antigen	9.22e+00
Borrelia KL11 antigen	9.22e+00
Borrelia M57 antigen v	9.22e+00
Borrelia B1TS antigen	9.22e+00
B. burgdorferi strain	9.22e+00
G-protein coupled odor	9.22e+00
G-protein coupled odor	9.22e+00
Odorant receptor clone	9.22e+00
Dialkylglycine decarbo	9.22e+00
2,2-dialkylglycine dec	9.22e+00
H. pylori inner membra	9.22e+00
Rat neuronal protein k	9.22e+00
Borrelia 297 antigen v	1.46e+01
Borrelia 257 antigen v	1.46e+01
Borrelia 297 antigen v	1.46e+01
Cyclophilin C.	1.46e+01
Flavobacterium GGGP sy	1.46e+01
Fungal lipase	1.46e+01
Transcriptional co-rep	1.46e+01
Plasmodium falciparum	1.46e+01
Sequence of truncated	2.31e+01
Human cytomegalovirus	2.31e+01
Human cytomegalovirus	2.31e+01
I-19 B-lymphocyte deri	2.31e+01
Hornet phospholipase D	2.31e+01
Mannose-1-phosphate tr	2.31e+01
Geranol/nerol 10-hydr	2.31e+01
Md-alpha-E7 malathion	2.31e+01
Bacillus subtilis srfA	2.31e+01
NMDA receptor channel	2.31e+01
Saccharomyces cerevisi	2.31e+01
S. cerevisiae scaurk	2.31e+01
Glutamic acid receptor	2.31e+01
Rat NMDA receptor subu	2.31e+01
Human N-methyl-D-aspar	2.31e+01
Human NMDA receptor R2	2.31e+01
Human excitatory amino	2.31e+01
Monocyte chemoattracta	3.62e+01
Monocyte chemoattracta	3.62e+01
Monocyte chemoattracta	3.62e+01
Monocyte chemoattracta	3.62e+01
(28-Asp) MCP-1.	3.62e+01
MCF.	3.62e+01
Sense MCP-1.	3.62e+01
H. pylori secreted or	3.62e+01
MCF.	3.62e+01
H. pylori secreted or	3.62e+01
APP haemolysin activat	3.62e+01
Mouse MD52 Cl.	3.62e+01
S-SPV-001 potential eu	3.62e+01
Human Yes-associated p	3.62e+01
Mouse Yes-associated p	3.62e+01
GroEL-1 protein.	3.62e+01
Fusion protein of 59-v	3.62e+01
A.nidulans phospheno	3.62e+01
HVTA antigen.	3.62e+01
Beat-galactosidase/hep	3.62e+01
Merozoite apical-end p	3.62e+01
PS17b acaride-active t	3.62e+01
Bacillus thuringiensis	3.62e+01
BT toxin 17b.	3.62e+01
BT toxin 17b.	3.62e+01
Toxin 17b.	3.62e+01
B. thuringiensis toxin	3.62e+01
Bacillus thuringiensis	3.62e+01
Protein tyrosine-kinas	3.62e+01
lktA::lacZ fusion prot	3.62e+01
LktA::lacZ fusion produ	3.62e+01
BT toxin 17a.	3.62e+01
Bacillus thuringiensis	3.62e+01

97 42 51.2 1411 1 R44201 Bacillus thuringiensis 3.62e+01
 98 42 51.2 1411 1 R20066 B.thuringiensis toxin 3.62e+01
 99 42 51.2 1411 1 R28803 BT toxin 17a. 3.62e+01
 100 42 51.2 1411 1 R58631 Bacillus thuringiensis 3.62e+01

ALIGNMENTS

RESULT 1
 ID R80619 standard; Protein; 12 AA.
 AC R80619;
 DT 28-FEB-1996 (first entry)
 DE Immunogenic peptide of tumour rejection antigen (MAGE-1).
 KW Tumour rejection antigen; MAGE-1; monoclonal antibody; Mab;
 KW diagnosis; immunoassay; cancer; immunogen; antisera.
 OS Homo sapiens.
 PN W09520974-A1.
 PD 10-AUG-1995.
 PF 05-JAN-1995; U000095.
 PR 01-FEB-1994; US-190411.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.
 PI Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;
 PI Stockert E, Van der bruggen P;
 DR WPI: 95-283606/37.
 DT New monoclonal antibody binding specifically to MAGE-1 - useful for
 PT diagnosis and monitoring of cancer, also new hybridomas, recombinant
 PT MAGE-1 and immunogenic peptide(s).
 PS Claim 12; Page 20; 33pp; English.
 CC A monoclonal antibody directed against the tumour rejection antigen
 CC (MAGE-1) can be used to detect MAGE-1 in samples by standard
 CC immunoassay methods for diagnosis and monitoring of cancer etc. The
 CC monoclonal antibody is designated MA454 and is produced by the
 CC hybridoma deposited as ATCC HB11540. The monoclonal antibody is
 CC specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
 CC Peptide fragments of MAGE-1 (See R80618-20) may be useful as
 CC immunogens for production of the monoclonal antibody and antisera.
 SQ Sequence 12 AA;

Query Match 100.0%; Score 82; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.60e-08;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 LFRVITKKVAD 38
 QY 1 LFRVITKKVAD 12
 |||||||

RESULT 2
 ID R70909 standard; Protein; 309 AA.
 AC R70909;
 DT 09-OCT-1995 (first entry)
 DE Human melanoma antigen MAGE-1.
 DE Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;
 KW HLA-restricted cytotoxic T-lymphocyte activity.
 OS Homo sapiens.
 PN W09504542-A.
 PD 16-FEB-1995.
 PF 02-AUG-1994; U08721.
 PR 06-AUG-1993; US-103623.
 PA (CYTE-) CYTEL CORP.
 PI Fikes JD, Livingston BD, Sette AD, Sidney JC;
 DR WPI: 95-090881/12.
 DR N-PSDB; Q85435.
 DT Human melanoma antigen, MAGE-1, peptide(s) - useful for
 PT stimulating immune response against melanoma
 PS Example 1; Fig 1; 59pp; English.
 CC Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used
 CC to produce the C-terminal MAGE-1 peptides described in R70915 to
 CC R70969. These peptides are useful for defining epitopes that
 CC engender a HLA-restricted cytotoxic lymphocyte activity against
 CC MAGE-1 antigens. Compsns. containing these peptides can be

CC administered, as a vaccine to patients susceptible to MAGE
 CC associated tumours, e.g. melanomas.
 SQ Sequence 309 AA;

Query Match 100.0%; Score 82; DB 1; Length 335;
 Best Local Similarity 100.0%; Pred. No. 1.60e-08;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 LFRVITKKVAD 134
 QY 1 LFRVITKKVAD 12
 |||||||

RESULT 3
 ID R47325 standard; Protein; 10 AA.
 AC R47325;
 DT 31-AUG-1994 (first entry)
 DE HLA-A3 MAGE 1 antigen peptide fragment 96-105.
 DE Immunogenic; HLA-A3.2; HLA-A1; binding motif; MHC molecule;
 KW immune response; viral infection; cancer; prostate cancer; lymphoma;
 KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
 OS Synthetic.
 PN W09403205-A.
 PD 17-FEB-1994.
 PF 06-AUG-1993; U07421.
 PR 07-AUG-1992; US-926666.
 PR 05-MAR-1993; US-027746.
 PA (CYTE-) CYTEL CORP.
 PA Celis E, Grey HM, Kubo RT, Sette A;
 DR WPI: 94-065403/08.
 DT Peptide which specifically binds selected MHC allele - used to
 PT induce an immune response for treatment or prevention of viral
 PT infection or cancer, or for diagnosis
 PS Example 8; Page 52; 150pp; English.
 CC The sequences given in R47304-33 and R49201-44 are immunogenic
 CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
 CC These peptides may be used in the composition of the invention.
 CC These peptides are capable of binding selected MHC molecules and
 CC inducing an immune response. They can be used to treat and/or
 CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
 CC hepatitis or AIDS. They can also be used to produce antibodies for
 CC use as diagnostic or therapeutic agents. The peptides can also be
 CC used as diagnostic agents.
 SQ Sequence 10 AA;

Query Match 79.3%; Score 65; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.04e-04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 LFRVITKK 36
 QY 1 LFRVITKK 9
 |||||||

RESULT 4
 ID R47324 standard; Protein; 9 AA.
 AC R47324;
 DT 31-AUG-1994 (first entry)
 DE HLA-A3 MAGE 1 antigen peptide fragment 96-104.
 DE Immunogenic; HLA-A3.2; HLA-A1; binding motif; MHC molecule;
 KW immune response; viral infection; cancer; prostate cancer; lymphoma;
 KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
 OS Synthetic.
 PN W09403205-A.
 PD 17-FEB-1994.
 PF 06-AUG-1993; U07421.
 PR 07-AUG-1992; US-926666.
 PR 05-MAR-1993; US-027746.
 PA (CYTE-) CYTEL CORP.
 PA Celis E, Grey HM, Kubo RT, Sette A;
 DR WPI: 94-065403/08.
 DT Peptide which specifically binds selected MHC allele - used to
 PT induce an immune response for treatment or prevention of viral

PT infection or cancer, or for diagnosis
 PS Example 8; Page 52; 150pp; English.
 CC The sequences given in R47304-33 and R49201-44 are immunogenic
 CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
 CC These peptides may be used in the composition of the invention.
 CC These peptides are capable of binding selected MHC molecules and
 CC inducing an immune response. They can be used to treat and/or
 CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
 CC hepatitis or AIDS. They can also be used to produce antibodies for
 CC use as diagnostic or therapeutic agents. The peptides can also be
 CC used as diagnostic agents.
 SQ Sequence 9 AA;

Query Match 70.7%; Score 58; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.37e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 LFRVAVTK 35
 |||||
 QY 1 LFRVAVTK 8

RESULT 5
 ID R65120 standard; peptide; 9 AA.
 AC R65120;
 DT 09-OCT-1995 (first entry)
 DE MAGE 1 immunogenic peptide 96-104.
 KW MAGE 1; immunogenic peptide 96-104; cytotoxic C cells;
 KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
 KW fungal infections; tuberculosis; hepatitis.
 OS Homo sapiens.
 PN WO9504817-A.
 PD 16-FEB-1995.
 PF 01-AUG-1994; U08672.
 PR 06-AUG-1993; US-103401.
 PA (CYTE-) CYTEL CORP.
 PI Cells E, Kubo R, Serra H, Tsai V, Wentworth P;
 DR WPI; 95-090895/12.
 PT In vitro activation of cytotoxic T cells for selected killing of
 PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
 PT incubating them with antigen presenting cells loaded with
 PT appropriate immunogenic peptide

PS Example 3; Page 35; 53pp; English.
 CC R65109-R65145 are immunogenic peptides, they are used in a new
 CC method for the in vitro activation of cytotoxic T cells (CTC).
 CC This is achieved by incubating the CTCs with antigen presenting
 CC cells loaded with an appropriate immunogenic peptide (e.g. one
 CC of the above peptides). By selecting the peptides used the
 CC following diseases and infections can be treated; cancer, AIDS,
 CC hepatitis, other viral and bacterial infections, malaria and
 CC tuberculosis.
 SQ Sequence 9 AA;

Query Match 70.7%; Score 58; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.37e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 LFRVAVTK 35
 |||||
 QY 1 LFRVAVTK 8

RESULT 6
 ID R49228 standard; Protein; 9 AA.
 AC R49228;
 DT 31-AUG-1994 (first entry)
 DE HLA-A11 MAGE 1 antigen peptide fragment 1072.13.
 KW Immunogenic; HLA-A3.2; HLA-A1; binding motif; MHC molecule;
 KW immune response; viral infection; cancer; prostate cancer; lymphoma;
 KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
 OS Synthetic.
 PN WO9403205-A.
 PD 17-FEB-1994.

PF 06-AUG-1993; U07421.
 PR 07-AUG-1992; US-926666.
 PR 05-MAR-1993; US-027746.
 PA (CYTE-) CYTEL CORP.
 PI Cells E, Grey HM, Kubo RT, Sette A;
 DR WPI; 94-063403/08.
 PT Peptide which specifically binds selected MHC allele - used to
 PT induce an immune response for treatment or prevention of viral
 PT infection or cancer, or for diagnosis.
 PS Example 16; Page 116; 150pp; English.
 CC The sequences given in R47304-33 and R49201-44 are immunogenic
 CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
 CC These peptides may be used in the composition of the invention.
 CC These peptides are capable of binding selected MHC molecules and
 CC inducing an immune response. They can be used to treat and/or
 CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
 CC hepatitis or AIDS. They can also be used to produce antibodies for
 CC use as diagnostic or therapeutic agents. The peptides can also be
 CC used as diagnostic agents.
 SQ Sequence 9 AA;

Query Match 70.7%; Score 58; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.37e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 LFRVAVTK 35
 |||||
 QY 1 LFRVAVTK 8

RESULT 7
 ID R65125 standard; peptide; 10 AA.
 AC R65125;
 DT 09-OCT-1995 (first entry)
 DE MAGE 1 immunogenic peptide 95-104.
 KW MAGE 1; immunogenic peptide 95-104; cytotoxic C cells;
 KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
 KW fungal infections; tuberculosis; hepatitis.
 OS Homo sapiens.
 PN WO9504817-A.
 PD 16-FEB-1995.
 PF 01-AUG-1994; U08672.
 PR 06-AUG-1993; US-103401.
 PA (CYTE-) CYTEL CORP.
 PI Cells E, Kubo R, Serra H, Tsai V, Wentworth P;
 DR WPI; 95-090895/12.
 PT In vitro activation of cytotoxic T cells for selected killing of
 PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
 PT incubating them with antigen presenting cells loaded with
 PT appropriate immunogenic peptide

PS Example 3; Page 35; 53pp; English.
 CC R65109-R65145 are immunogenic peptides, they are used in a new
 CC method for the in vitro activation of cytotoxic T cells (CTC).
 CC This is achieved by incubating the CTCs with antigen presenting
 CC cells loaded with an appropriate immunogenic peptide (e.g. one
 CC of the above peptides). By selecting the peptides used the
 CC following diseases and infections can be treated; cancer, AIDS,
 CC hepatitis, other viral and bacterial infections, malaria and
 CC tuberculosis.
 SQ Sequence 10 AA;

Query Match 70.7%; Score 58; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.37e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 LFRVAVTK 36
 |||||
 QY 1 LFRVAVTK 8

RESULT 8
 ID R49230 standard; Protein; 10 AA.
 AC R49230;

31-AUG-1994 (first entry)
 HLA-A11 MAGE 1 antigen peptide fragment 1072.15.
 Immunogenic: HLA-A3.2, HLA-A1; binding motif; MHC molecule;
 immune response; viral infection; cancer; prostate cancer; lymphoma;
 hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
 OS Synthetic.
 PN WO9403205-A.
 PD 17-FEB-1994.
 PF 06-AUG-1993; U07421.
 PR 07-AUG-1992; US-926666.
 PR 05-MAR-1993; US-027746.
 PA (CYTE-) CYTEL CORP.
 PI Celis E, Grey HM, Kubo RT, Sette A;
 WPI; 94-065403/08.
 DR Peptide which specifically binds selected MHC allele - used to
 induce an immune response for treatment or prevention of viral
 infection or cancer, or for diagnosis.
 PT Example 16; Page 116; 150pp; English.
 PS The sequences given in R47304-33 and R49201-44 are immunogenic
 CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
 CC These peptides may be used in the composition of the invention.
 CC These peptides are capable of binding selected MHC molecules and
 CC inducing an immune response. They can be used to treat and/or
 CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
 CC hepatitis or AIDS. They can also be used to produce antibodies for
 CC use as diagnostic or therapeutic agents. The peptides can also be
 CC used as diagnostic agents.
 SQ Sequence 10 AA;

Query Match 70.7%; Score 58; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.37e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 LFRVITVK 36
 |||||
 QY 1 LFRVITVK 8

RESULT 9
 ID W11578 standard; Protein; 578 AA.
 AC W11578;
 DE 23-MAR-1997 (first entry)
 DE Bacillus licheniformis maltogenic amylase.
 KW BLMA; amylolytic enzyme; maltogenic amylase; alpha-1,6-linkage;
 KW branched oligosaccharide; pullulan; cyclodextrin; hydrolysis;
 KW sugar transferase activity.
 OS Bacillus licheniformis (AFCC 27811).
 FH Key Location/Qualifiers
 FT Region 238..244
 FT /label= conserved_motif
 FT /note= Putative calcium binding domain"
 FT Region 319..326
 FT /label= conserved_motif
 FT /note= "sequence conserved among amylases"
 FT Region 349..352
 FT /label= conserved_motif
 FT /note= "sequence conserved among amylases"
 FT Region 411..416
 FT /label= conserved_motif
 FT /note= "sequence conserved among amylases"
 PN US583039-A.
 PD 10-DEC-1996.
 PF 07-JUN-1990; 534679.
 PR 07-JUN-1990; US-534679.
 PR 12-NOV-1993; US-152271.
 PA (DOOS-) DOOSAN TECH CENT.
 PA (SUNH-) SUNHILL GLUCOSE CO LTD.
 PA (SUNK-) SUNKYONG IND LTD.
 PI Cha JH, Choi YD, Jang SY, Kim IC, Kim JR, Kim KH;
 PI Park KH, Seo BC;
 DR WPI; 97-042316/04.
 DR N-PSDB; T58548.
 - Recombinant E. coli strain - contg. gene coding for Bacillus

PT licheniformis maltogenic amylase
 PS Claim 2; Fig 2; 21pp; English.
 CC A genomic library was constructed from EcoRI- and BamHI-partially
 CC digested chromosomal DNA of Bacillus licheniformis. The DNA
 CC fragments were cloned into plasmid pBR322 and transformed into
 CC E.coli HB101. Ampicillin-resistant colonies were screened for
 CC amylolytic activity on starch agar. One positive colony showed starch
 CC hydrolysing phenotype after the cell membrane was disrupted
 CC with D-cycloserine. The DNA insert from positive transformants was
 CC 3.5 kb long. A subfragment containing an open reading frame of 1740
 CC nucleotides was sequenced. The gene product has the present deduced
 CC amino acid sequence and is a B.licheniformis maltogenic amylase
 CC (BLMA) which hydrolyses starch, pullulan and cyclodextrin at an optimum
 CC temperature of 50 deg.C and pH 7. The enzyme also has sugar
 CC transferase activity in the presence of glucose. A previously
 CC reported BLMA enzyme was thermostable and only hydrolysed starch.
 CC The new BLMA can be used for synthesising branched oligosaccharides
 CC with alpha-1,6-linkages.
 SQ Sequence 578 AA;

Query Match 58.5%; Score 48; DB 1; Length 604;
 Best Local Similarity 50.0%; Pred. No. 2.22e+00;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 247 LFRVWVR 254
 |||:|:
 QY 1 LFRVITVK 8

RESULT 10
 ID R67916 standard; Protein; 309 AA.
 AC R67916;
 DE 14-SEP-1995 (first entry)
 DE (1-3)-beta-D-glucan sensitive factor.
 DE (1-3)-beta-D-glucan sensitive factor; antifungal agent;
 KW mycosis diagnosis.
 OS Limulus sp.

FH Key Location/Qualifiers
 FT Peptide 1..31
 FT /label= sig_peptide
 FN WO9501432-A.
 PD 12-JAN-1995.
 PF 29-JUN-1994; J01057.
 PR 29-JUN-1993; JP-184403.
 PA (SEKG) SEIKAGAKU KOGYO CO LTD.
 PI Iwanaga S, Muta T, Oda T, Seki N;
 DR WPI; 95-060996/08.
 DR N-PSDB; Q81335.
 DR DNA encoding a polypeptide comprising a tetrapeptide motif at
 PT least once - which may be used as an antibacterial and
 PT antifungal.
 PS Claim 11; Pages 32-38; 51pp; Japanese.
 CC Q81335 encodes R67916 a (1-3)-beta-D-glucan sensitive factor, it
 CC has a high affinity for the (1-3)-beta-D-glucan found in fungal
 CC cell walls. The protein is therefore useful for clinically
 CC diagnosing mycosis, and as an antifungal agent for the removal
 CC of fungi.
 SQ Sequence 309 AA;

Query Match 57.3%; Score 47; DB 1; Length 335;
 Best Local Similarity 50.0%; Pred. No. 3.59e+00;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 66 FRPVITRIIG 75
 ||:|:|:
 QY 2 FRVITKKVA 11

RESULT 11
 ID R98227 standard; Protein; 722 AA.
 AC R98227;
 DE 23-SEP-1996 (first entry)
 DE Rat neuronal protein kinase MARK-2.

KW Neuronal protein kinase; NPK; microtubule associated protein;
 KW MAP; tau protein; phosphorylation; NPK inhibitor; Alzheimer disease;
 KW cancer; therapy; diagnosis.
 OS Rattus norvegicus.
 PN W09613592-A2.
 PD 09-MAY-1996.
 PR 30-OCT-1995; E04258.
 PR 28-OCT-1994; EP-117122.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PI Biernat J, Drewes G, Mandelkow E;
 DR WPI; 96-251461/25.
 PT DNA encoding neuronal protein kinase (NPK) - useful for identifying
 PT NPK inhibitors for treatment of Alzheimer's disease and cancer.
 PS Claim 1; Page 44-45; 77pp; English.
 CC A novel rat neuronal protein kinase (R98227), designated NPK MARK-2,
 CC is capable of phosphorylating a XGS sequence motif in tau protein
 CC and microtubule associated proteins MAP4, MAP2 and MAP2c (see also
 CC R98229-39 and W00850-54), causing their dissociation from microtubules.
 CC Phosphorylation of human tau Ser-262 is indicative of the onset of
 CC Alzheimer's disease. MARK-1 is the product of a cDNA clone obtd.
 CC from a rat brain cDNA library by screening with probes derived
 CC from pig brain peptide sequences (see also R98240-50). Another NPK,
 CC MARK-1 (R98226), was similarly isolated. Inhibitors (e.g. antibodies)
 CC of NPKs are used to treat Alzheimer's disease and cancer. NPKs are
 CC themselves used for in vitro diagnosis and/or monitoring of
 CC Alzheimer's disease and cancer.
 SQ Sequence 722 AA;

Query Match 57.3%; Score 47; DB 1; Length 748;
 Best Local Similarity 60.0%; Pred. No. 3.59e+00;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 123 LFEVRIMKV 132
 QY 1 LFRVITKKV 10
 ||| | :||

RESULT 12
 ID P91891 standard; protein; 140 AA.
 AC P91891;
 DT 29-APR-1990 (first entry)
 DE Part of the sequence of the Brazil nut 2S-albumin as encoded in the
 DE PBN2S1 plasmid
 KW 2S-albumin; Brazil nut; PBN2S1; storage protein gene;
 KW heterologous polypeptide.
 OS Brazil nut.
 FH Key Location/Qualifiers
 FT peptide 1..30
 FT /note="signal peptide"
 FT protein 31..38
 FT /note="mature small subunit"
 FT region 39..43
 FT /note="processing site"
 FT protein 44..136
 FT /note="mature large subunit"
 PN W08903867-A.
 PD 05-MAY-1989.
 PF 20-OCT-1988; E00944.
 PR 20-OCT-1987; EP-402348.
 PA (PLAN-) Plant Genetic Syst.
 PI Vandekerckhove JS, Krebbers E, Botterman J, Leemans J;
 DR WPI; 89-150783/20.
 DR N-PSDB; N91699.
 PT Recombinant DNA expression in plants
 PT - using modified storage protein genes for expressing
 PT heterologous polypeptide(s) in the seeds
 PS Figure 4; 12lpp; English.
 CC The entire 2S-albumin storage protein precursor including
 CC signal peptide. It is to be inserted into plants under the control of
 CC a seed-specific promoter and expressed at high levels only or mostly
 CC in the seed forming stage and produced mostly in the seeds.
 SQ Sequence 140 AA;

Query Match 56.1%; Score 46; DB 1; Length 166;
 Best Local Similarity 45.5%; Pred. No. 5.77e+00;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Db 43 FRATVTTTVE 53
 QY 2 FRATVTRKQAD 12
 ||| :|| :
 RESULT 13
 ID P81996 standard; protein; 330 AA.
 AC P81996;
 DT 17-DEC-1990 (first entry)
 DE Sequence encoded by nodulation regulatory gene 2 (nodD-2) of
 DE Bradyrhizobium japonicum strain USDA 123
 KW Rhizobium; symbiosis; legume.
 OS Bradyrhizobium japonicum USDA 123.
 PN W08707910-A.
 PD 30-DEC-1987.
 PF 17-JUN-1987; U01421.
 PR 7-JUN-1986; US-875297.
 PR 11-JUN-1987; US-061848.
 PA (LUBR) Lubrizol Genetics I.
 PI Appelbaum ER, Hennecke H, Lamb JW, Gottfert M;
 DR WPI; 88-014399/02.
 DR N-PSDB; N82007.
 PT DNA contg. nodulation regulatory genes (nod D) -
 PT from Bradyrhizobium japonicum strains, useful for selective
 PT expression of structural genes
 PS Disclosure; 4-4; 88pp; English.
 CC DNA sequence of the nodD-1 gene coding region of B.japonicum USDA 110 is
 CC almost identical to that of USDA 123 (N82006) with single base change in
 CC codon 139 which is GAC in USDA 110. The deduced protein sequences of the
 CC two nodD-1 differ by one AA at position 139, which is Asp in USDA 110.
 CC nodD-2 may be used to enhance competitiveness of strains for nodulation
 CC and in the selective manipulation of nodulation host range of strains.
 SQ Sequence 330 AA;

Query Match 56.1%; Score 46; DB 1; Length 356;
 Best Local Similarity 50.0%; Pred. No. 5.77e+00;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 137 LFRNVVAR 144
 QY 1 LFRAVITK 8
 ||| |:::

RESULT 14
 ID W07702 standard; Protein; 543 AA.
 AC W07702;
 DT 06-APR-1997 (first entry)
 DE Mouse ETS2 repressor factor (ERF).
 KW ETS2 repressor factor; ERF; transcriptional repressor;
 KW tumour suppressor; tumour; cancer; oncoprotein; therapy.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT Domain 21..98
 FT /label= DNA_binding_domain
 FT /note= "ets-like DNA binding domain"
 FT Domain 466..525
 FT /label= Active_repressor_domain
 PN W09639517-A1.
 PD 12-DEC-1996.
 PF 04-JUN-1996; U10177.
 PR 05-JUN-1995; US-469412.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Achanasious MA, Beal GJ, Blair DG, Fisher RJ, Mavrothalassitis GJ;
 DR WPI; 97-043139/04.
 DR N-PSDB; T47200.
 PT New DNA encoding ETS2 repressor factor - useful for reducing
 PT tumorigenicity, esp. oncogene associated tumour cells
 PS Disclosure; Page 70-72; 10lpp; English.

DT. 29-JUN-1996 (first entry)

CC recombinant antigen pro
SO Sequence 159 AA:

CC recombinant antigen pro
SO Sequence 159 AA:

Query Match 54.9%; Score 45; DB 1; Length 185;
 Best Local Similarity 55.6%; Pred. No. 9.22e+00;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKITD 57
 :||:|:|:
 QY 4 AVITKKVAD 12

RESULT 18

ID R62793 standard; Protein; 173 AA.
 AC R62793;
 DT 25-MAY-1995 (first entry)
 DE Borrelia Kll1 antigen vaccine.
 KW OspC antigen; vaccine; Lyme disease; borreliosis; immunogen;
 KW serovar typing; restriction fragment length polymorphism;
 KW RFLP; Pichia pastoris.
 OS Borrelia burgdorferi Kll1.
 PN W09425596-A.
 PD 10-NOV-1994.
 PF 29-APR-1994; E01365.
 PR 29-APR-1993; US-053863.
 PA (IMMO) IMMUNO AG.
 PI Crowe B, Dörner F, Livey I;
 DR WPI: 94-358273/44.
 DR N-PSDB; Q73905.
 PT Immunogenic composition comprising OspC antigens - for the
 PT treatment of Lyme borreliosis in different, specific geographical
 PT areas.
 PS Disclosure: Fig. 9; 115pp; English.
 CC A vaccine for Lyme disease includes selected OspC antigen
 CC formulations based on defined OspC families resolved by serovar
 CC typing and RFLP typing. Partial sequences of OspC genes selected
 CC from different RFLP types are given in Q73883-905 (encoded peptides,
 CC comprising the first 92% of mature OspC, are given in R62771-93).
 CC Complete sequences of these novel OspC genes, including the 3' end,
 CC plus sequences for the OspC genes of Borrelia strains H13 and 28691
 CC are given in Q73857-82, and encoded proteins in R60884-909. The
 CC DNA sequences may be expressed in e.g. Pichia pastoris for
 CC recombinant antigen production.
 SQ Sequence 173 AA;

Query Match 54.9%; Score 45; DB 1; Length 199;
 Best Local Similarity 55.6%; Pred. No. 9.22e+00;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKITD 57
 :||:|:|:
 QY 4 AVITKKVAD 12

RESULT 19

ID R60508 standard; Protein; 173 AA.
 AC R60508;
 DT 25-MAY-1995 (first entry)
 DE Borrelia PBI antigen vaccine.
 KW OspC antigen; vaccine; Lyme disease; borreliosis; immunogen;
 KW serovar typing; restriction fragment length polymorphism;
 KW RFLP; Pichia pastoris.
 OS Borrelia burgdorferi PBI.
 PN W09425596-A.
 PD 10-NOV-1994.
 PF 29-APR-1994; E01365.
 PR 29-APR-1993; US-053863.
 PA (IMMO) IMMUNO AG.
 PI Crowe B, Dörner F, Livey I;
 DR WPI: 94-358273/44.
 DR N-PSDB; Q73881.
 PT Immunogenic composition comprising OspC antigens - for the
 PT treatment of Lyme borreliosis in different, specific geographical
 PT areas.
 PS Disclosure: Fig. 9a; 115pp; English.

CC A vaccine for Lyme disease includes selected OspC antigen
 CC formulations based on defined OspC families resolved by serovar
 CC typing and RFLP typing. Partial sequences of OspC genes selected
 CC from different RFLP types are given in Q73883-905 (encoded peptides,
 CC comprising the first 92% of mature OspC, are given in R62771-93).
 CC Complete sequences of these novel OspC genes, including the 3' end,
 CC plus sequences for the OspC genes of Borrelia strains H13 and 28691
 CC are given in Q73857-82, and encoded proteins in R60884-909. The
 CC DNA sequences may be expressed in e.g. Pichia pastoris for
 CC recombinant antigen production.
 SQ Sequence 173 AA;

Query Match 54.9%; Score 45; DB 1; Length 199;
 Best Local Similarity 55.6%; Pred. No. 9.22e+00;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKITD 57
 :||:|:|:
 QY 4 AVITKKVAD 12

RESULT 20

ID R62786 standard; Protein; 174 AA.
 AC R62786;
 DT 25-MAY-1995 (first entry)
 DE Borrelia VSDA antigen vaccine.
 KW OspC antigen; vaccine; Lyme disease; borreliosis; immunogen;
 KW serovar typing; restriction fragment length polymorphism;
 KW RFLP; Pichia pastoris.
 OS Borrelia burgdorferi VSDA.
 PN W09425596-A.
 PD 10-NOV-1994.
 PF 29-APR-1994; E01365.
 PR 29-APR-1993; US-053863.
 PA (IMMO) IMMUNO AG.
 PI Crowe B, Dörner F, Livey I;
 DR WPI: 94-358273/44.
 DR N-PSDB; Q73898.
 PT Immunogenic composition comprising OspC antigens - for the
 PT treatment of Lyme borreliosis in different, specific geographical
 PT areas.
 PS Disclosure: Fig. 9; 115pp; English.
 CC A vaccine for Lyme disease includes selected OspC antigen
 CC formulations based on defined OspC families resolved by serovar
 CC typing and RFLP typing. Partial sequences of OspC genes selected
 CC from different RFLP types are given in Q73883-905 (encoded peptides,
 CC comprising the first 92% of mature OspC, are given in R62771-93).
 CC Complete sequences of these novel OspC genes, including the 3' end,
 CC plus sequences for the OspC genes of Borrelia strains H13 and 28691
 CC are given in Q73857-82, and encoded proteins in R60884-909. The
 CC DNA sequences may be expressed in e.g. Pichia pastoris for
 CC recombinant antigen production.
 SQ Sequence 174 AA;

Query Match 54.9%; Score 45; DB 1; Length 200;
 Best Local Similarity 55.6%; Pred. No. 9.22e+00;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKITD 57
 :||:|:|:
 QY 4 AVITKKVAD 12

RESULT 21

ID R62784 standard; Protein; 175 AA.
 AC R62784;
 DT 25-MAY-1995 (first entry)
 DE Borrelia M57 antigen vaccine.
 KW OspC antigen; vaccine; Lyme disease; borreliosis; immunogen;
 KW serovar typing; restriction fragment length polymorphism;
 KW RFLP; Pichia pastoris.
 OS Borrelia burgdorferi M57.
 PN W09425596-A.

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PD 10-NOV-1994.
PF 29-APR-1994; E01365.
PR 29-APR-1993; US-053863.
PA (IMMO ) IMMUNO AG.
PI Crowe B, Dörner F, Livey I;
DR WPI; 94-358273/44.
DR N-PSDB; Q73896.
PT Immunogenic composition comprising OspC antigens - for the
PT treatment of Lyme borreliosis in different, specific geographical
PT areas.
PS Disclosure; Fig. 9; 115pp; English.
CC A vaccine for Lyme disease includes selected OspC antigen
CC formulations based on defined OspC families resolved by serovar
CC typing and RFLP typing. Partial sequences of OspC genes selected
CC from different RFLP types are given in Q73883-905 (encoded peptides,
CC comprising the first 92% of mature OspC, are given in R62771-93).
CC Complete sequences of these novel ospC genes, including the 3' end,
CC plus sequences for the ospC genes of Borrelia strains H13 and 28691
CC are given in Q73857-82, and encoded proteins in R60884-909. The
CC DNA sequences may be expressed in e.g. Pichia pastoris for
CC recombinant antigen production.
CC Sequence 175 AA;

Query Match 54.9%; Score 45; DB 1; Length 201;
Best Local Similarity 55.6%; Pred. No. 9.22e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKITD 57
QY 4 AVITKKVAD 12

RESULT 22
ID R60904 standard; Protein; 177 AA.
AC R60904;
DT 25-MAY-1995 (first entry)
DE Borrelia IP90 antigen vaccine.
KW OspC antigen; vaccine; Lyme disease; borreliosis; immunogen;
KW serovar typing; restriction fragment length polymorphism;
KW RFLP; Pichia pastoris.
OS Borrelia burgdorferi IP90.
PN WO9425596-A.
PD 10-NOV-1994.
PF 29-APR-1994; E01365.
PR 29-APR-1993; US-053863.
PA (IMMO ) IMMUNO AG.
PI Crowe B, Dörner F, Livey I;
DR WPI; 94-358273/44.
DR N-PSDB; Q60904.
PT Immunogenic composition comprising OspC antigens - for the
PT treatment of Lyme borreliosis in different, specific geographical
PT areas.
PS Disclosure; Fig. 9a; 115pp; English.
CC A vaccine for Lyme disease includes selected OspC antigen
CC formulations based on defined OspC families resolved by serovar
CC typing and RFLP typing. Partial sequences of OspC genes selected
CC from different RFLP types are given in Q73883-905 (encoded peptides,
CC comprising the first 92% of mature OspC, are given in R62771-93).
CC Complete sequences of these novel ospC genes, including the 3' end,
CC plus sequences for the ospC genes of Borrelia strains H13 and 28691
CC are given in Q73857-82, and encoded proteins in R60884-909. The
CC DNA sequences may be expressed in e.g. Pichia pastoris for
CC recombinant antigen production.
CC Sequence 177 AA;

Query Match 54.9%; Score 45; DB 1; Length 203;
Best Local Similarity 55.6%; Pred. No. 9.22e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKITD 57
QY 4 AVITKKVAD 12

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RESULT 23
ID R62792 standard; Protein; 177 AA.
AC R62792;
DT 25-MAY-1995 (first entry)
DE Borrelia BITS antigen vaccine.
KW OspC antigen; vaccine; Lyme disease; borreliosis; immunogen;
KW serovar typing; restriction fragment length polymorphism;
KW RFLP; Pichia pastoris.
OS Borrelia burgdorferi BITS.
PN WO9425596-A.
PD 10-NOV-1994.
PF 29-APR-1994; E01365.
PR 29-APR-1993; US-053863.
PA (IMMO ) IMMUNO AG.
PI Crowe B, Dörner F, Livey I;
DR WPI; 94-358273/44.
DR N-PSDB; Q73904.
PT Immunogenic composition comprising OspC antigens - for the
PT treatment of Lyme borreliosis in different, specific geographical
PT areas.
PS Disclosure; Fig. 9; 115pp; English.
CC A vaccine for Lyme disease includes selected OspC antigen
CC formulations based on defined OspC families resolved by serovar
CC typing and RFLP typing. Partial sequences of OspC genes selected
CC from different RFLP types are given in Q73883-905 (encoded peptides,
CC comprising the first 92% of mature OspC, are given in R62771-93).
CC Complete sequences of these novel ospC genes, including the 3' end,
CC plus sequences for the ospC genes of Borrelia strains H13 and 28691
CC are given in Q73857-82, and encoded proteins in R60884-909. The
CC DNA sequences may be expressed in e.g. Pichia pastoris for
CC recombinant antigen production.
CC Sequence 177 AA;

Query Match 54.9%; Score 45; DB 1; Length 203;
Best Local Similarity 55.6%; Pred. No. 9.22e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKITD 57
QY 4 AVITKKVAD 12

RESULT 24
ID R62790 standard; Protein; 177 AA.
AC R62790;
DT 25-MAY-1995 (first entry)
DE Borrelia IP90 antigen vaccine.
KW OspC antigen; vaccine; Lyme disease; borreliosis; immunogen;
KW serovar typing; restriction fragment length polymorphism;
KW RFLP; Pichia pastoris.
OS Borrelia burgdorferi IP90.
PN WO9425596-A.
PD 10-NOV-1994.
PF 29-APR-1994; E01365.
PR 29-APR-1993; US-053863.
PA (IMMO ) IMMUNO AG.
PI Crowe B, Dörner F, Livey I;
DR WPI; 94-358273/44.
DR N-PSDB; Q73902.
PT Immunogenic composition comprising OspC antigens - for the
PT treatment of Lyme borreliosis in different, specific geographical
PT areas.
PS Disclosure; Fig. 9; 115pp; English.
CC A vaccine for Lyme disease includes selected OspC antigen
CC formulations based on defined OspC families resolved by serovar
CC typing and RFLP typing. Partial sequences of OspC genes selected
CC from different RFLP types are given in Q73883-905 (encoded peptides,
CC comprising the first 92% of mature OspC, are given in R62771-93).
CC Complete sequences of these novel ospC genes, including the 3' end,
CC plus sequences for the ospC genes of Borrelia strains H13 and 28691
CC are given in Q73857-82, and encoded proteins in R60884-909. The
CC DNA sequences may be expressed in e.g. Pichia pastoris for

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CC recombinant antigen production.
SQ Sequence 177 AA;

Query Match 54.9%; Score 45; DB 1; Length 203;
Best Local Similarity 55.6%; Pred. No. 9.22e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKTD 57
:||||:|
QY 4 AVITKKVAD 12

RESULT 25

ID R60907 standard; Protein; 189 AA.

AC R60907; 1995 (first entry)

DE Borrelia KL11 antigen vaccine.

KW OSpC antigen; vaccine; Lyme disease; borreliosis; immunogen;

KW serovar typing; restriction fragment length polymorphism;

KW RFLP; Pichia pastoris.

OS Borrelia burgdorferi KL11.

PN W09425596-A.

PD 10-NOV-1994.

PF 29-APR-1994; E01365.

PR 29-APR-1993; US-053863.

PA (IMMO) IMMUNO AG.

PI Crowe B, Dörner F, Livey I;

DR WPI; 94-358273/44.

DR N-PSDB; Q73880.

PT Immunogenic composition comprising OSpC antigens - for the

PT treatment of Lyme borreliosis in different, specific geographical

PT areas.

PS Disclosure; Fig. 9a; 115pp; English.

CC A vaccine for Lyme disease includes selected OSpC antigen

CC formulations based on defined OSpC families resolved by serovar

CC typing and RFLP typing. Partial sequences of OSpC genes selected

CC from different RFLP types are given in Q73883-905 (encoded peptides,

CC comprising the first 92% of mature OSpC, are given in R62771-93).

CC Complete sequences of these novel OSpC genes, including the 3' end,

CC plus sequences for the OSpC genes of Borrelia strains H13 and 28691

CC are given in Q73857-82, and encoded proteins in R60884-909. The

CC DNA sequences may be expressed in e.g. Pichia pastoris for

CC recombinant antigen production.

CC Sequence 189 AA;

Query Match 54.9%; Score 45; DB 1; Length 215;
Best Local Similarity 55.6%; Pred. No. 9.22e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKTD 57
:||||:|
QY 4 AVITKKVAD 12

RESULT 26

ID R60898 standard; Protein; 191 AA.

AC R60898;

DE Borrelia M57 antigen vaccine.

KW OSpC antigen; vaccine; Lyme disease; borreliosis; immunogen;

KW serovar typing; restriction fragment length polymorphism;

KW RFLP; Pichia pastoris.

OS Borrelia burgdorferi M57.

PN W09425596-A.

PD 10-NOV-1994.

PF 29-APR-1994; E01365.

PR 29-APR-1993; US-053863.

PA (IMMO) IMMUNO AG.

PI Crowe B, Dörner F, Livey I;

DR WPI; 94-358273/44.

DR N-PSDB; Q73871.

PT Immunogenic composition comprising OSpC antigens - for the

PT treatment of Lyme borreliosis in different, specific geographical

PT areas.

PS Disclosure; Fig. 9a; 115pp; English.

CC A vaccine for Lyme disease includes selected OSpC antigen

CC formulations based on defined OSpC families resolved by serovar

CC typing and RFLP typing. Partial sequences of OSpC genes selected

CC from different RFLP types are given in Q73883-905 (encoded peptides,

CC comprising the first 92% of mature OSpC, are given in R62771-93).

CC Complete sequences of these novel OSpC genes, including the 3' end,

CC plus sequences for the OSpC genes of Borrelia strains H13 and 28691

CC are given in Q73857-82, and encoded proteins in R60884-909. The

CC DNA sequences may be expressed in e.g. Pichia pastoris for

CC recombinant antigen production.

CC Sequence 191 AA;

Query Match 54.9%; Score 45; DB 1; Length 217;
Best Local Similarity 55.6%; Pred. No. 9.22e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKTD 57
:||||:|
QY 4 AVITKKVAD 12

RESULT 27

ID R60906 standard; Protein; 193 AA.

AC R60906;

DE Borrelia B1TS antigen vaccine.

KW OSpC antigen; vaccine; Lyme disease; borreliosis; immunogen;

KW serovar typing; restriction fragment length polymorphism;

KW RFLP; Pichia pastoris.

OS Borrelia burgdorferi B1TS.

PN W09425596-A.

PD 10-NOV-1994.

PF 29-APR-1994; E01365.

PR 29-APR-1993; US-053863.

PA (IMMO) IMMUNO AG.

PI Crowe B, Dörner F, Livey I;

DR WPI; 94-358273/44.

DR N-PSDB; Q73879.

PT Immunogenic composition comprising OSpC antigens - for the

PT treatment of Lyme borreliosis in different, specific geographical

PT areas.

PS Disclosure; Fig. 9a; 115pp; English.

CC A vaccine for Lyme disease includes selected OSpC antigen

CC formulations based on defined OSpC families resolved by serovar

CC typing and RFLP typing. Partial sequences of OSpC genes selected

CC from different RFLP types are given in Q73883-905 (encoded peptides,

CC comprising the first 92% of mature OSpC, are given in R62771-93).

CC Complete sequences of these novel OSpC genes, including the 3' end,

CC plus sequences for the OSpC genes of Borrelia strains H13 and 28691

CC are given in Q73857-82, and encoded proteins in R60884-909. The

CC DNA sequences may be expressed in e.g. Pichia pastoris for

CC recombinant antigen production.

CC Sequence 193 AA;

Query Match 54.9%; Score 45; DB 1; Length 219;
Best Local Similarity 55.6%; Pred. No. 9.22e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 49 TVISKKTD 57
:||||:|
QY 4 AVITKKVAD 12

RESULT 28

ID R75730 standard; Protein; 207 AA.

AC R75730;

DE B. burgdorferi strain pTrob outer surface protein C (OspC-pTrob).

KW Strain pTrob; outer surface protein; OSpC; antigenic domain;

KW chimeric protein; treatment; diagnosis; infection; vaccine;

KW Lyme borreliosis; immunodiagnostic assay; antibody;

KW T-cell reactivity; chimeric.
 OS Borrelia burgdorferi.
 PN W09512676-A1.
 PD 11-MAY-1995.
 PF 27-OCT-1994; U12352.
 PR 01-NOV-1993; US-148191.
 PR 29-APR-1994; US-235836.
 PA (ASUY-) ASSOC UNIVERSITIES INC.
 PI Dunn JJ, Luft BJ;
 DR WPI; 95-215034/28.
 DR N-PSDB; Q90717.
 PT Chimeric protein comprising 2 or more antigenic Borrelia
 PT polypeptide(s) - useful in a vaccine against Lyme borreliosis and in
 PT immuno:diagnostic assays
 PS Example 1; Fig 15; 200pp; English.
 CC The present sequence is the B. burgdorferi strain pTrob, outer
 CC surface protein C (OspC-pTrob). Using chemical or enzymatic methods,
 CC peptide fragments of OspC-pTrob were prep'd., and analysed by western
 CC blot to assess their ability to bind different anti-OspC monoclonal
 CC antibodies. The information obt'd. was used to locate antigenic
 CC domains in OspC-pTrob, the epitopes of which were mapped with the
 CC aid of site directed mutagenesis. Identical analyses were performed
 CC on a selection of Osp purified from a variety of B. burgdorferi
 CC strains, the results from which were utilised in the prep'n. of a
 CC pool of antigenic Borrelia polypeptides, and corresponding
 CC polynucleotides. Chimeric proteins comprising 2 or more antigenic
 CC Borrelia polypeptides, that do not naturally occur in the same
 CC protein, can be used in the treatment and diagnosis of Borrelia
 CC infections, i.e. as a vaccine against Lyme borreliosis, in
 CC immunodiagnostic assays to detect anti-Borrelia antibodies or to
 CC measure T-cell reactivity.
 SQ Sequence 207 AA;

Query Match 54.9%; Score 45; DB 1; Length 233;
 Best Local Similarity 55.6%; Pred. No. 9.22e+00;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 67 TVISKKIID 75
 QY 4 AVITRKVD 12

RESULT 29
 ID R75728 standard; Protein; 209 AA.
 AC R75728; 1996 (first entry)
 DE B. burgdorferi strain K48 outer surface protein C (OspC-K48).
 KW Strain K48; outer surface protein; OspC; antigenic domain;
 KW chimeric protein; treatment; diagnosis; infection; vaccine;
 KW Lyme borreliosis; immunodiagnostic assay; antibody;
 KW T-cell reactivity; chimeric.
 OS Borrelia burgdorferi.
 PN W09512676-A1.
 PD 11-MAY-1995.
 PF 27-OCT-1994; U12352.
 PR 01-NOV-1993; US-148191.
 PR 29-APR-1994; US-235836.
 PA (ASUY-) ASSOC UNIVERSITIES INC.
 PI Dunn JJ, Luft BJ;
 DR WPI; 95-215034/28.
 DR N-PSDB; Q90715.
 PT Chimeric protein comprising 2 or more antigenic Borrelia
 PT polypeptide(s) - useful in a vaccine against Lyme borreliosis and in
 PT immuno:diagnostic assays
 PS Example 1; Fig 13; 200pp; English.
 CC The present sequence is the B. burgdorferi strain K48, outer
 CC surface protein C (OspC-K48). Using chemical or enzymatic methods,
 CC peptide fragments of OspC-K48 were prep'd., and analysed by western
 CC blot to assess their ability to bind different anti-OspC monoclonal
 CC antibodies. The information obt'd. was used to locate antigenic
 CC domains in OspC-K48, the epitopes of which were mapped with the
 CC aid of site directed mutagenesis. Identical analyses were performed
 CC on a selection of Osp purified from a variety of B. burgdorferi

CC strains, the results from which were utilised in the prep'n. of a
 CC pool of antigenic Borrelia polypeptides, and corresponding
 CC polynucleotides. Chimeric proteins comprising 2 or more antigenic
 CC Borrelia polypeptides, that do not naturally occur in the same
 CC protein, can be used in the treatment and diagnosis of Borrelia
 CC infections, i.e. as a vaccine against Lyme borreliosis, in
 CC immunodiagnostic assays to detect anti-Borrelia antibodies or to
 CC measure T-cell reactivity.
 SQ Sequence 209 AA;

Query Match 54.9%; Score 45; DB 1; Length 235;
 Best Local Similarity 55.6%; Pred. No. 9.22e+00;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 67 TVISKKIID 75
 QY 4 AVITRKVD 12

RESULT 30
 ID W02719 standard; peptide; 277 AA.
 AC W02719;
 DT 13-NOV-1996 (first entry)
 DE G-protein coupled odorant receptor I14.
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrania; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomagalovirus; serotonergic.
 OS Synthetic.
 PN US5508384-A.
 PD 16-APR-1996.
 PF 10-SEP-1992; 943236.
 PR 10-SEP-1992; US-943236.
 PR 09-SEP-1993; US-118270.
 PA (UYNV) UNIV NEW YORK STATE.
 PI Murphy RB, Schuster DI;
 DR WPI; 96-208785/21.
 PT New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 PT for treating schizophrania
 PS Disclosure: Column 159-160; 184pp; English.
 CC Proteins W02657-W02730 represent a range of G-protein coupled receptor
 CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, opsin,
 CC odorant, cytomagaloviral and other GPR proteins. The receptor proteins
 CC were used to design polypeptides, pref. based on the transmembrane
 CC domains, for use in G-protein coupled receptor ligand binding assays.
 CC The polypeptide fragments retain biological activity such as binding a
 CC GPR ligand or modulating GPR ligand binding to a GPR (see W02747-W02999
 CC for examples of polypeptide fragments). The polypeptide fragments can
 CC be used in compositions for treating subjects suffering from a pathology
 CC related to a GPR abnormality e.g. a psychotic disorder such as
 CC schizophrania.
 SQ Sequence 277 AA;

Query Match 54.9%; Score 45; DB 1; Length 303;
 Best Local Similarity 45.5%; Pred. No. 9.22e+00;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 292 LIRVICTRKIS 302
 QY 1 LFRVITRKVA 11

RESULT 31
 ID R48747 standard; Protein; 277 AA.
 AC R48747;
 DT 07-JUN-1996 (first entry)
 DE G-protein coupled odorant receptor I14 protein.
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW psychotic disorder; schizophrania; dopamine; cAMP; adenosine; thrombin;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomagalovirus.
 OS Synthetic.

PN W09405695-A1.
 PD 17-MAR-1994.
 PF 09-SEP-1993; U08528.
 PR 10-SEP-1992; US-943236.
 PA (UIN) UNIV NEW YORK STATE.
 PI Murphy RB, Schuster DI;
 DR WPI: 94-101120/12.
 PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 binding GPR ligands or modulating GPR binding.
 PS Disclosure, Page 122-123; 160pp; English.
 CC Proteins R4865-R48758 represent a range of G-protein coupled receptor
 proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 binding assays. The polypeptide fragments retain biological activity
 CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see R48759-R48758, R50569-R50807 and R89189-R89195 for examples of
 CC polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to
 CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 SQ Sequence 277 AA;

Query Match 54.9%; Score 45; DB 1; Length 303;
 Best Local Similarity 45.5%; Pred. No. 9.22e+00;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 292 LIRVICTKKIS 302
 I : I : I : I : I :
 QY 1 LFRVITKKVA 11

RESULT 32
 ID R27875 standard; Protein; 312 AA.
 AC R27875;
 DT 15-MAR-1993 (first entry)
 DE Odorant receptor clone 114.
 KW hormone; G-protein; insect; vertebrate; fish; mammal; neurotransmitter;
 KW Sprague-Dawley rat; amplify; primer; polymerase chain reaction;
 KW multigene family; ligand binding domain.
 OS Ratus rattus.
 PN W09217585-A.
 PD 15-OCT-1992.
 PF 06-APR-1992; U02741.
 PR 05-APR-1991; US-681880.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PI Axel R, Buck LB;
 DR WPI: 92-366257/44.
 DR N-PSDB; Q29863.
 PT Nucleic acid encoding an odorant receptor - can be used to
 PT control insect populations or for detecting odours e.g. alcohol,
 PT explosives, natural gas etc.
 PS Claim 44: Fig 17: 195pp; English.
 CC The sequences given in R27867-89 are encoded by odorant receptor
 CC clones derived from an insect, a vertebrate, a fish or a mammal.
 CC These clones form a family of neurotransmitters and hormone receptors
 CC which transduce intracellular signals by activation of specific G-
 CC proteins. Each of these receptors is a member of a superfamily of
 CC surface receptors which traverse the membrane seven times. These
 CC clones are only expressed in the olfactory epithelium. These clones
 CC were isolated using probes derived from RNA prepared from the
 CC olfactory epithelia of Sprague-Dawley rats. Isolated cDNA's were
 CC amplified using primers which correspond to transmembrane domain 2
 CC and 7. PCR products of the appropriate size were isolated and
 CC sequenced. The deduced protein sequences of these cDNA's defined a
 CC new multigene family which shared sequence and structural properties
 CC with the superfamily of neurotransmitter and hormone receptors which
 CC traverse the membrane seven times. This novel family, however
 CC exhibits features different from any other member of the superfamily
 CC identified so far. There is a striking divergence within the third,
 CC fourth and fifth transmembrane domains between the olfactory proteins.

CC This divergence in the potential ligand binding domain is consistent
 CC with the idea that the family of molecules cloned is capable of
 CC associating with a large number of odorant of diverse molecular
 CC structure. 312 AA;
 SQ Sequence 312 AA;

Query Match 54.9%; Score 45; DB 1; Length 338;
 Best Local Similarity 45.5%; Pred. No. 9.22e+00;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 327 LIRVICTKKIS 337
 I : I : I : I : I :
 QY 1 LFRVITKKVA 11

RESULT 33
 ID R62042 standard; Protein; 434 AA.
 AC R62042;
 DT 05-JUL-1995 (first entry)
 DE Dialkylglycine decarboxylase.
 DE Dialkylglycine decarboxylase.
 KW Dialkylglycine decarboxylase; dgdR; repressor; repression;
 KW regulation; gene expression.
 OS Pseudomonas cepacia.
 PN US5356796-A.
 PD 18-OCT-1994.
 PF 30-MAR-1990; 501814.
 PR 30-MAR-1990; US-501814.
 PR 28-SEP-1992; US-952817.
 PA (UYAL-) UNIV ALASKA.
 PI Keller JW;
 DR WPI: 94-332342/41.
 DR N-PSDB; Q72718.
 PT 2,2-di-alkyl-glycine decarboxylase (DD) repressor protein - and
 PT vectors comprising its coding sequence and operators, useful for
 PT prep. of Pseudomonas cepacia DB and for regulating gene
 PT expression
 PS Disclosure; Figure 3; 52pp; English.
 CC E.coli may be transformed with vectors comprising the gene encoding
 CC the 2,2-dialkylglycine decarboxylase sequence (the gene is induced
 CC by the presence of dialkylglycines), with the specific aim of
 CC producing and isolating the enzyme. A repressor gene (Q72717) is
 CC useful for regulating expression of 2,2-dialkylglycine carboxylase.
 CC The use of the repressor gene and its product allows the rate of
 CC 2,2-dialkylglycine decarboxylase production to be controlled.
 SQ Sequence 434 AA;

Query Match 54.9%; Score 45; DB 1; Length 460;
 Best Local Similarity 33.3%; Pred. No. 9.22e+00;
 Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 104 LFSGIVSRPVD 115
 I : I : I : I : I :
 QY 1 LFRVITKKVAD 12

RESULT 34
 ID R36724 standard; Protein; 434 AA.
 AC R36724;
 DT 03-SEP-1993 (first entry)
 DE 2,2-dialkylglycine decarboxylase of Pseudomonas cepacia.
 DE Pyridoxyl 5'-phosphate dependent 2,2-dialkylglycine decarboxylase;
 KW pyruvate; EC 4.1.1.64; soil bacterium; decarboxylation;
 KW aminotransferase; repression-induction system.
 OS Pseudomonas cepacia.
 FH Key Location/Qualifiers
 FT Peptide 2..20
 FT /note= "sequenced directly"
 FT Peptide 261..276
 FT /note= "sequenced directly"
 PN US5210025-A.
 PD 11-MAY-1993.
 PF 30-MAR-1990; 501814.
 PR 30-MAR-1990; US-501814.

PA (UYAL-) UNIV ALASKA.
 PI Keller JW;
 DR WPI: 93-166958/20.
 DR N-PSDB; 041259.
 PT Prepn. of 2,2-di:alkyl:glycine decarboxylase of *Pseudomonas*
 PT cepacia - in *E. coli* cells transformed with vectors regulated by
 PT repressor protein
 PS Disclosure; Fig 3; 23pp; English.
 CC A 3969 bp PstI-PstI fragment of *P. cepacia* DNA containing the gene
 CC for 2,2-dialkylglycine decarboxylase was cloned in *E. coli*. The
 CC C-terminus of the deduced amino acid of the decarboxylase is
 CC homologous with the C-terminus of the mammalian ornithine amino-
 CC transferase and the active site is similar to several other
 CC aminotransferases. No homologues with known decarboxylase sequences
 CC could be found. Expression of the decarboxylase is controlled by a
 CC 687-nucleotide sequence upstream of and diverging from the
 CC structural gene. Expression is induced by S-isovaline,
 CC 2-methylalanine and D-2-aminobutanoic acid, but not by glycine,
 CC D- or L-alanine, L-2-aminobutanoic acid, R-isovaline, or other
 CC alkyl amino acids. See R36725 for repressor sequence.
 SQ Sequence 434 AA;

Query Match 54.9%; Score 45; DB 1; Length 460;
 Best Local Similarity 33.3%; Pred. No. 9.22e+00;
 Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

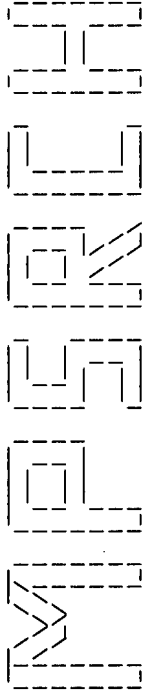
Db 104 LFGIVSRPVVD 115
 || : : : : ||
 QY 1 LFRVITKKVAD 12

RESULT 35
 ID W20991 standard; protein; 614 AA.
 AC W20991;
 DT 21-JUL-1997 (first entry)
 DE H. pylori inner membrane protein, hp3ell168orf29.
 KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;
 KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
 KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
 OS- Helicobacter pylori.
 PN W09640893-AL.
 PD 19-DEC-1996.
 PF 06-JUN-1996; U09122.
 PR 07-JUN-1995; US-487032.
 PR 01-APR-1996; US-630405.
 PA (ASTR) ASTRA AB.
 PI Berglindh OT, Smith D, Mellgaerd BL;
 DR WPI: 97-052306/05.
 DR N-PSDB; T68244.
 PT Helicobacter pylori nucleic acid sequences and related
 PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
 PT infection, and to detect Helicobacter
 PS Claim 56; Page 1379-1380; 1481pp; English.
 CC The present sequence is a H. pylori inner membrane protein.
 CC The protein may be used in a vaccine to prevent or treat H. pylori
 CC infection or to identify H. pylori polypeptide binding compounds,
 CC useful as potential H. pylori life cycle activators or inhibitors.
 CC The genomic sequence of H. pylori (ATCC 55679) was determined from
 CC overlapping contigs generated by mechanically shearing the bacterial
 CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
 CC and the predicted coding regions defined by computer evaluation. To
 CC identify likely H. pylori antigens for vaccine development, the amino
 CC acid sequences predicted from various ORF were analysed for significant
 CC homology to other known or exported membrane proteins. Having identified
 CC and determined the sequences of interest, particular regions can be
 CC isolated from H. pylori by PCR amplification for recombinant polypeptide
 CC production, e.g. in *E. coli* hosts.
 SQ Sequence 614 AA;

Query Match 54.9%; Score 45; DB 1; Length 640;
 Best Local Similarity 50.0%; Pred. No. 9.22e+00;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 571 FREIRKEVS 580
 || : | | | :
 QY 2 FRAVITKKVA 11

Search completed: Tue Apr 7 08:41:11 1998
 Job time : 7 secs.



(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:44:52 1998; MasPar time 2.51 Seconds
Tabular output not generated. 26.281 Million cell updates/sec

Title: >US-08-190-411A-3
Description: (1-12) from 5541104 pep
Perfect Score: 82
Sequence: 1 LFRVITKKVAD 12

Scoring table:

Searched: 60183 seqs, 5492030 residues
Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCP90
10:PCP91 11:PCP92 12:PCP93 13:PCP94 14:PCP95 15:PCP96

Statistics: Mean 16.538; Variance 48.719; scale 0.339

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match %	Length	ID	Description	Pred. No.
1	82	100.0	12	6	US-08-190- Sequence 3, Applicatio	4.26e-03
2	45	54.9	277	12	PCP-US93-0 Sequence 68, Applicati	8.88e+01
3	45	54.9	277	6	US-08-118- Sequence 68, Applicati	8.88e+01
4	45	54.9	434	4	US-07-952- Sequence 14, Applicati	8.88e+01
5	45	54.9	434	4	US-07-952- Sequence 9, Applicatio	8.88e+01
6	45	54.9	434	1	5210025-2 Patent No. 5210025.	8.88e+01
7	45	54.9	434	1	5210025-7 Patent No. 5210025.	8.88e+01
8	43	52.4	121	13	PCP-US94-0 Sequence 22, Applicati	1.44e+02
9	43	52.4	121	6	US-08-180- Sequence 22, Applicati	1.44e+02
10	43	52.4	121	5	US-08-142- Sequence 5, Applicatio	1.44e+02
11	43	52.4	295	6	US-08-118- Sequence 79, Applicati	1.44e+02
12	43	52.4	295	12	PCP-US93-0 Sequence 79, Applicati	1.44e+02
13	43	52.4	317	13	PCP-US94-0 Sequence 17, Applicati	1.44e+02
14	43	52.4	317	7	US-08-385- Sequence 17, Applicati	1.44e+02
15	43	52.4	317	6	US-08-180- Sequence 17, Applicati	1.44e+02
16	43	52.4	317	6	US-08-180- Sequence 17, Applicati	1.44e+02
17	43	52.4	788	5	US-08-194- Sequence 12, Applicati	1.44e+02
18	43	52.4	1486	6	US-08-026- Sequence 8, Applicatio	1.44e+02
19	43	52.4	1486	6	US-08-026- Sequence 2, Applicatio	1.83e+02
20	42	51.2	76	6	US-08-250- Sequence 1, Applicatio	1.83e+02
21	42	51.2	76	7	US-08-235- Sequence 1, Applicatio	1.83e+02
22	42	51.2	76	5	US-07-956- Sequence 1, Applicatio	1.83e+02

96 40 48.8 778 12 PCT-US93-0 Sequence 4, Applicatio 2.94e+02
97 40 48.8 1513 12 PCT-US93-0 Sequence 2, Applicatio 2.94e+02
98 40 48.8 2616 1 5206163-3 Patent No. 5206163. 2.94e+02
99 39 47.6 235 13 PCT-US94-0 Sequence 13, Applicati 3.71e+02
100 39 47.6 1480 12 PCT-US93-1 Sequence 2, Applicatio 3.71e+02

ALIGNMENTS

RESULT 1
ID US-08-190-411A-3 STANDARD; PRT; 12 AA.

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Sequence 3, Application US/08190411A.
Patent No. 5541104
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
NANT MAGE-1.
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBI
NANT MAGE-1.
TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,411A
FILING DATE: 01-FEBRUARY-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5541104man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5354
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acid residues

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 12 AA; 1361 MW; 791 CN;

Query Match 100.0%; Score 82; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.26e-03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 LFRVITKKVAD 12
QY 1 LFRVITKKVAD 12

RESULT 2
ID PCT-US93-08528-68 STANDARD; PRT; 277 AA.

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Sequence 68, Application PC/TUS9308528.
Sequence 68, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 277 AA; 31920 MW; 451947 CN;

Query Match 54.9%; Score 45; DB 12; Length 277;
Best Local Similarity 45.5%; Pred. No. 8.88e-01;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 266 LIRVICTKKIS 276
QY 1 LFRVITKKVA 11

CC COUNTRY: US
CC ZIP: 20005-3315
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/952,817
CC FILING DATE: 19920928
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Meyers, Kenneth J.
CC REGISTRATION NUMBER: 25,146
CC REFERENCE/DOCKET NUMBER: 01120.0002-01000
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-408-4000
CC TELEFAX: 202-408-4400
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 434 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 434 AA; 46545 MW; 886275 CN;

Query Match 54.9%; Score 45; DB 4; Length 434;
Best Local Similarity 33.3%; Pred. No. 8.88e+01;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 78 LFGSIVSRPVD 89
|| : : : : ||
QY 1 LFRVITKKVAD 12

RESULT 6
ID 5210025-2 STANDARD; PRT; 470 AA.
XX 6
AC xxxxxx
XX 01-JAN-1900
DT Patent No. 5210025.
DE Patent No. 5210025
XX APPLICANT: KELLER, JOHN W.
CC TITLE OF INVENTION: REPRESSOR PROTEIN GENE FOR REGULATING
CC EXPRESSION OF POLYPEPTIDES AND ITS USE IN THE PREPARATION OF
CC 2,2-DIALKYLGLYCINE DECARBOXYLASE OF PSEUDOMONAS CEPACIA
CC NUMBER OF SEQUENCES: 18
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/501,814
CC FILING DATE: 30-MAR-1990
CC SEQ ID NO:2:
CC LENGTH: 434
CC SEQUENCE 470 AA; 50510 MW; 1154124 CN;

Query Match 54.9%; Score 45; DB 1; Length 434;
Best Local Similarity 33.3%; Pred. No. 8.88e+01;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 78 LFGSIVSRPVD 89
|| : : : : ||
QY 1 LFRVITKKVAD 12

RESULT 7
ID 5210025-7 STANDARD; PRT; 470 AA.
XX 7
AC xxxxxx
XX 01-JAN-1900
DT Patent No. 5210025.
DE Patent No. 5210025
XX APPLICANT: KELLER, JOHN W.
CC TITLE OF INVENTION: REPRESSOR PROTEIN GENE FOR REGULATING
CC EXPRESSION OF POLYPEPTIDES AND ITS USE IN THE PREPARATION OF
CC 2,2-DIALKYLGLYCINE DECARBOXYLASE OF PSEUDOMONAS CEPACIA
CC NUMBER OF SEQUENCES: 18
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/501,814
CC FILING DATE: 30-MAR-1990
CC SEQ ID NO:2:
CC LENGTH: 434
CC SEQUENCE 470 AA; 50510 MW; 1154124 CN;

DE Patent No. 5210025.
XX 5210025
CC Patent No. 5210025
CC APPLICANT: KELLER, JOHN W.
CC TITLE OF INVENTION: REPRESSOR PROTEIN GENE FOR REGULATING
CC EXPRESSION OF POLYPEPTIDES AND ITS USE IN THE PREPARATION OF
CC 2,2-DIALKYLGLYCINE DECARBOXYLASE OF PSEUDOMONAS CEPACIA
CC NUMBER OF SEQUENCES: 18
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/501,814
CC FILING DATE: 30-MAR-1990
CC SEQ ID NO:7:
CC LENGTH: 434
CC SEQUENCE 470 AA; 50542 MW; 1153697 CN;

Query Match 54.9%; Score 45; DB 1; Length 434;
Best Local Similarity 33.3%; Pred. No. 8.88e+01;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 78 LFGSIVSRPVD 89
|| : : : : ||
QY 1 LFRVITKKVAD 12

RESULT 8
ID PCT-US94-02629-22 STANDARD; PRT; 121 AA.
XX 8
AC xxxxxx
XX 01-JAN-1900
DT Sequence 22, Application PC/TUS9402629.
DE Sequence 22, Application PC/TUS9402629.
XX 22
CC Sequence 22, Application PC/TUS9402629
CC GENERAL INFORMATION:
CC APPLICANT: King, Te-Piao
CC TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
CC 2,2-DIALKYLGLYCINE DECARBOXYLASE OF PSEUDOMONAS CEPACIA
CC NUMBER OF SEQUENCES: 18
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/02629
CC FILING DATE: 10-MAR-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/031,400
CC FILING DATE: 11-MAR-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Jackson Esq., David A.
CC REGISTRATION NUMBER: 26,742
CC REFERENCE/DOCKET NUMBER: 600-1-074 PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 201 487-5800
CC TELEFAX: 201 343-1684
CC TELEX: 133521
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 121 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 121 AA; 13168 MW; 74343 CN;

Query Match 52.4%; Score 43; DB 13; Length 121;
Best Local Similarity 45.5%; Pred. No. 1.44e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 14 FIAMIACKLVE 24
| | | | | :
QY 2 FRAVITKKVAD 12

RESULT 9
ID US-08-180-209B-22 STANDARD; PRT; 121 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX Sequence 22, Application US/08180209B.
DE Patent No. 5593877
CC CC
CC GENERAL INFORMATION:
CC APPLICANT: King, Te-Piao
CC TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
CC TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
CC TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED
CC TITLE OF INVENTION: THEREON
CC NUMBER OF SEQUENCES: 62
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Klauber & Jackson
CC STREET: 411 Hackensack Avenue
CC CITY: Hackensack
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07601
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/180,209B
CC FILING DATE: 11-JAN-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/031,400
CC FILING DATE: 11-MAR-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Jackson Esq., David A.
CC REGISTRATION NUMBER: 26,742
CC REFERENCE/DOCKET NUMBER: 600-1-074 CIP
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 201 487-5800
CC TELEFAX: 201 343-1684
CC TELEX: 133521
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 121 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 121 AA; 13168 MW; 74343 CN;

Query Match 52.4%; Score 43; DB 6; Length 121;
Best Local Similarity 45.5%; Pred. No. 1.44e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 14 FIAMIACKLVE 24
| | | | | :
QY 2 FRAVITKKVAD 12

RESULT 10
ID US-08-385-745-22 STANDARD; PRT; 121 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX Sequence 22, Application US/08385745.
DE Patent No. 5612209
CC CC
CC GENERAL INFORMATION:
CC APPLICANT: King, Te Piao
CC TITLE OF INVENTION: Cloning and Recombinant Production of
CC TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Th
CC erapies
CC TITLE OF INVENTION: Based Thereon
CC NUMBER OF SEQUENCES: 27
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: U.S.A.
CC ZIP: 10036-2711
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/385,745
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/031,400
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Misrock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 3288-020
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212 790-9090
CC TELEFAX: 212 869-8864/9741
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 121 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 121 AA; 13168 MW; 74343 CN;

Query Match 52.4%; Score 43; DB 7; Length 121;
Best Local Similarity 45.5%; Pred. No. 1.44e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 14 FIAMIACKLVE 24
| | | | | :
QY 2 FRAVITKKVAD 12

RESULT 11
ID US-08-142-897-5 STANDARD; PRT; 212 AA.
XX AC xxxxxx

[illegible]

CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/08528
CC FILING DATE: 09-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/943,236
CC FILING DATE: 10-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Townsend, Kevin G.
CC REGISTRATION NUMBER: 34,033
CC REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-628-5197
CC TELEFAX: 202-737-3528
CC TELEX: 248633
CC INFORMATION FOR SEQ ID NO: 79:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 295 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 295 AA; 34191 MW; 498086 CN;

Query Match 52.4%; Score 43; DB 12; Length 295;
Best Local Similarity 75.0%; Pred. No. 1.44e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 133 FMVITKK 140
| | | | |
QY 2 FRAVITKK 9

RESULT 14
ID PCT-US94-02629-17 STANDARD; PRT; 317 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 17, Application PC/TUS9402629.

XX SEQUENCE 17, Application PC/TUS9402629

CC GENERAL INFORMATION:

CC APPLICANT: King, Te-Piao

CC TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
CC TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
CC TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED
CC THEREON

CC NUMBER OF SEQUENCES: 62

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Klauber & Jackson

CC STREET: 411 Hackensack Avenue

CC CITY: Hackensack

CC STATE: New Jersey

CC COUNTRY: USA

CC ZIP: 07601

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US94/02629

CC FILING DATE: 10-MAR-1994

CC CLASSIFICATION:

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/180,209

CC FILING DATE: 11-JAN-1994

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/031,400

CC FILING DATE: 11-MAR-1993

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Jackson Esq., David A.
CC REGISTRATION NUMBER: 26,742
CC REFERENCE/DOCKET NUMBER: 600-1-074 PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 201 487-5800
CC TELEFAX: 201 343-1684
CC TELEX: 133521
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 317 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 317 AA; 35708 MW; 516933 CN;

Query Match 52.4%; Score 43; DB 13; Length 317;
Best Local Similarity 45.5%; Pred. No. 1.44e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 129 FIAMIKKLVE 139

QY 2 FRAVITKKVAD 12

RESULT 15
ID US-08-385-745-17 STANDARD; PRT; 317 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 17, Application US/08385745.

XX SEQUENCE 17, Application US/08385745

CC PATENT NO. 5612209

CC GENERAL INFORMATION:

CC APPLICANT: King, Te Piao

CC TITLE OF INVENTION: Cloning and Recombinant Production of

CC TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Th

CC erapies

CC TITLE OF INVENTION: Based Thereon

CC NUMBER OF SEQUENCES: 27

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Pennie & Edmonds

CC STREET: 1155 Avenue of the Americas

CC CITY: New York

CC STATE: New York

CC COUNTRY: U.S.A.

CC ZIP: 10036-2711

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/385,745

CC FILING DATE:

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US/08/031,400

CC FILING DATE:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Misrock, S. Leslie

CC REGISTRATION NUMBER: 18,872

CC REFERENCE/DOCKET NUMBER: 3288-020

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 212 790-9090

CC TELEFAX: 212 869-8864/9741

CC TELEX: 66141 PENNIE

CC INFORMATION FOR SEQ ID NO: 17:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 317 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear
SQ MOLECULE TYPE: protein
SEQUENCE 317 AA; 35708 MW; 516933 CN;
Query Match 52.4%; Score 43; DB 7; Length 317;
Best Local Similarity 45.5%; Pred. No. 1.44e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Db 129 FIAMIAKLVE 139
| :|:|:| :
QY 2 FRAVITRKVAD 12

RESULT 16
ID US-08-180-209B-17 STANDARD; PRT; 317 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 17, Application US/08180209B.
XX
CC Sequence 17, Application US/08180209B
CC Patent No. 5593877
CC GENERAL INFORMATION:
CC APPLICANT: King, Te-Piao
CC TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
CC TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
CC TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED
CC TITLE OF INVENTION: THEREON
CC NUMBER OF SEQUENCES: 62
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Klauber & Jackson
CC STREET: 411 Hackensack Avenue
CC CITY: Hackensack
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07601
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/180,209B
CC FILING DATE: 11-JAN-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/031,400
CC FILING DATE: 11-MAR-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Jackson Esq., David A.
CC REGISTRATION NUMBER: 26,742
CC REFERENCE/DOCKET NUMBER: 600-1-074 CIP
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 201 487-5800
CC TELEFAX: 201 343-1684
CC TELEX: 133521
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 317 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 317 AA; 35708 MW; 516933 CN;
Query Match 52.4%; Score 43; DB 6; Length 317;
Best Local Similarity 45.5%; Pred. No. 1.44e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Db 129 FIAMIAKLVE 139
| :|:|:| :
QY 2 FRAVITRKVAD 12

CC TOPOLOGY: linear
SQ MOLECULE TYPE: protein
SEQUENCE 317 AA; 35708 MW; 516933 CN;
Query Match 52.4%; Score 43; DB 7; Length 317;
Best Local Similarity 45.5%; Pred. No. 1.44e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Db 129 FIAMIAKLVE 139
| :|:|:| :
QY 2 FRAVITRKVAD 12

RESULT 17
ID US-08-194-338-12 STANDARD; PRT; 788 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 12, Application US/08194338.
XX
CC Sequence 12, Application US/08194338
CC Patent No. 5474898
CC GENERAL INFORMATION:
CC APPLICANT: Venter, John C.
CC APPLICANT: Fraser, Claire M.
CC APPLICANT: McCombie, William R.
CC TITLE OF INVENTION: OCTOPAMINE RECEPTOR
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Knobbe, Martens, Olson and Bear
CC STREET: 620 Newport Center Drive, Sixteenth Floor
CC CITY: Newport Beach
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92660
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/194,338
CC FILING DATE: 08-FEB-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/676,174
CC FILING DATE: 28-MAR-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Israelsen, Ned A.
CC REGISTRATION NUMBER: 29,655
CC REFERENCE/DOCKET NUMBER: NIH101.001DV1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 235-8550
CC TELEFAX: (619) 235-0176
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 788 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: internal
CC SEQUENCE 788 AA; 85060 MW; 3068211 CN;
Query Match 52.4%; Score 43; DB 5; Length 788;
Best Local Similarity 45.5%; Pred. No. 1.44e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Db 21 LFRVTVTSTTT 31
| :|:|:| :
QY 1 LFRVITRKVA 11

RESULT 18
ID US-08-026-138E-8 STANDARD; PRT; 1456 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX

DE Sequence 8, Application US/08026138E.
XX
CC Sequence 8, Application US/08026138E
CC Patent No. 5502166
CC GENERAL INFORMATION:
CC APPLICANT: Masayoshi MISHINA
CC TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Nishiohata Residence 1-107
CC STREET: 5214, Nishiohata-machi
CC CITY: Niigata-shi
CC STATE: Niigata-ken
CC COUNTRY: JAPAN
CC ZIP: 951
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: MS-DOS v.5
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/026,138E
CC FILING DATE: 26-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 39563/1992
CC FILING DATE: 26-FEB-1992
CC APPLICATION NUMBER: JP 173155/1992
CC FILING DATE: 30-JUN-1992
CC APPLICATION NUMBER: JP 215017/1992
CC FILING DATE: 12-AUG-1992
CC APPLICATION NUMBER: JP 303878/1992
CC FILING DATE: 13-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hamburg, C.Bruce
CC REGISTRATION NUMBER: 22,389
CC REFERENCE/DOCKET NUMBER: F-4551
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 986-2340
CC TELEFAX: (212) 953-7733
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1456 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single strand
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORGANISM: mouse
CC TISSUE TYPE: brain
CC PUBLICATION INFORMATION:
CC AUTHORS: Masayoshi MISHINA
CC TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
CC RELEVANT RESIDUES IN SEQ ID NO: 8: FROM 1 to 4368
SQ SEQUENCE 1456 AA; 162890 MW; 10978415 CN;

Query Match 52.4%; Score 43; DB 6; Length 1456;
Best Local Similarity 62.5%; Pred. No. 1.44e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1393 FRALVTNK 1400
QY 2 FRAVITKK 9
|||:|:|

RESULT 19
ID US-08-026-138E-2 STANDARD; PRT; 1482 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application US/08026138E.
XX

CC Sequence 2, Application US/08026138E
CC Patent No. 5502166
CC GENERAL INFORMATION:
CC APPLICANT: Masayoshi MISHINA
CC TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Nishiohata Residence 1-107
CC STREET: 5214, Nishiohata-machi
CC CITY: Niigata-shi
CC STATE: Niigata-ken
CC COUNTRY: JAPAN
CC ZIP: 951
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: MS-DOS v.5
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/026,138E
CC FILING DATE: 26-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 39563/1992
CC FILING DATE: 26-FEB-1992
CC APPLICATION NUMBER: JP 173155/1992
CC FILING DATE: 30-JUN-1992
CC APPLICATION NUMBER: JP 215017/1992
CC FILING DATE: 12-AUG-1992
CC APPLICATION NUMBER: JP 303878/1992
CC FILING DATE: 13-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hamburg, C.Bruce
CC REGISTRATION NUMBER: 22,389
CC REFERENCE/DOCKET NUMBER: F-4551
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 986-2340
CC TELEFAX: (212) 953-7733
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1482 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single strand
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORGANISM: mouse
CC TISSUE TYPE: brain
CC PUBLICATION INFORMATION:
CC AUTHORS: Masayoshi MISHINA
CC TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
CC RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 to 1482
SQ SEQUENCE 1482 AA; 165957 MW; 11386804 CN;

Query Match 52.4%; Score 43; DB 6; Length 1482;
Best Local Similarity 62.5%; Pred. No. 1.44e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1419 FRALVTNK 1426
QY 2 FRAVITKK 9
|||:|:|

RESULT 20
ID US-08-250-958-1 STANDARD; PRT; 76 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 1, Application US/08250958.
XX
DE Sequence 1, Application US/08250958
CC Patent No. 5571713
CC

CC GENERAL INFORMATION:
CC APPLICANT: LYLE, LEON R.
CC APPLICANT: KUNKEL, STEVEN L.
CC APPLICANT: STRIETER, ROBERT M.
CC TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING
CC TITLE OF INVENTION: VASCULAR RESTENOSIS
CC NUMBER OF SEQUENCES: 10
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Rothwell, Figg, Ernst & Kurz
CC STREET: Suite 701-E, 555 Thirteenth St., N.W
CC CITY: Washington
CC STATE: D. C.
CC COUNTRY: U.S.A.
CC ZIP: 20004
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/250,958
CC FILING DATE: 27-MAY-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/965,678
CC FILING DATE: 22-OCT-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WALKER, Barbara W.
CC REGISTRATION NUMBER: 35,400
CC REFERENCE/DOCKET NUMBER: 2077-206A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202)783-6040
CC TELEFAX: (202)783-6031
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 76 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC FRAGMENT TYPE: N-terminal
CC SEQUENCE 76 AA; 8614 MW; 31299 CN;
SQ
Query Match 51.2%; Score 42; DB 6; Length 76;
Best Local Similarity 20.0%; Pred. No. 1.83e+02;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Db 42 IFKTIVAKEI 51
QY 1 LFRAVITKKV 10
RESULT 21
ID US-08-235-659-1 STANDARD; PRT; 76 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 1, Application US/08235659.
XX Sequence 1, Application US/08235659
CC Patent No. 5605671
CC GENERAL INFORMATION:
CC APPLICANT: Lyle, Leon R.
CC APPLICANT: Kunkel, Steven L.
CC APPLICANT: Strieter, Robert M.
CC TITLE OF INVENTION: LABELLED CHEMOKINE MATERIALS AND
CC TITLE OF INVENTION: MEDICAL USES THEREOF
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Rothwell, Figg, Ernst & Kurz

CC STREET: Suite 701-E, 555 Thirteenth St., N.W
CC CITY: Washington
CC STATE: D. C.
CC COUNTRY: U.S.A.
CC ZIP: 20004
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/235,659
CC FILING DATE: 29-APR-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/956,862
CC FILING DATE: 05-OCT-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/956,863
CC FILING DATE: 05-OCT-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WALKER, Barbara W.
CC REGISTRATION NUMBER: 35,400
CC REFERENCE/DOCKET NUMBER: 2077-205A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202)783-6040
CC TELEFAX: (202)783-6031
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 76 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: N-terminal
CC SEQUENCE 76 AA; 8667 MW; 31314 CN;
SQ
Query Match 51.2%; Score 42; DB 7; Length 76;
Best Local Similarity 20.0%; Pred. No. 1.83e+02;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Db 42 IFKTIVAKEI 51
QY 1 LFRAVITKKV 10
RESULT 22
ID US-07-956-862A-1 STANDARD; PRT; 76 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 1, Application US/07956862A.
XX Sequence 1, Application US/07956862A
CC Patent No. 5413778
CC GENERAL INFORMATION:
CC APPLICANT: KUNKEL, STEVEN L.
CC APPLICANT: LYLE, LEON R.
CC APPLICANT: STRIETER, ROBERT M.
CC TITLE OF INVENTION: LABELLED MONOCYTE CHEMAOTTRACTANT
CC TITLE OF INVENTION: PROTEIN MATERIAL AND MEDICAL USES
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 1
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Rothwell, Figg, Ernst & Kurz
CC STREET: Suite 701-E, 555 Thirteenth St., N.W
CC CITY: Washington
CC STATE: D. C.
CC COUNTRY: U.S.A.
CC ZIP: 20004
CC COMPUTER READABLE FORM:

CC TELEPHONE: (617) 542-3070
CC TELEFAX: (617) 542-8906
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 78 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC

CC MOLECULE TYPE: peptide
SQ SEQUENCE 78 AA; 8953 MW; 32898 CN;
Query Match 51.2%; Score 42; DB 7; Length 78;
Best Local Similarity 20.0%; Pred. No. 1.83e+02;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Db 44 IFKTIKAKEI 53
:|:|:|:|:|:
QY 1 LFRAVITKKV 10
RESULT 25
ID PCT-US96-10087-5 STANDARD; PRT; 99 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 5, Application PC/TUS9610087.
XX
CC Sequence 5, Application PC/TUS9610087
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Monocyte Chemotactic Protein-4
CC NUMBER OF SEQUENCES: 6
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US96/10087
CC FILING DATE: 07-JUN-1996
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/479,126
CC FILING DATE: 07-JUN-1995
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 99 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 99 AA; 11025 MW; 51738 CN;
Query Match 51.2%; Score 42; DB 15; Length 99;
Best Local Similarity 20.0%; Pred. No. 1.83e+02;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Db 65 IFKTIKAKEI 74
:|:|:|:|:|:
QY 1 LFRAVITKKV 10
RESULT 26
ID 5212073-2 STANDARD; PRT; 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Patent No. 5212073.
XX
CC Patent No. 5212073
CC APPLICANT: ROLLINS, BARRETT; STILES, CHARLES; WONG, GORDON G.
CC TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
CC NUMBER OF SEQUENCES: 1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/351.008
CC FILING DATE: 12-MAY-1989
CC , SEQ ID NO: 2:
CC , LENGTH: 99

SQ SEQUENCE 107 AA; 11906 MW; 65752 CN;
Query Match 51.2%; Score 42; DB 1; Length 99;
Best Local Similarity 20.0%; Pred. No. 1.83e+02;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Db 65 IFKTIKAKEI 74
:|:|:|:|:|:
QY 1 LFRAVITKKV 10
RESULT 27
ID US-08-347-492B-8 STANDARD; PRT; 99 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 8, Application US/08347492B.
XX
CC Sequence 8, Application US/08347492B
CC Patent No. 5602008
CC GENERAL INFORMATION:
CC APPLICANT: Wilde, Craig G.
CC APPLICANT: Hawkins, Phillip R.
CC APPLICANT: Bandman, Olga
CC APPLICANT: Seilhamer, Jeffrey J.
CC TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
CC TITLE OF INVENTION: PRODUCTION AND USES
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Incyte Pharmaceuticals, Inc.
CC STREET: 3174 Porter Drive
CC CITY: Palo Alto
CC STATE: CA
CC COUNTRY: U.S.
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/347,492B
CC FILING DATE: 29-NOV-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/303,241
CC FILING DATE: 07-SEP-1994
CC APPLICATION NUMBER: 08/320,011
CC FILING DATE: 05-OCT-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Luther, Barbara J
CC REGISTRATION NUMBER: 33,954
CC REFERENCE/DOCKET NUMBER: PF-0024
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-855-0555
CC TELEFAX: 415-852-0195
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 99 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC LIBRARY: GENBANK
CC CLONE: GI 487124
CC SEQUENCE 99 AA; 11025 MW; 51738 CN;
Query Match 51.2%; Score 42; DB 7; Length 99;
Best Local Similarity 20.0%; Pred. No. 1.83e+02;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 65 IFKTIIVAKEI 74
:|:|:|:|:|:
QY 1 LFRVITKKV 10

RESULT 28
ID US-08-482-847-35 STANDARD; PRT; 99 AA.
AC xxxxxx
XX
DT 01-JAN-1900
DE Sequence 35, Application US/08482847.
XX Sequence 35, Application US/08482847
CC Patent No. 5556757
CC GENERAL INFORMATION:
CC APPLICANT: VAN ALSTYNE, Diane
CC APPLICANT: SHARMA, Lawrence Rajendra
CC TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
CC TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND
CC THEIR
CC TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
CC NUMBER OF SEQUENCES: 40
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Foley & Lardner
CC STREET: 3000 K Street, N.W., Suite 500
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: USA
CC ZIP: 20007-5109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/482,847
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/127,499
CC FILING DATE: 28-SEP-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BENT, Stephen A.
CC REGISTRATION NUMBER: 29,768
CC REFERENCE/DOCKET NUMBER: 51916/104/INBI
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202)672-5300
CC TELEFAX: (202)672-5399
CC TELEX: 904136
CC INFORMATION FOR SEQ ID NO: 35:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 99 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: unknown
CC SEQUENCE 99 AA; 11025 MW; 51738 CN;

Query Match 51.2%; Score 42; DB 6; Length 99;
Best Local Similarity 20.0%; Pred. No. 1.83e+02;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 65 IFKTIIVAKEI 74
:|:|:|:|:|:
QY 1 LFRVITKKV 10

RESULT 29
ID US-08-480-449-19 STANDARD; PRT; 99 AA.
XX
AC xxxxxx
XX

DT 01-JAN-1900
XX
DE Sequence 19, Application US/08480449.
XX
CC Sequence 19, Application US/08480449
CC Patent No. 5688927
CC GENERAL INFORMATION:
CC APPLICANT: Godiska, Ronald
CC APPLICANT: Gray, Patrick W.
CC TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: United States of America
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/480,449
CC FILING DATE:
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Gass, David A.
CC REGISTRATION NUMBER: 38,153
CC REFERENCE/DOCKET NUMBER: 27866/32779
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6300
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 19:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 99 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FEATURE:
CC NAME/KEY: misc-feature
CC OTHER INFORMATION: "Hu MCP-1"
CC SEQUENCE 99 AA; 11025 MW; 51738 CN;

Query Match 51.2%; Score 42; DB 7; Length 99;
Best Local Similarity 20.0%; Pred. No. 1.83e+02;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 65 IFKTIIVAKEI 74
:|:|:|:|:|:
QY 1 LFRVITKKV 10

RESULT 30
ID US-08-127-499A-35 STANDARD; PRT; 99 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 35, Application US/08127499A.
XX
CC Sequence 35, Application US/08127499A
CC Patent No. 5510264
CC GENERAL INFORMATION:
CC APPLICANT: VAN ALSTYNE, Diane
CC APPLICANT: SHARMA, Lawrence Rajendra
CC TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
CC TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
CC NUMBER OF SEQUENCES: 40
XX

CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Foley & Lardner
CC STREET: 3000 K Street, N.W., Suite 500
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: USA
CC ZIP: 20007-5109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/127,499A
CC FILING DATE: 28-SEP-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BENT, Stephen A.
CC REGISTRATION NUMBER: 29,768
CC REFERENCE/DOCKET NUMBER: 51916/102/INBI
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202)672-5300
CC TELEFAX: (202)672-5399
CC TELEX: 904136
CC INFORMATION FOR SEQ ID NO: 35:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 99 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: unknown
CC SQ SEQUENCE 99 AA; 11025 MW; 51738 CN;

Query Match 51.2%; Score 42; DB 6; Length 99;
Best Local Similarity 20.0%; Pred. No. 1.83e+02;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 65 IFTTIVAKEI 74
:|:::|:
Qy 1 LFRVITKKV 10

RESULT 31
ID PCT-US93-00324-8 STANDARD; PRT; 100 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX Sequence 8, Application PC/TUS9300324.

XX Sequence 8, Application PC/TUS9300324

XX GENERAL INFORMATION:

XX APPLICANT: Cochran Ph.D., Mark D

XX APPLICANT: Junker M.S., David E

XX TITLE OF INVENTION: Recombinant Swinepox Virus

XX NUMBER OF SEQUENCES: 42

XX CORRESPONDENCE ADDRESS:

XX ADDRESSEE: John P. White

XX STREET: 30 Rockefeller Plaza

XX CITY: New York

XX STATE: New York

XX COUNTRY: USA

XX ZIP: 10112

XX COMPUTER READABLE FORM: disk

XX MEDIUM TYPE: Floppy disk

XX COMPUTER: IBM PC compatible

XX OPERATING SYSTEM: PC-DOS/MS-DOS

XX SOFTWARE: PatentIn Release #1.0, Version #1.25

XX CURRENT APPLICATION DATA:

XX APPLICATION NUMBER: PCT/US93/00324

XX FILING DATE: 19930113

XX CLASSIFICATION:

XX ATTORNEY/AGENT INFORMATION:

XX NAME: White, John P

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212)977-9550
CC TELEFAX: (212)664-0525
CC TELEX: 422523
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 100 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: YES
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: C-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Swinepox virus
CC STRAIN: Kasza
CC POSITION IN GENOME:
CC MAP POSITION: -23.2
CC UNITS: %G
CC SQ SEQUENCE 100 AA; 11740 MW; 54002 CN;

Query Match 51.2%; Score 42; DB 12; Length 100;
Best Local Similarity 44.4%; Pred. No. 1.83e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 25 LYRILIVKR 33

:|:::|:
Qy 1 LFRVITKK 9

RESULT 32
ID US-07-820-154A-8 STANDARD; PRT; 100 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX Sequence 8, Application US/07820154A.

XX Sequence 8, Application US/07820154A

XX Patent No. 5382425

XX GENERAL INFORMATION:

XX APPLICANT: Cochran Ph.D., Mark D

XX APPLICANT: Junker M.S., David E

XX TITLE OF INVENTION: Recombinant Swinepox Virus

XX NUMBER OF SEQUENCES: 40

XX CORRESPONDENCE ADDRESS:

XX ADDRESSEE: John P. White

XX STREET: 30 Rockefeller Plaza

XX CITY: New York

XX STATE: New York

XX COUNTRY: USA

XX ZIP: 10112

XX COMPUTER READABLE FORM: disk

XX COMPUTER: IBM PC compatible

XX OPERATING SYSTEM: PC-DOS/MS-DOS

XX SOFTWARE: PatentIn Release #1.0, Version #1.25

XX CURRENT APPLICATION DATA:

XX APPLICATION NUMBER: US/07/820,154A

XX FILING DATE: 19920113

XX CLASSIFICATION: 424

XX ATTORNEY/AGENT INFORMATION:

XX NAME: White, John P

XX TELECOMMUNICATION INFORMATION:

XX TELEPHONE: (212)977-9550

XX TELEFAX: (212)664-0525

XX TELEX: 422523

XX INFORMATION FOR SEQ ID NO: 8:

XX SEQUENCE CHARACTERISTICS:

XX LENGTH: 100 amino acids

XX TYPE: AMINO ACID

```
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: YES
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: C-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Swinepox virus
CC STRAIN: Kasza
CC POSITION IN GENOME:
CC MAP POSITION: -23.2
CC UNITS: %G
SQ SEQUENCE 100 AA; 11740 MW; 54002 CN;

Query Match 51.2%; Score 42; DB 4; Length 100;
Best Local Similarity 44.4%; Pred. No. 1.83e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 25 LYRILIVKR 33
|:|:|:|:|
QY 1 LFRVITKK 9

RESULT 33
ID PCT-US95-17025-17 STANDARD; PRT; 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 17, Application PC/TUS9517025.
XX
CC Sequence 17, Application PC/TUS9517025
CC GENERAL INFORMATION:
CC APPLICANT: James E. Darnell, Jr.
CC APPLICANT: Zilong Wen
CC APPLICANT: Curt M. Horvath
CC APPLICANT: Zhong Zhong
CC TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
CC TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT)
PROTEINS
CC NUMBER OF SEQUENCES: 39
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Klauber & Jackson
CC STREET: 411 Hackensack Avenue
CC CITY: Hackensack
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07601
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/17025
CC FILING DATE: 28-DEC-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/369,796
CC FILING DATE: 06-JAN-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Jackson Esq., David A.
CC REGISTRATION NUMBER: 26,742
CC REFERENCE/DOCKET NUMBER: 600-1-116
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 201 487-5800
CC TELEX: 133521
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC FRAGMENT TYPE: internal
CC SEQUENCE 107 AA; 11984 MW; 59812 CN;

Query Match 51.2%; Score 42; DB 8; Length 107;
Best Local Similarity 40.0%; Pred. No. 1.83e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Cc 5 LFKNLLKKI 14
|:|:|:|:|
QY 1 LFRVITKKV 10

RESULT 34
ID US-08-369-796-17 STANDARD; PRT; 107 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 17, Application US/08369796.
XX
CC Sequence 17, Application US/08369796
CC Patent No. 5716622
CC GENERAL INFORMATION:
CC APPLICANT: James E. Darnell, Jr.
CC APPLICANT: Zilong Wen
CC APPLICANT: Curt M. Horvath
CC APPLICANT: Zhong Zhong
CC TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
CC TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT)
PROTEINS
CC NUMBER OF SEQUENCES: 39
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Klauber & Jackson
CC STREET: 411 Hackensack Avenue
CC CITY: Hackensack
CC STATE: New Jersey
CC COUNTRY: USA
CC ZIP: 07601
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/369,796
CC FILING DATE: 06-JAN-1995
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Jackson Esq., David A.
CC REGISTRATION NUMBER: 26,742
CC REFERENCE/DOCKET NUMBER: 600-1-116
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 201 487-5800
CC TELEX: 201 343-1684
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: NO
CC FRAGMENT TYPE: internal
CC SEQUENCE 107 AA; 11984 MW; 59812 CN;
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Best Local Similarity 40.0%; Pred. No. 1.83e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 5 LFKNLLKKI 14
||: :||:
Qy 1 LFRVITKKV 10

RESULT 35
ID PCT-US94-14277-4 STANDARD; PRT; 200 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 4, Application PC/TUS9414277.

CC Sequence 4, Application PC/TUS9414277

CC GENERAL INFORMATION:

CC APPLICANT: Aguet, Michel

CC APPLICANT: Bohni, Ruth

CC APPLICANT: Hemmi, Silvio

CC TITLE OF INVENTION: Receptor Subunit Polypeptides

CC NUMBER OF SEQUENCES: 8

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Genentech, Inc.

CC STREET: 460 Point San Bruno Blvd

CC CITY: South San Francisco

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94080

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: patin (Genentech)

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US94/14277

CC FILING DATE: 07-DEC-1994

CC CLASSIFICATION:

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/164596

CC FILING DATE: 09-DEC-1993

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Love, Richard B.

CC REGISTRATION NUMBER: 34,659

CC REFERENCE/DOCKET NUMBER: 866PCT

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 415/225-5530

CC TELEFAX: 415/952-9881

CC TELEX: 910/371-7168

CC INFORMATION FOR SEQ ID NO: 4:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 200 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

SQ SEQUENCE 200 AA; 22525 MW; 227601 CN;

Query Match 51.2%; Score 42; DB 13; Length 200;

Best Local Similarity 62.5%; Pred. No. 1.83e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 175 LFRALLNK 182

||||:|

Qy 1 LFRVITK 8

Search completed: Tue Apr 7 08:45:06 1998

Job time : 14 secs.

WQISREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:40:32 1998; MasPar time 4.22 Seconds
Tubular output not generated. 121.776 Million cell updates/sec

Title: >US-08-190-411A-3
Description: (1-12) from 5541104.pap
Perfect Score: 82
Sequence: 1 LFRVITKKVAD 12

Scoring table: PAM 150
Gap 15

Searched: 195121 seqs, 42852602 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: pir55
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 19.923; Variance 56.762; scale 0.351

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	82	100.0	280	JC2358	TOIG of: jc2358 check 6.02e-02	
2	60	73.2	124	I38663	A:Title: Structure, ch 2.29e+01	
3	55	67.1	875	J55377	A:CROSS-references: EM 8.10e+01	
4	54	65.9	693	JN0573	TOIG of: jn0573 check 1.04e+02	
5	54	65.9	701	JN0574	TOIG of: jn0574 check 1.04e+02	
6	54	65.9	885	S59660	TOIG of: S59660 check 1.04e+02	
7	53	64.6	236	F64964	A:Title: The complete 1.33e+02	
8	53	64.6	904	G64840	A:Title: The complete 1.33e+02	
9	52	63.4	126	S64131	TOIG of: S64131 check 1.70e+02	
10	52	63.4	317	JC2359	A:Accession: PH1298. 1.70e+02	
11	52	63.4	317	I38661	A:Accession: PH1297. 1.70e+02	
12	52	63.4	489	S40731	TOIG of: S40731 check 1.70e+02	
13	51	62.2	234	I38667	A:Title: Structure, ch 2.16e+02	
14	51	62.2	736	A27477	C:Genetics: 2.16e+02	
15	51	62.2	980	S45444	TOIG of: S45444 check 2.16e+02	
16	51	62.2	1729	S57596	TOIG of: S57596 check 2.16e+02	
17	50	61.0	348	I38521	A:Accession: S18521. 2.75e+02	
18	50	61.0	394	Y0B2DH	TOIG of: y0b2dh check 2.75e+02	
19	50	61.0	690	S64646	TOIG of: S64646 check 2.75e+02	
20	50	61.0	890	F64591	A:Title: The complete 2.75e+02	
21	50	61.0	2360	I40457	TOIG of: I40457 check 2.75e+02	
22	50	61.0	2560	B69681	A>Status: preliminary; 2.75e+02	
23	49	59.8	224	WMBERG	A:Accession: JQ1494. 3.49e+02	

24	49	59.8	236	H54425	A:Authors: Borodovsky, 3.49e+02
25	49	59.8	274	S18857	TOIG of: s18857 check 3.49e+02
26	49	59.8	274	XNECSD	A:Title: The complete 3.49e+02
27	49	59.8	287	H64538	A:Authors: Hayes, W.S. 3.49e+02
28	49	59.8	303	H64133	A:Authors: Cotton, M.D 3.49e+02
29	49	59.8	405	MTTILTSTR	This is a DE line. 3.49e+02
30	49	59.8	468	A54926	TOIG of: a54926 check 3.49e+02
31	49	59.8	528	S32593	TOIG of: s32593 check 3.49e+02
32	49	59.8	660	S40098	TOIG of: s40098 check 3.49e+02
33	49	59.8	1454	S53398	TOIG of: S53398 check 3.49e+02
34	49	59.8	1906	S68235	F:1451-1708/Domain: pr 3.49e+02
35	48	58.5	193	C64328	A:Authors: Borodovsky, 4.42e+02
36	48	58.5	319	C69507	A:Accession: C69507. 4.42e+02
37	48	58.5	320	B37767	TOIG of: b37767 check 4.42e+02
38	48	58.5	336	C64410	A:Authors: Borodovsky, 4.42e+02
39	48	58.5	458	D64708	A:Authors: Hayes, W.S. 4.42e+02
40	48	58.5	516	A31270	A:Accession: S05962. 4.42e+02
41	48	58.5	578	A44326	TOIG of: a44326 check 4.42e+02
42	48	58.5	580	S25010	TOIG of: s25010 check 4.42e+02
43	48	58.5	754	S62561	TOIG of: s62561 check 4.42e+02
44	48	58.5	793	S77402	A:Accession: S77402. 4.42e+02
45	47	57.3	61	B33833	TOIG of: B33833 check 5.59e+02
46	47	57.3	70	S55110	TOIG of: S55110 check 5.59e+02
47	47	57.3	80	S59636	A:CROSS-references: EM 5.59e+02
48	47	57.3	87	S69542	A:CROSS-references: EM 5.59e+02
49	47	57.3	87	D64076	A:Accession: F69542. 5.59e+02
50	47	57.3	149	D64076	A:Authors: Cotton, M.D 5.59e+02
51	47	57.3	173	C1PGAA	This is a DE line. 5.59e+02
52	47	57.3	173	CYMNAA	TOIG of: cymnAA check 5.59e+02
53	47	57.3	173	CYLEAA	TOIG of: cyleAA check 5.59e+02
54	47	57.3	173	CYRNAA	This is a DE line. 5.59e+02
55	47	57.3	173	CYLPAA	TOIG of: cyLPAA check 5.59e+02
56	47	57.3	173	CYGCAR	TOIG of: cyGCAa check 5.59e+02
57	47	57.3	225	Q0BE42	A:Title: DNA sequence 5.59e+02
58	47	57.3	249	S21935	TOIG of: s21935 check 5.59e+02
59	47	57.3	249	S09654	TOIG of: s09654 check 5.59e+02
60	47	57.3	268	H64435	A:Authors: Borodovsky, 5.59e+02
61	47	57.3	301	S45597	TOIG of: s45597 check 5.59e+02
62	47	57.3	309	B49878	A:CROSS-references: GB 5.59e+02
63	47	57.3	314	JC2361	A:Title: Human gene MA 5.59e+02
64	47	57.3	353	S34347	A:Accession: S65461. 5.59e+02
65	47	57.3	354	S33309	A:CROSS-references: EM 5.59e+02
66	47	57.3	355	A41534	A:Accession: A41534. 5.59e+02
67	47	57.3	359	RGMSQ	F:183/Modified site: A 5.59e+02
68	47	57.3	359	S45700	TOIG of: s45700 check 5.59e+02
69	47	57.3	359	S45699	TOIG of: s45699 check 5.59e+02
70	47	57.3	359	S30359	TOIG of: s30359 check 5.59e+02
71	47	57.3	359	RGHUCY	F:183/Modified site: A 5.59e+02
72	47	57.3	359	RGMS11	F:183/Modified site: A 5.59e+02
73	47	57.3	360	JN0115	TOIG of: jn0115 check 5.59e+02
74	47	57.3	370	A41891	TOIG of: a41891 check 5.59e+02
75	47	57.3	399	F69034	A:Accession: F69034. 5.59e+02
76	47	57.3	401	A31266	TOIG of: a31266 check 5.59e+02
77	47	57.3	468	A64601	A:Authors: Hayes, W.S. 5.59e+02
78	47	57.3	628	S22396	A:Accession: S22396. 5.59e+02
79	47	57.3	745	G01025	TOIG of: g01025 check 5.59e+02
80	47	57.3	774	I48609	TOIG of: i48609 check 5.59e+02
81	47	57.3	775	S31333	TOIG of: s31333 check 5.59e+02
82	47	57.3	998	S41397	TOIG of: s41397 check 5.59e+02
83	47	57.3	1147	A41674	F:702-710/Region: prot 5.59e+02
84	47	57.3	1176	JN0583	F:731-739/Region: prot 5.59e+02
85	47	57.3	1450	S78050	A:CROSS-references: EM 5.59e+02
86	46	56.1	175	G69833	A:Experimental source: 7.05e+02
87	46	56.1	215	B26473	TOIG of: b26473 check 7.05e+02
88	46	56.1	261	MPKWDRLM	This is a DE line. 7.05e+02
89	46	56.1	273	S67622	TOIG of: S67622 check 7.05e+02
90	46	56.1	342	MGSGLALKH	This is a DE line. 7.05e+02
91	46	56.1	357	G69290	A:Accession: G69290. 7.05e+02
92	46	56.1	396	AJM2RB	A:Accession: B28180. 7.05e+02
93	46	56.1	489	B36395	TOIG of: b36395 check 7.05e+02
94	46	56.1	509	D64435	A:Authors: Borodovsky, 7.05e+02
95	46	56.1	548	S59133	A:Accession: S59133. 7.05e+02
96	46	56.1	732	S73089	A:CROSS-references: EM 7.05e+02

97 46 56.1 863 2 S38140 TOIG of: s38140 check 7.05e+02
98 46 56.1 893 2 S46442 F:536-610/Domain: cyto 7.05e+02
99 46 56.1 1265 2 S57968 TOIG of: s57968 check 7.05e+02
100 46 56.1 1556 2 S76781 A:Accession: S76781. 7.05e+02

ALIGNMENTS

RESULT 1
ID JC2358 STANDARD; PRT; 280 AA.

XX AC xxxxxx

DT 01-JAN-1900

DE TOIG of: jc2358 check: 467 from: 1 to: 280.

CC TOIG of: jc2358 check: 467 from: 1 to: 280

CC >P1:JC2358

CC tumor-associated antigen , MAGE-1 - human

CC C:Species: Homo sapiens (man)

CC C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Mar-19

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CC C:Accession: JC2358

CC R:Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.

CC Biochem. Biophys. Res. Commun. 202, 549-555, 1994

CC A:Title: Cloning and analysis of MAGE-1-related genes.

CC A:Reference number: JC2358

CC A:Accession: JC2358

CC A:Molecule type: mRNA

CC A:Residues: 1-280 <DIN>

CC A:Experimental source: melanoma cell line DM150

CC C:Genetics:

CC A:Gene: MAGE

CC F:161-169/Region: HLA-A1 binding #status predicted

SQ SEQUENCE 280 AA; 30932 MW; 426797 CN;

Query Match 100.0%; Score 82; DB 2; Length 280;

Best Local Similarity 100.0%; Pred. No. 6.02e-02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 97 LFRVITKKVAD 108

XX |||||

QY 1 LFRVITKKVAD 12

RESULT 2

ID I38663 STANDARD; PRT; 124 AA.

XX AC xxxxxx

DT 01-JAN-1900

DE A:Title: Structure, chromosomal localization, and expression of 12 genes o
f the MAGE family.

CC A:Title: Structure, chromosomal localization, and expression of 12 genes
of the MAGE family.

CC A:Reference number: I38659; MUID:95012457

CC A:Accession: I38663

CC A:Status: preliminary; translated from GB/EMBL/DBJ

CC A:Molecule type: DNA

CC A:Residues: 1-124 <RES>

CC A:Cross-references: EMBL:U10689; NID:g533518; PID:g533519

CC A:Note: MAGE-5a antigen

CC A:Accession: I38664

CC A:Status: preliminary; translated from GB/EMBL/DBJ

CC A:Molecule type: DNA

CC A:Residues: 1-124 <RES>

CC A:Cross-references: EMBL:U10690; NID:g533520; PID:g533521

CC A:Note: MAGE-5b antigen

CC C:Genetics:

CC A:Gene: GDB:MAGE5
CC A:Cross-references: GDB:331120
CC A:Map position: Xq28-Xq28
CC A:Introns: #status absent
SQ SEQUENCE 124 AA; 13015 MW; 83534 CN;

Query Match 73.2%; Score 60; DB 2; Length 124;

Best Local Similarity 66.7%; Pred. No. 2.29e+01;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 104 VERAALSKKVAD 115

QY 1 LFRVITKKVAD 12

RESULT 3

ID S75377 STANDARD; PRT; 875 AA.

XX AC xxxxxx

DT 01-JAN-1900

DE A:Cross-references: EMBL:Y08257; NID:gl707772; PID:e283825; PID:gl707782.

CC A:Cross-references: EMBL:Y08257; NID:gl707772; PID:e283825; PID:gl707782

CC A:Experimental source: strain P2

CC A:Note: the nucleotide sequence was submitted to the EMBL Data Library, S

epetember 1996

CC C:Genetics:

CC A:Start codon: TTG

SQ SEQUENCE 875 AA; 100392 MW; 4004557 CN;

Query Match 67.1%; Score 55; DB 2; Length 875;

Best Local Similarity 77.8%; Pred. No. 8.10e+01;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 193 LFRNLITKK 201

QY 1 LFRVITKK 9

RESULT 4

ID JN0673 STANDARD; PRT; 693 AA.

XX AC xxxxxx

DT 01-JAN-1900

DE TOIG of: jn0673 check: 7105 from: 1 to: 693.

XX TOIG of: jn0673 check: 7105 from: 1 to: 693

CC >P1:JN0673

CC ubiquitin-like fusion protein Anla - African clawed frog

CC C:Species: Xenopus laevis (African clawed frog)

CC C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 08-Sep-19

97

CC C:Accession: JN0673

CC R:Linnen, J.M.; Bailey, C.P.; Weeks, D.L.

CC Gene 128, 181-188, 1993

CC A:Title: Two related localized mRNAs from Xenopus laevis encode ubiquitin

-like fusion proteins.

CC A:Reference number: JN0673

CC A:Accession: JN0673

CC A:Status: nucleic acid sequence not shown

CC A:Molecule type: mRNA

CC A:Residues: 1-693 <DIN>

CC C:Genetics:

CC A:Gene: Anla

CC C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

CC C:Keywords: fusion protein; zinc; zinc finger

CC F:28-103/Region: ubiquitin-like protein

CC F:28-103/Domain: ubiquitin homology <UBH>

```
CC F:625-693/Region: zinc finger
SQ SEQUENCE 693 AA; 76844 MW; 2512772 CN;

Query Match 65.9%; Score 54; DB 2; Length 693;
Best Local Similarity 50.0%; Pred. No. 1.04e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 474 LFRSVEVRNIAD 485
|||:| :|||
QY 1 LFRVITKKVAD 12

RESULT 5
ID JN0674 STANDARD; PRT; 701 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: jn0674 check: 3367 from: 1 to: 701.
XX
CC TOIG of: jn0674 check: 3367 from: 1 to: 701
CC
CC >P1:JN0674
CC ubiquitin-like fusion protein Anlb - African clawed frog
CC C:Species: Xenopus laevis (African clawed frog)
CC C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 08-Sep-19
97
CC C:Accession: JN0674
CC R:Linnen, J.M.; Bailey, C.P.; Weeks, D.L.
CC Gene 128, 181-188, 1993
CC A:Title: Two related localized mRNAs from Xenopus laevis encode ubiquitin
CC -like fusion proteins.
CC A:Reference number: JN0673
CC A:Accession: JN0674
CC A:Status: nucleic acid sequence not shown
CC A:Molecule type: mRNA
CC A:Residues: 1-701 <LIN>
CC C:Gene: Anlb
CC C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
CC C:Keywords: fusion protein; zinc; zinc finger
CC F:28-103/Region: ubiquitin-like protein
CC F:28-103/Domain: ubiquitin homology <UBH>
CC F:633-701/Region: zinc finger
SQ SEQUENCE 701 AA; 78581 MW; 2611877 CN;

Query Match 65.9%; Score 54; DB 2; Length 701;
Best Local Similarity 50.0%; Pred. No. 1.04e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 481 LFRSVEVRNIAD 492
|||:| :|||
QY 1 LFRVITKKVAD 12

RESULT 6
ID S59660 STANDARD; PRT; 885 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: s59660 check: 8781 from: 1 to: 885.
XX
CC TOIG of: s59660 check: 8781 from: 1 to: 885
CC
CC >P1:S59660
CC anaphase spindle elongation protein ASE1 - yeast (Saccharomyces cerevisia
e)
CC N:Alternate names: protein 02806; protein YOR058c
CC C:Species: Saccharomyces cerevisiae
CC C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Dec-19

97
CC C:Accession: S59660; S66941
CC R:Pellman, D.; Fink, G.R.
CC submitted to the EMBL Data Library, January 1995
CC A:Description: Yeast microtubule-associated proteins required for anaphas
e spindle elongation.
CC A:Reference number: S59660
CC A:Accession: S59660
CC A:Molecule type: DNA
CC A:Residues: 1-885 <PEL>
CC A:Cross-references: EMBL:U20235; NID:g972941; PID:g972942
CC R:Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens
, M.
CC submitted to the Protein Sequence Database, July 1996
CC A:Reference number: S66929
CC A:Accession: S66941
CC A:Molecule type: DNA
CC A:Residues: 1-885 <BOH>
CC A:Cross-references: EMBL:Z74966; NID:g1420196; PID:e252338; PID:g1420197;
MIPS:YOR058c
CC A:Experimental source: strain S288C
CC C:Genetics:
CC A:Gene: SGD:ASE1
CC A:Cross-references: SGD:S0005584
CC A:Map position: 15R
SQ SEQUENCE 885 AA; 101623 MW; 3976412 CN;

Query Match 65.9%; Score 54; DB 2; Length 885;
Best Local Similarity 60.0%; Pred. No. 1.04e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 328 EKSVLTKKVS 337
|::|:|::|
QY 2 FRVITKKVA 11

RESULT 7
ID F64964 STANDARD; PRT; 236 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A:Title: The complete genome sequence of Escherichia coli K-12.
CC A:Title: The complete genome sequence of Escherichia coli K-12.
CC A:Reference number: A64720; MUID:97426617
CC A:Accession: F64964
CC A:Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A:Molecule type: DNA
CC A:Residues: 1-236 <BLAT>
CC A:Cross-references: GB:AE000291; GB:U00096; NID:g1788298; PID:g1788308; U
WGP:bl999
CC A:Experimental source: strain K-12, substrain MG1655
SQ SEQUENCE 236 AA; 27074 MW; 286157 CN;

Query Match 64.6%; Score 53; DB 2; Length 236;
Best Local Similarity 50.0%; Pred. No. 1.33e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 4 LFRVISEQIID 15
|||:| :|
QY 1 LFRVITKKVAD 12

RESULT 8
ID G64840 STANDARD; PRT; 904 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
```

```
DE A:Title: The complete genome sequence of Escherichia coli K-12.
XX
CC A:Title: The complete genome sequence of Escherichia coli K-12.
CC A:Reference number: A64720; MUID:97426617
CC A:Accession: G64840
CC A>Status: preliminary; nucleic acid sequence not shown; translation not s
      hown
CC A:Molecule type: DNA
CC A:Residues: 1-904 <BLAT>
CC A:Cross-references: GB:AE000201; GB:U00096; NID:g2367113; PID:g1787227; U
      WCP:D0993
CC A:Experimental source: strain K-12, substrain MG1655
CC C:Genetics:
CC A:Gene: torS
CC C:Keywords: phosphotransferase
SQ SEQUENCE 904 AA; 99738 MW; 3808259 CN;

      Query Match      64.6%; Score 53; DB 2; Length 904;
      Best Local Similarity 54.5%; Pred. No. 1.33e+02;
      Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 766 LFRGIIPKVP 776
  |||:| | | :
Qy 1 LFRAVITKKVA 11

RESULT 9
ID S64131 STANDARD; PRT; 126 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE TOIG of: s64131 check: 414 from: 1 to: 126.
XX
XX TOIG of: s64131 check: 414 from: 1 to: 126
CC
CC >PL:S64131
CC hypothetical protein YGL121c - yeast (Saccharomyces cerevisiae)
CC N:Alternate names: hypothetical protein G2913
CC C:Species: Saccharomyces cerevisiae
CC C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 14-Nov-19
      97
CC C:Accession: S64131
CC R:Lauquin, G.
CC submitted to the Protein Sequence Database, May 1996
CC A:Reference number: S64122
CC A:Accession: S64131
CC A:Molecule type: DNA
CC A:Residues: 1-126 <LAU>
CC A:Cross-references: EMBL:Z72643; NID:gl322678; PID:e243349; PID:gl322679;
      MIPS:YGL121c
CC A:Experimental source: strain S288C
CC C:Genetics:
CC A:Map position: 7L
SQ SEQUENCE 126 AA; 14922 MW; 82947 CN;

      Query Match      63.4%; Score 52; DB 2; Length 126;
      Best Local Similarity 33.3%; Pred. No. 1.70e+02;
      Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 82 LYDVLKMKSE 93
  |||:| | | :
Qy 1 LFRAVITKKVAD 12

RESULT 10
ID JC2359 STANDARD; PRT; 317 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE TOIG of: s64131 check: 414 from: 1 to: 126.
XX
XX TOIG of: s64131 check: 414 from: 1 to: 126
CC
CC >PL:S64131
CC hypothetical protein YGL121c - yeast (Saccharomyces cerevisiae)
CC N:Alternate names: hypothetical protein G2913
CC C:Species: Saccharomyces cerevisiae
CC C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 14-Nov-19
      97
CC C:Accession: S64131
CC R:Lauquin, G.
CC submitted to the Protein Sequence Database, May 1996
CC A:Reference number: S64122
CC A:Accession: S64131
CC A:Molecule type: DNA
CC A:Residues: 1-126 <LAU>
CC A:Cross-references: EMBL:Z72643; NID:gl322678; PID:e243349; PID:gl322679;
      MIPS:YGL121c
CC A:Experimental source: strain S288C
CC C:Genetics:
CC A:Map position: 7L
SQ SEQUENCE 126 AA; 14922 MW; 82947 CN;

      Query Match      63.4%; Score 52; DB 2; Length 126;
      Best Local Similarity 33.3%; Pred. No. 1.70e+02;
      Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 82 LYDVLKMKSE 93
  |||:| | | :
Qy 1 LFRAVITKKVAD 12

RESULT 11
ID I38661 STANDARD; PRT; 317 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE A:Accession: PH1297.
XX
XX A:Accession: PH1297
CC A:Molecule type: DNA
CC A:Residues: 169-177 <TRA>
CC C:Genetics:
CC A:Gene: GDB:MAGE4
CC A:Cross-references: GDB:331119
CC A:Map position: Xq28-Xq28
CC A:Introns: #status absent
SQ SEQUENCE 317 AA; 34899 MW; 528124 CN;

      Query Match      63.4%; Score 52; DB 2; Length 317;
      Best Local Similarity 41.7%; Pred. No. 1.70e+02;
      Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 105 LFREALSKNVDE 116
  |||:| | | :
Qy 1 LFRAVITKKVAD 12

RESULT 12
ID S40731 STANDARD; PRT; 489 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE TOIG of: s40731 check: 4937 from: 1 to: 489.
XX
XX TOIG of: s40731 check: 4937 from: 1 to: 489
CC
CC >PL:S40731
CC ATP-dependent RNA helicase homolog T26G10.1 - Caenorhabditis elegans
CC C:Species: Caenorhabditis elegans
CC C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-19
      97
CC C:Accession: S40731
CC R:Berkas, M.
```

CC submitted to the EMBL Data Library, December 1993
 CC A:Reference number: S40731
 CC A:Accession: S40731
 CC A:Molecule type: DNA
 CC A:Residues: 1-489 <BER>
 CC A:Cross-references: EMBL:Z29115; NID:G439259; PID:G439260
 CC C:Genetics:
 CC A:Introns: 26/1; 319/3; 403/1
 CC A:Introns: 489 AA; 54227 MW; 1183591 CN;
 SQ SEQUENCE 489 AA; 54227 MW; 1183591 CN;

Query Match 63.4%; Score 52; DB 2; Length 489;
 Best Local Similarity 63.6%; Pred. No. 1.70e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 223 LFSATMTKKVS 233
 ||| : |||:
 QY 1 LFRVITTKVA 11

RESULT 13
 ID I38667 STANDARD; PRT; 234 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900

DE A:Title: Structure, chromosomal localization, and expression of 12 genes o
 f the MAGE family.
 XX

CC A:Title: Structure, chromosomal localization, and expression of 12 genes
 of the MAGE family.
 CC A:Reference number: I38659; MUID:95012457
 CC A:Accession: I38667
 CC A>Status: preliminary; translated from GB/EMBL/DBJ
 CC A:Molecule type: DNA
 CC A:Residues: 1-234 <RES>
 CC A:Cross-references: EMBL:U10693; NID:G533525; PID:G533526
 CC C:Genetics:
 CC A:Gene: GDB:MAGE8
 CC A:Cross-references: GDB:331123
 CC A:Map position: Xq28-Xq28
 CC A:Introns: #status absent
 SQ SEQUENCE 234 AA; 25197 MW; 296950 CN;

Query Match 62.2%; Score 51; DB 2; Length 234;
 Best Local Similarity 50.0%; Pred. No. 2.16e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 107 LFEALDEKVAE 118
 ||| : |||:
 QY 1 LFRVITTKVAD 12

RESULT 14
 ID A27477 STANDARD; PRT; 736 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900

DE C:Genetics:
 XX

CC C:Genetics:
 CC A:Gene: SGD:CDL24; CLS4; TSL1
 CC A:Cross-references: SGD:S0000039
 CC A:Map position: 1L
 CC C:Superfamily: CDC24 homology
 CC F:160-336/Domain: CDC24 homology <CD24>
 SQ SEQUENCE 736 AA; 83960 MW; 2862170 CN;

Query Match 62.2%; Score 51; DB 2; Length 736;
 Best Local Similarity 63.6%; Pred. No. 2.16e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 399 LFEVVTTKSA 409
 ||| : |||:
 QY 1 LFRVITTKVA 11

RESULT 15
 ID S45444 STANDARD; PRT; 980 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900

DE TOIG of: s45444 check: 8660 from: 1 to: 980.
 XX
 CC TOIG of: s45444 check: 8660 from: 1 to: 980

CC
 CC >P1;S45444

CC BEM1 protein-binding protein BOB1 - yeast (Saccharomyces cerevisiae)
 CC N:Alternate names: protein YBL0717; protein YBL085W
 CC C:Species: Saccharomyces cerevisiae
 CC C:Date: 09-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 05-Dec-19

CC C:Accession: S45444; S45421; S45826; S59218
 CC R:Bender, A.; Bender, L.; Kokojan, V.
 CC submitted to the EMBL Data Library, April 1994
 CC A:Description: Yeast Bobip (Bemip-binding protein) binds to the SH3 domai
 n-containing protein Bemip.

CC A:Reference number: S45444
 CC A:Accession: S45444
 CC A:Molecule type: DNA
 CC A:Residues: 1-980 <BEN>
 CC A:Cross-references: EMBL:L31406; NID:G829041; PID:G466436
 CC R:Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
 CC submitted to the EMBL Data Library, May 1994
 CC A:Description: Sequence analysis of a 78,6 kb segment of the left end of
 Saccharomyces cerevisiae chromosome II.

CC A:Reference number: S45387
 CC A:Accession: S45421
 CC A:Molecule type: DNA
 CC A:Residues: 1-980 <OBE>
 CC A:Cross-references: EMBL:X79489; NID:G496661; PID:G496694
 CC R:Domdey, H.; Gassenhuber, H.; Obermaier, B.; Piravandi, E.
 CC submitted to the Protein Sequence Database, August 1994
 CC A:Reference number: S45816
 CC A:Accession: S45826
 CC A:Molecule type: DNA
 CC A:Residues: 1-980 <DON>
 CC A:Cross-references: EMBL:Z35846; NID:G536137; PID:G536138; MIPS:YBL085W
 CC R:Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.

CC Yeast 11, 1103-1112, 1995
 CC A:Title: Sequence analysis of a 78.6 kb segment of the left end of Saccha
 romyces cerevisiae chromosome II.

CC A:Reference number: S59184
 CC A:Accession: S59218
 CC A>Status: nucleic acid sequence not shown; translation not shown
 CC A:Molecule type: DNA

CC A:Residues: 1-980 <OBW>
 CC A:Cross-references: EMBL:X79489; NID:G496661; PID:G496694
 CC A:Note: the nucleotide sequence was submitted to the EMBL Data Library, M
 ay 1994

CC C:Genetics:
 CC A:Gene: SGD:BOB1; BOB1
 CC A:Cross-references: MIPS:YBL085W; SGD:S0000181
 CC A:Map position: 2L
 CC C:Superfamily: SH3 homology
 CC F:20-72/Domain: SH3 homology <SH3>
 SQ SEQUENCE 980 AA; 109294 MW; 5181201 CN;

Query Match 62.2%; Score 51; DB 2; Length 980;
 Best Local Similarity 54.5%; Pred. No. 2.16e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

Db 66 LYPVFTKRIA 76
   I: ||:|:|:|
QY 1 LFRVITRKVA 11

RESULT 16
ID S57596 STANDARD; PRT; 1729 AA.
XX AC xxxxxx
XX AC xxxxxx
DT 01-JAN-1900
DE TOIG of: s57596 check: 3679 from: 1 to: 1729.
CC TOIG of: s57596 check: 3679 from: 1 to: 1729
CC TOIG of: s57596 check: 3679 from: 1 to: 1729
CC >P1:S57596
CC hypothetical protein YMR229c - yeast (Saccharomyces cerevisiae)
CC N:Alternate names: hypothetical protein YM9959.11c
CC C:Species: Saccharomyces cerevisiae
CC C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Dec-19
97
CC C:Accession: S57596
CC R:Skellton, J.; Churcher, C.M.
CC submitted to the EMBL Data Library, June 1995
CC A:Reference number: S57587
CC A:Accession: S57596
CC A:Molecule type: DNA
CC A:Residues: 1-1729 <SKE>
CC A:CROSS-references: EMBL:249939; NID:g887599; PID:g887610; MIPS:YMR229c
CC A:Experimental source: strain AB972
CC C:Genetics:
CC A:Gene: SGD.FM11
CC A:CROSS-references: SGD:S0004842
CC A:Map position: 13R
CC SEQUENCE 1729 AA; 193133 MW; 15516437 CN;

Query Match 62.2%; Score 51; DB 2; Length 1729;
Best Local Similarity 54.5%; Pred. No. 2.16e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1674 LFERIITRKIT 1684
   I: ||:|:|:|
QY 1 LFRVITRKVA 11

RESULT 17
ID S18521 STANDARD; PRT; 348 AA.
XX AC xxxxxx
XX AC xxxxxx
DT 01-JAN-1900
DE A:Accession: S18521.
XX A:Accession: S18521
XX A:Molecule type: DNA
CC A:Residues: 1-348 <KIT>
CC A:CROSS-references: EMBL:X61672; NID:g4977; PID:g4978
CC C:Keywords: G protein-coupled receptor; transmembrane protein
SQ SEQUENCE 348 AA; 39285 MW; 700740 CN;

Query Match 61.0%; Score 50; DB 2; Length 348;
Best Local Similarity 55.6%; Pred. No. 2.75e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 229 LFRVILIRK 237
   I: ||:|:|:|
QY 1 LFRVITRK 9

RESULT 18
ID YQBZDH STANDARD; PRT; 394 AA.

```

```

XX xxxxxx
AC 01-JAN-1900
DT 01-JAN-1900
DE TOIG of: yqbzdh check: 2838 from: 1 to: 394.
XX TOIG of: yqbzdh check: 2838 from: 1 to: 394
CC >P1:YQBZDH
CC fimD protein - Dichelobacter nodosus (serotype H1)
CC C:Species: Dichelobacter nodosus
CC C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Sep-19
97
CC C:Accession: S15255
CC R:Hobbs, M.; Dalrymple, B.P.; Cox, P.T.; Livingstone, S.P.; Delaney, S.F.
CC ; Mattick, J.S.
CC Mol. Microbiol. 5, 543-560, 1991
CC A:Title: Organization of the fimbrial gene region of Bacteroides nodosus:
CC class I and class II strains.
CC A:Reference number: S15240; MUID:91260439
CC A:Accession: S15255
CC A:Molecule type: DNA
CC A:Residues: 1-394 <HO>
CC A:CROSS-references: EMBL:X52390; NID:g39703; PID:g580812
CC A:Note: the source is designated as Bacteroides nodosus
CC C:Genetics:
CC A:Gene: fimD
CC A:Start codon: GTG
CC C:Superfamily: fimD protein
CC C:Keywords: fimbria
CC SEQUENCE 394 AA; 45105 MW; 815478 CN;

Query Match 61.0%; Score 50; DB 1; Length 394;
Best Local Similarity 72.7%; Pred. No. 2.75e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 365 FRAASTKTKAD 375
   I: ||:|:|:|
QY 2 FRVITRKVAD 12

RESULT 19
ID S64646 STANDARD; PRT; 690 AA.
XX AC xxxxxx
XX AC xxxxxx
DT 01-JAN-1900
DE TOIG of: s64646 check: 478 from: 1 to: 690.
XX TOIG of: s64646 check: 478 from: 1 to: 690
CC >P1:S64646
CC biotin--[acetyl-CoA-carboxylase] ligase (EC 6.3.4.15) - yeast (Saccharomyces cerevisiae)
CC N:Alternate names: biotin-apoptein ligase; protein D2140; protein YDL14
1W
CC C:Species: Saccharomyces cerevisiae
CC C:Date: 12-Jul-1996 #sequence_revision 23-Aug-1996 #text_change 05-Dec-19
97
CC C:Accession: S64646; S67687; S67688
CC R:Cronan Jr., J.E.; Wallace, J.C.
CC FEMS Microbiol. Lett. 130, 221-230, 1995
CC A:Title: The gene encoding the biotin-apoptein ligase of Saccharomyces cerevisiae.
CC A:Reference number: S64646
CC A:Accession: S64646
CC A:Molecule type: DNA
CC A:Residues: 1-690 <CRO>
CC A:CROSS-references: EMBL:U27182; NID:g886080; PID:g886081
CC R:Saluz, H.P.; Woelfl, S.; Hanemann, V.
CC submitted to the Protein Sequence Database, July 1996

```

```
CC A;Reference number: S67677
CC A;Accession: S67687
CC A;Molecule type: DNA
CC A;Residues: 1-690 <SAL>
CC A;Cross-references: EMBL:Z74189; NID:g1431218; PID:e253238; PID:g1431219;
MIPS:YDL141w
CC A;Experimental source: strain S288C
CC R;Baron, L.; Legros, Y.; Biteau, N.; Monnet, A.; Granotier, C.
CC submitted to the Protein Sequence Database, July 1996
CC A;Reference number: S67688
CC A;Accession: S67688
CC A;Molecule type: DNA
CC A;Residues: 1-291 <BAR>
CC A;Cross-references: EMBL:Z74189; MIPS:YDL141w
CC A;Experimental source: strain S288C
CC C;Genetics:
CC A;Gene: SGD:BPL1
CC A;Cross-references: SGD:S0002300
CC A;Map position: 4L
CC C;Keywords: ligase; transmembrane protein
CC F;458-474/Domain: transmembrane status predicted <TM>
CC SEQUENCE 690 AA; 76362 MW; 2564839 CN;

Query Match 61.0%; Score 50; DB 2; Length 690;
Best Local Similarity 50.0%; Pred. No. 2.75e+02;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 679 IFKSLIAKKV 688
:|::|::|
QY 1 LFRVITKKV 10

RESULT 20
ID F64991 STANDARD; PRT; 890 AA.
XX
AC xxxxxx
DT 01-JAN-1900
DE A;Title: The complete genome sequence of Escherichia coli K-12.
CC
CC A;Title: The complete genome sequence of Escherichia coli K-12.
CC A;Reference number: A64720; MUID:97426617
CC A;Accession: F64991
CC A;Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A;Molecule type: DNA
CC A;Residues: 1-890 <BLAT>
CC A;Cross-references: GB:AE000310; GB:U00096; NID:g2367131; PID:g1788545; U
WGP:b2216
CC A;Experimental source: strain K-12, substrain MG1655
CC C;Genetics:
CC A;Gene: yojN
CC SEQUENCE 890 AA; 100371 MW; 3869027 CN;

Query Match 61.0%; Score 50; DB 2; Length 890;
Best Local Similarity 60.0%; Pred. No. 2.75e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 377 RTVISNKIAD 386
:|::|::|
QY 3 RAVITRKVAD 12

RESULT 21
ID I40457 STANDARD; PRT; 2560 AA.
XX
AC xxxxxx
DT 01-JAN-1900
DE TOIG of: 140457 check: 9702 from: 1 to: 2560.
XX
```

```
CC TOIG of: i40457 check: 9702 from: 1 to: 2560
CC >P1:I40457
CC peptide-synthetase 2 - Bacillus subtilis
CC N;Alternate names: pps2
CC C;Species: Bacillus subtilis
CC C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 18-Jul-19
97
CC C;Accession: I40457; S49134
CC R;Tognoni, A.; Franchi, E.; Magistrelli, C.; Colombo, E.; Cosmina, P.; Gr
andi, G.
CC Microbiology 141, 645-648, 1995
CC A;Title: A putative new peptide synthase operon in Bacillus subtilis: par
tial characterization.
CC A;Reference number: I40454; MUID:95227362
CC A;Accession: I40457
CC A;Status: preliminary; translated from GB/EMBL/DBJ
CC A;Molecule type: DNA
CC A;Residues: 1-2560 <RES>
CC A;Cross-references: EMBL:Z34883; NID:g509465; PID:g509469
CC C;Genetics:
CC A;Gene: pps2
CC C;Superfamily: gramicidin S synthetase I repeat homology; acetate-CoA li
gase homology; acyl carrier protein homology
CC F;456-1036/Domain: gramicidin S synthetase I repeat homology <GRS1>
CC F;515-952/Domain: acetate-CoA ligase homology <ACL1>
CC F;988-1036/Domain: acyl carrier protein homology <ACP1>
CC F;1486-2076/Domain: gramicidin S synthetase I repeat homology <GRS2>
CC F;1546-1992/Domain: acetate-CoA ligase homology <ACL2>
CC F;2009-2076/Domain: acyl carrier protein homology <ACP2>
CC SEQUENCE 2560 AA; 290162 MW; 32837003 CN;

Query Match 61.0%; Score 50; DB 2; Length 2560;
Best Local Similarity 41.7%; Pred. No. 2.75e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 63 IERTIFIKEVPD 74
:|::|::|
QY 1 LFRVITKKVAD 12

RESULT 22
ID B69681 STANDARD; PRT; 2560 AA.
XX
AC xxxxxx
DT 01-JAN-1900
DE A;Status: preliminary; nucleic acid sequence not shown; translation not sh
own.
XX
CC A;Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A;Molecule type: DNA
CC A;Residues: 1-2560 <KUN>
CC A;Experimental source: strain 168
CC C;Genetics:
CC A;Gene: ppsB
CC SEQUENCE 2560 AA; 290162 MW; 32837003 CN;

Query Match 61.0%; Score 50; DB 2; Length 2560;
Best Local Similarity 41.7%; Pred. No. 2.75e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 63 IERTIFIKEVPD 74
:|::|::|
QY 1 LFRVITKKVAD 12

RESULT 23
ID WMBEHC STANDARD; PRT; 224 AA.
XX
AC xxxxxx
```

```
XX 01-JAN-1900
DT
XX
DE A:Accession: J01494.
XX
CC A:Accession: J01494
CC A:Molecule type: DNA
CC A:Residues: 1-224 <MCG>
CC A:Cross-references: GB:D10470; DDBJ:D01127; NID:g221791; PID:d1001734; PI
D:g221792
CC C:Genetics:
CC A:Gene: UL1
CC C:Superfamily: varicella-zoster virus gene 60 protein
SQ SEQUENCE 224 AA; 25192 MW; 242721 CN;

Query Match 59.8%; Score 49; DB 1; Length 224;
Best Local Similarity 50.0%; Pred. No. 3.49e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 27 VLRSVIAKEVGD 38
QY 1 LFRVITKKVAD 12
:|:|:|:|:|

RESULT 24
ID H64425 STANDARD; PRT; 236 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE A:Authors: Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
C.R.; Venter, J.C.
CC A:Authors: Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
C.R.; Venter, J.C.
CC A:Title: Complete genome sequence of the methanogenic archaeon, Methanoco-
ccus jannaschii.
CC A:Reference number: A64300; MUID:96337999
CC A:Accession: H64425
CC A>Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A:Molecule type: DNA
CC A:Residues: 1-236 <BUL>
CC A:Cross-references: GB:U67543; GB:L77117; NID:g1591663; PID:g1591668; TIG
R:MJ1009; PID:g1511039
CC C:Genetics:
CC A:Map position: REV939905-939195
SQ SEQUENCE 236 AA; 27426 MW; 265381 CN;

Query Match 59.8%; Score 49; DB 2; Length 236;
Best Local Similarity 33.3%; Pred. No. 3.49e+02;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 161 LYRSMISKIEN 172
QY 1 LFRVITKKVAD 12
|:|:|:|:|:|

RESULT 25
ID S18857 STANDARD; PRT; 274 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE TIG of: s18857 check: 6782 from: 1 to: 274.
XX
CC TOIG of: s18857 check: 6782 from: 1 to: 274
CC
CC >P1:S18857
CC 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase (EC 2.3.1.
117).- Actinobacillus pleuropneumoniae
```

```
CC N:Alternate names: tetrahydridipicolinate N-succinyltransferase
CC C:Species: Actinobacillus pleuropneumoniae
CC C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Oct-19
97
CC C:Accession: S18857
CC R:Denich, K.; O'Hanley, P.; Lalonde, G.
CC submitted to the EMBL Data Library, November 1991
CC A:Description: Cloning and sequence analysis of the DAPD gene from Actino-
bacillus pleuropneumonia.
CC A:Reference number: S18857
CC A:Accession: S18857
CC A>Status: preliminary
CC A:Molecule type: DNA
CC A:Residues: 1-274 <DEN>
CC A:Cross-references: EMBL:X63201; NID:g38946; PID:g38947
CC C:Superfamily: 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransfe-
rase
CC C:Keywords: acyltransferase; aminotransferase; diaminopimelate biosynthes-
is; lysine biosynthesis; pyridoxal phosphate
SQ SEQUENCE 274 AA; 29761 MW; 412362 CN;

Query Match 59.8%; Score 49; DB 2; Length 274;
Best Local Similarity 70.0%; Pred. No. 3.49e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 246 LYCAVIVKKV 255
QY 1 LFRVITKKV 10
|:|:|:|:|

RESULT 26
ID XNECSD STANDARD; PRT; 274 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE A:Title: The complete genome sequence of Escherichia coli K-12.
XX
CC A:Title: The complete genome sequence of Escherichia coli K-12.
CC A:Reference number: A64720; MUID:97426617
CC A:Accession: F64740
CC A>Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A:Molecule type: DNA
CC A:Residues: 1-274 <BLAT>
CC A:Cross-references: GB:AE000126; GB:U00096; NID:g1786358; PID:g1786362; U
WGP:b0166
CC A:Experimental source: strain K-12, substrain MG1655
CC R:Richaud, C.; Richaud, F.; Martin, C.; Haziza, C.; Patte, J.C.
CC J. Biol. Chem. 259, 14824-14828, 1984
CC A:Title: Regulation of expression and nucleotide sequence of the Escheric-
hia coli dapD gene.
CC A:Reference number: A00601; MUID:85054973
CC A:Accession: A00601
CC A:Molecule type: DNA
CC A:Residues: 1-30, 'D', '32-162, 'R', '164-176, 'M', '178-189, 'L', '191-274 <R1C>
R:Fujita, N.
CC submitted to the EMBL Data Library, January 1994
CC A:Reference number: S45181
CC A:Accession: S45231
CC A>Status: preliminary
CC A:Molecule type: DNA
CC A:Residues: 1-274 <FUJ>
CC A:Cross-references: EMBL:D26562; NID:g473770; PID:d1006154; PID:g473821
R:van Heeswijk, W.C.; Rabenberg, M.; Westerhoff, H.V.; Kahn, D.
CC Mol. Microbiol. 9, 443-457, 1993
CC A:Title: The genes of the glutamine synthetase adenylation cascade are
not regulated by nitrogen in Escherichia coli.
CC A:Reference number: S36254
CC A:Accession: S36255
CC A:Molecule type: DNA
CC A:Residues: 1-14 <VAN>
```



```
CC A;Cross-references: EMBL:Z21842
CC C;Genetics:
CC A;Gene: dapD
CC A;Map position: 4 min
CC C;Superfamily: 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransfe
      rase
CC C;Keywords: acyltransferase; diaminopimelate biosynthesis; lysine biosynt
      hesis; pyridoxal phosphate
SQ SEQUENCE 274 AA; 29892 MW; 403030 CN;

Query Match          59.8%; Score 49; DB 1; Length 274;
Best Local Similarity 70.0%; Pred. No. 3.49e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 247 LYCAVIVKKV 256
   |: ||| |||
QY 1 LFRVAVITKKV 10

RESULT 27
ID H64538 STANDARD; PRT; 287 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A;Authors: Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
   C.M.; Venter, J.C.
XX
CC A;Authors: Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
   C.M.; Venter, J.C.
CC A;Title: The complete genome sequence of the gastric pathogen Helicobacte
   r pylori.
CC A;Reference number: A64520; MUID:97394467
CC A;Accession: H64538
CC A;Status: preliminary; nucleic acid sequence not shown; translation not s
      hown
CC A;Molecule type: DNA
CC A;Residues: 1-287 <TOM>
CC A;Cross-references: GB:AE000536; GB:AE000511; NID:92313230; PID:92313242;
      TIGR:HP0152
CC C;Genetics:
CC A;Start codon: TTG
SQ SEQUENCE 287 AA; 32948 MW; 428117 CN;

Query Match          59.8%; Score 49; DB 2; Length 287;
Best Local Similarity 55.6%; Pred. No. 3.49e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 189 LYRAILIKK 197
   |: |||: ||
QY 1 LFRVAVITKK 9

RESULT 28
ID H64133 STANDARD; PRT; 303 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A;Authors: Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saude
   k, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.
XX
CC A;Authors: Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saud
   ek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.
CC Fuhrmann, J.L.; Geohagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Small, K.
   V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
CC A;Title: Whole-genome random sequencing and assembly of Haemophilus influ
      enzae Rd.
CC A;Reference number: A64000; MUID:95350630
CC A;Accession: H64133
CC A;Status: nucleic acid sequence not shown; translation not shown
```

```
CC A;Molecule type: DNA
CC A;Residues: 1-303 <TIGR>
CC A;Cross-references: GB:U32836; GB:L42023; NID:gl574473; PID:gl574480; TIG
      R:H11634
CC C;Genetics:
CC A;Start codon: GTG
CC C;Superfamily: 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransfe
      rase
CC C;Keywords: acyltransferase; diaminopimelate biosynthesis; lysine biosynt
      hesis; pyridoxal phosphate
SQ SEQUENCE 303 AA; 32817 MW; 503347 CN;

Query Match          59.8%; Score 49; DB 2; Length 303;
Best Local Similarity 70.0%; Pred. No. 3.49e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 275 LYCAVIVKKV 284
   |: ||| |||
QY 1 LFRVAVITKKV 10

RESULT 29
ID MTYIITSTFRNLSTTSKWALRESVRPLSCSSQVQSAPAVQTSKKTAKPNLKNIVVVEGVRIPFLLSGT
STANDARD; PRT; 405 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE This is a DE line.
XX
SQ SEQUENCE 405 AA; 43796 MW; 794088 CN;

Query Match          59.8%; Score 49; DB 2; Length 405;
Best Local Similarity 50.0%; Pred. No. 3.49e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 19 LYRTNIPKDVVD 30
   |: | | | |
QY 1 LFRVAVITKKVAD 12

RESULT 30
ID A54926 STANDARD; PRT; 468 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: a54926 check: 8551 from: 1 to: 468.
XX
CC TOIG of: a54926 check: 8551 from: 1 to: 468
CC
CC >P1:A54926
CC UDPglucose 6-dehydrogenase (EC 1.1.1.22) - bovine
CC C;Species: Bos primigenius taurus (cattle)
CC C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 04-Nov-19
      94
CC C;Accession: A54926
CC R;Hempel, J.; Perozich, J.; Romovacek, H.; Hinrich, A.; Kuo, I.; Feingold,
      D.S.
CC Protein Sci. 3, 1074-1080, 1994
CC A;Title: UDP-glucose dehydrogenase from bovine liver: primary structure a
      nd relationship to other dehydrogenases.
CC A;Reference number: A54926
CC A;Accession: A54926
CC A;Status: preliminary
CC A;Molecule type: protein
CC A;Residues: 1-468 <HEM>
CC C;Keywords: NAD; oxidoreductase
SQ SEQUENCE 468 AA; 52171 MW; 1108556 CN;

Query Match          59.8%; Score 49; DB 2; Length 468;
```



```
ID S68235 STANDARD; PRT; 1906 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE F:1451-1708/Domain: protein kinase homology <KIN>.
XX
CC F:1451-1708/Domain: protein kinase homology <KIN>
CC F:1459-1467/Region: protein kinase ATP-binding motif
CC F:1750-1906/Product: telokin #status predicted <TKN>
SQ SEQUENCE 1906 AA; 210445 MW; 18691293 CN;

Query Match 59.8%; Score 49; DB 2; Length 1906;
Best Local Similarity 50.0%; Pred. No. 3.49e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

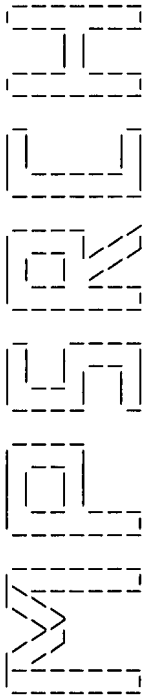
Db 909 FRDILGKVS 918
OY 2 FRVITKVA 11
|| : |||

RESULT 35
ID C64328 STANDARD; PRT; 193 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A;Authors: Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
C.R.; Venter, J.C.
XX A;Authors: Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
C.R.; Venter, J.C.
CC A;Title: Complete genome sequence of the methanogenic archaeon, Methanoco-
ccus jannaschii.
CC A;Reference number: A64300; MUID:96337999
CC A;Accession: C64328
CC A;Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A;Molecule type: DNA
CC A;Residues: 1-193 <BUL>
CC A;Cross-references: GB:U67478; GB:L77117; NID:g1590958; PID:g1590963; TIG
R:MJ0226; PID:g1510334
CC C;Genetics:
CC A;Map position: FOR216394-216975
CC A;Start codon: TTG
SQ SEQUENCE 193 AA; 22202 MW; 192384 CN;

Query Match 58.5%; Score 48; DB 2; Length 193;
Best Local Similarity 25.0%; Pred. No. 4.42e+02;
Matches 3; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 129 LFKGIVKGRVSE 140
OY 1 LFRVITKKVAD 12
|| : |||
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Search completed: Tue Apr 7 08:40:46 1998
Job time : 14 secs.



(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:39:32 1998; MasPar time 3.95 Seconds
Tabular output not generated. 76.145 Million cell updates/sec

Title: >US-08-190-411A-3
Description: (1-12) from 5541104.pep
Perfect Score: 82
Sequence: 1 LFRVITKKVAD 12

Scoring table: PAM 150
Gap 15

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 25.999; Variance 27.975; scale 0.929

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	82	100.0	309	1	MAG1_HUMAN	MELANOMA-ASSOCIATED AN	7.13e-08
2	60	73.2	124	1	MAG5_HUMAN	MELANOMA-ASSOCIATED AN	4.58e-02
3	54	65.9	885	1	ASE1_YEAST	ANAPHASE SPINDLE ELONG	1.14e+00
4	53	64.6	236	1	YEEL_ECOLI	HYPOTHETICAL 27.1 KD P	1.89e+00
5	53	64.6	904	1	TORS_ECOLI	SENSOR PROTEIN TORS (E	1.89e+00
6	52	63.4	126	1	YGM1_YEAST	HYPOTHETICAL 14.9 KD P	3.13e+00
7	52	63.4	317	1	MAG4_HUMAN	MELANOMA-ASSOCIATED AN	3.13e+00
8	52	63.4	489	1	Y2N1_CAEEL	PUTATIVE ATP-DEPENDENT	3.13e+00
9	51	62.2	234	1	MAG8_HUMAN	MELANOMA-ASSOCIATED AN	5.14e+00
10	51	62.2	854	1	CC24_YEAST	CELL DIVISION CONTROL	5.14e+00
11	51	62.2	980	1	BOB1_YEAST	BOB1 PROTEIN (BEM1-BIN	5.14e+00
12	51	62.2	1729	1	RRP5_YEAST	RRNA BIOGENESIS PROTEI	5.14e+00
13	50	61.0	348	1	NAM2_SCHPO	PEROMONE P-FACTOR REC	8.37e+00
14	50	61.0	394	1	FMDH_BACNO	POSSIBLE FIBRILAL ASSE	8.37e+00
15	50	61.0	690	1	BPL1_YEAST	BIOTIN--PROTEIN LIGASE	8.37e+00
16	50	61.0	890	1	YOJN_ECOLI	PROBABLE SENSOR PROTEI	8.37e+00
17	50	61.0	2560	1	PPS2_BACSU	PEPTIDE SYNTHETASE 2.	8.37e+00
18	49	59.8	224	1	VGLE_HSV2H	GLYCOPROTEIN L PRECURS	1.35e+01
19	49	59.8	274	1	DAPD_ACTPL	2,3,4,5-TETRAHYDROPYR	1.35e+01
20	49	59.8	274	1	DAPD_ECOLI	2,3,4,5-TETRAHYDROPYR	1.35e+01
21	49	59.8	275	1	DAPD_HAEIN	2,3,4,5-TETRAHYDROPYR	1.35e+01
22	49	59.8	432	1	GBAL_CRYNE	GUANINE NUCLEOTIDE-BIN	1.35e+01
23	49	59.8	475	1	ECHB_RAT	MITOCHONDRIAL TRIFUNCT	1.35e+01

528	1	CTK1_YEAST	CTD KINASE ALPHA SUBUN	1.35e+01
1906	1	KML2_CHICK	MYOSIN LIGHT CHAIN KIN	1.35e+01
193	1	Y226_METJA	HYPOTHETICAL PROTEIN M	2.16e+01
266	1	FLIP_CAUCR	FLAGELLAR BIOSYNTHETIC	2.16e+01
320	1	THI4_FUSOX	THIAZOLE BIOSYNTHETIC	2.16e+01
351	1	B3AR_CAVPO	BETA-3 ADRENERGIC RECE	2.16e+01
424	1	FADH_METMR	GLUTATHIONE-DEPENDENT	2.16e+01
516	1	RSP3_CHLRE	RADIAL SPOKE PROTEIN 3	2.16e+01
578	1	AYTM_BACLI	MALTOGENIC ALPHA-AMYL	2.16e+01
754	1	YAJ3_SCHPO	PUTATIVE ATP-DEPENDENT	2.16e+01
69	1	RM39_YEAST	MITOCHONDRIAL 60S RIBO	3.43e+01
149	1	RL9_HAEIN	50S RIBOSOMAL PROTEIN	3.43e+01
173	1	CRAA_CERSI	ALPHA CRYSTALLIN A CHA	3.43e+01
173	1	CRAA_MUSVI	ALPHA CRYSTALLIN A CHA	3.43e+01
173	1	CRAA_EULFU	ALPHA CRYSTALLIN A CHA	3.43e+01
173	1	CRAA_PIG	ALPHA CRYSTALLIN A CHA	3.43e+01
225	1	CRAA_PERPO	ALPHA CRYSTALLIN A CHA	3.43e+01
225	1	UL92_EBV	PROTEIN BDLF4.	3.43e+01
249	1	H1_DROHY	HISTONE H1.	3.43e+01
301	1	THI2_SCHPO	THIAZOLE BIOSYNTHETIC	3.43e+01
314	1	MAG3_HUMAN	MELANOMA-ASSOCIATED AN	3.43e+01
353	1	GBQ_LYMF	GUANINE NUCLEOTIDE-BIN	3.43e+01
353	1	GBQ_CANFA	GUANINE NUCLEOTIDE-BIN	3.43e+01
353	1	GBQ_HUMAN	GUANINE NUCLEOTIDE-BIN	3.43e+01
353	1	GBQ3_DROME	GUANINE NUCLEOTIDE-BIN	3.43e+01
353	1	GBQ1_DROME	GUANINE NUCLEOTIDE-BIN	3.43e+01
353	1	GBQ_MOUSE	GUANINE NUCLEOTIDE-BIN	3.43e+01
353	1	GBQ_XENLA	GUANINE NUCLEOTIDE-BIN	3.43e+01
354	1	GBQ_LOLFO	GUANINE NUCLEOTIDE-BIN	3.43e+01
355	1	GB14_MOUSE	GUANINE NUCLEOTIDE-BIN	3.43e+01
359	1	GB11_XENLA	GUANINE NUCLEOTIDE-BIN	3.43e+01
359	1	GB11_HUMAN	GUANINE NUCLEOTIDE-BIN	3.43e+01
359	1	GB11_MOUSE	GUANINE NUCLEOTIDE-BIN	3.43e+01
359	1	GB11_MELGA	GUANINE NUCLEOTIDE-BIN	3.43e+01
370	1	FLG1_CAUCR	FLAGELLAR P-RING PROTE	3.43e+01
401	1	ALKB_PSEOL	ALKANE-1 MONOOXYGENASE	3.43e+01
441	1	FUS6_ARATH	FUSCA PROTEIN FUS6.	3.43e+01
468	1	ASPA_HELPY	ASPARTATE AMMONIA-LYAS	3.43e+01
523	1	YTD5_PAPSO	TYROSINE/DOPA DECARBOX	3.43e+01
648	1	Y084_HUMAN	HYPOTHETICAL PROTEIN K	3.43e+01
708	1	KMK_MOUSE	MRE11 HOMOLOG.	3.43e+01
774	1	REK1_MOUSE	PUTATIVE SERINE/THREON	3.43e+01
1450	1	RP01_ASEB7	DNA-DIRECTED RNA POLYM	3.43e+01
146	1	2S5_BEREX	2S-RELATED RICH SEED S	5.39e+01
206	1	RALB_HUMAN	RAS-RELATED PROTEIN RA	5.39e+01
215	1	CAT3_STAAR	CHLORAMPHENICOL ACETYL	5.39e+01
215	1	CAT2_STAAR	CHLORAMPHENICOL ACETYL	5.39e+01
215	1	CAT_STAIN	CHLORAMPHENICOL ACETYL	5.39e+01
215	1	CAT_STRAG	CHLORAMPHENICOL ACETYL	5.39e+01
274	1	T2B1_HERAU	TYPE II RESTRICTION EN	5.39e+01
285	1	WC2B_ARATH	PLASMA MEMBRANE INTRIN	5.39e+01
285	1	WC2C_ARATH	PLASMA MEMBRANE INTRIN	5.39e+01
324	1	THI4_FUSSH	THIAZOLE BIOSYNTHETIC	5.39e+01
327	1	GSFK_ECOLI	PUTATIVE GENERAL SECRE	5.39e+01
331	1	Y244_METJA	HYPOTHETICAL PROTEIN M	5.39e+01
357	1	GBA2_DICDI	GUANINE NUCLEOTIDE-BIN	5.39e+01
369	1	KG12_YEAST	PROBABLE SERINE/THREON	5.39e+01
395	1	YKC8_CAEEL	PROBABLE NUCLEAR HORMO	5.39e+01
396	1	ASSY_METBA	ARGININOSUCCINATE SYNT	5.39e+01
432	1	AMIB_HAEIN	PROBABLE N-ACETYLMURAM	5.39e+01
489	1	CP56_YEAST	CYTCHROME P450-DIT2 (5.39e+01
548	1	ERF_HUMAN	ETS-RELATED PROTEIN ER	5.39e+01
564	1	BMRP_CANAL	BENOMYL/METHOPREXATE R	5.39e+01
593	1	PUR9_CHICK	PHOSPHORIBOSYLAMINOIM	5.39e+01
697	1	UL44_HCMVA	VLIRON PROTEIN UL104.	5.39e+01
705	1	STI3_MOUSE	OLIGOSACCHARYL TRANSFE	5.39e+01
705	1	STI3_HUMAN	OLIGOSACCHARYL TRANSFE	5.39e+01
754	1	Y4OF_RHIS	PROBABLE PEPTIDASE Y4O	5.39e+01
793	1	DCMA_METSO	CARBON MONOXIDE DEHYDR	5.39e+01
842	1	PHSH_VICFA	ALPHA-GLUCAN PHOSPHORY	5.39e+01
856	1	AAPL_YEAST	ALANINE/ARGININE AMINO	5.39e+01
863	1	YK44_YEAST	PUTATIVE 101.8 KD TRAN	5.39e+01
893	1	NIA_LEPMC	NITRATE REDUCTASE (NAD	5.39e+01

97 46 56.1 909 1 CTIA_FUSSO CUTINASE TRANSCRIPTION 5.39e+01
98 46 56.1 1480 1 PANI_YEAST PANI PROTEIN. 5.39e+01
99 46 56.1 1556 1 GLFS_VSNY3 FERREDOXIN-DEPENDENT G 5.39e+01
100 45 54.9 235 1 COLL_RAT CORTICOTROPIN-LIPOTROP 8.40e+01

ALIGNMENTS

RESULT 1
ID MAG1_HUMAN STANDARD; PRT; 309 AA.
AC P43355; O00346;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 1 (MAGE-1 ANTIGEN) (ANTIGEN MZ2-E).
GN MAGE1 OR MAGE1 OR MAGE1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92086861.
RA VAN DER BRUGGEN P., TRAVERSARI C., CHOMEZ P., LURQUIN C., DE PLAEN E.,
RA VAN DEN EYNDE B., KNUTH A., BOON T.;
RL SCIENCE 254:1643-1647(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE; 94311935.
RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA GLOCKNER G., RUMP A., NORDSIEK G., HINZMANN B., KIOSCHIS P.,
RA HEISS N., POUSTKA A., BAUER D., DRESCHER B., KNOB A., ROSENTHAL A.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP MUTAGENESIS.
RC TISSUE=LOOD;
RX MEDLINE; 94157413.
RA GAUGLER B., VAN DEN EYNDE B., VAN DER BRUGGEN P., ROMERO P.,
RA GAFORIO J.J., DE PLAEN E., LETHE B., BRASSEUR F., BOON T.;
RL J. EXP. MED. 179:921-930(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CYTOLYTIC T LYMPHOCYTES.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CARCINOMA AND BREAST CARCINOMA, *BUT NOT IN NORMAL TISSUES EXCEPT
FOR TESTES. NEVER EXPRESSED IN KIDNEY TUMORS, LEUKEMIAS AND
LYMPHOMAS.
CC -!- POLYMORPHISM: THE VARIANT AT POSITION 32 LIKELY REPRESENTS A
POLYMORPHISM OF THE MAGE-1 GENE.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
DR EMBL; M77481; G416115; -.
DR EMBL; U82672; G2078527; -.
DR MIM; 300016; -.
KW ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.
FT VARIANT 32 32 T -> A.
FT DOMAIN 33 36 POLY-SER.
FT MUTAGEN 163 163 D->A: ABOLISHES HLA-A1 BINDING.
FT MUTAGEN 169 169 Y->A: ABOLISHES HLA-A1 BINDING.
FT CONFLICT 72 72 R -> Q (IN REF. 3).
SQ SEQUENCE 309 AA; 34342 MW; E6CB1300 CRC32;

Query Match 100.0%; Score 82; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 7.13e-08;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 97 LFRVITKKVAD 108
1 LFRVITKKVAD 12

RESULT 2
ID MAG5_HUMAN STANDARD; PRT; 124 AA.
AC P43359;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 5 (MAGE-5 ANTIGEN).
GN MAGE5 OR MAGE5.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENEE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE TUMOR TRANSFORMATION
OR PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
FOR TESTES.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
DR EMBL; U10690; G533521; -.
DR EMBL; U10689; G533519; -.
KW ANTIGEN; MULTIGENE FAMILY.
FT DOMAIN 40 43 POLY-SER.
SQ SEQUENCE 124 AA; 13015 MW; 7216B8C8 CRC32;

Query Match 73.2%; Score 60; DB 1; Length 124;
Best Local Similarity 66.7%; Pred. No. 4.58e-02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 104 VFRAALSKKQAD 115
1 LFRVITKKVAD 12

RESULT 3
ID ASEL_YEAST STANDARD; PRT; 885 AA.
AC P50275;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ANAPHASE SPINDLE ELONGATION PROTEIN.
GN ASEL OR YOR058C OR YOR29-09.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMICETES.
RN [1]
RP SEQUENCE FROM N.A.
RA PELLMAN D., FINK G.R.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97279235.
RA VALENS M., BOHN C., DAIGNAN-FORNIER B., DANG V., BOLOTIN-FUKUHARA M.;
RL YEAST 13:379-390(1997).
CC -!- FUNCTION: REQUIRED FOR ANAPHASE SPINDLE ELONGATION.
DR EMBL; U20235; G972942; -.
DR EMBL; Z74966; E252338; -.
DR EMBL; Z70678; E234104; -.
DR SGD; L0000125; ASEL.
SQ SEQUENCE 885 AA; 101623 MW; FF00B6B9 CRC32;

Query Match 65.9%; Score 54; DB 1; Length 885;
Best Local Similarity 60.0%; Pred. No. 1.14e+00;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 328 FKSVLTKKVS 337

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QY      1:1:1:1:1:1:
2 FRVITKKVA 11

RESULT 4
ID YEEP_ECOLI STANDARD; PRT; 236 AA.
AC P76359; P94754;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE HYPOTHETICAL 27.1 KD PROTEIN IN COBU-SBMC INTERGENIC REGION.
GN YEEP.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
CC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RA BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 97251358.
RA ITOH T., AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T.,
RA ISONO K., KASAI H., KIMURA S., KITAKAWA M., KITAGAWA M.,
RA MAKINO K., MIKI T., MIZOBUCHI K., MORI H., MORI T., MOTOMURA K.,
RA NAKADE S., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T.,
RA SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H.,
RA TAKEIDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.;
RL DNA RES. 3:379-392(1996).
CC -1- SIMILARITY: TO E.COLI YFJP AND YKFA.
DR EMBL; AE000291; G1788308; -.
DR EMBL; D90838; G1736669; ALT_INIT.
DR ECOGENE; EG13384; YEEP.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 236 AA; 27074 MW; 69582534 CRC32;

Query Match 64.6%; Score 53; DB 1; Length 236;
Best Local Similarity 50.0%; Pred. No. 1.89e+00;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 4 LFRVVISQIID 15
QY 1 LFRVITKKVAD 12
1:1:1:1:1:1:

RESULT 5
ID TORS_ECOLI STANDARD; PRT; 904 AA.
AC P39453; P75887;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE SENSOR PROTEIN TORS (EC 2.7.3.-).
GN TORS.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
CC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC MEJEAN V.;
RA SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RA BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE OF 1-104 FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 94364937.
RA SIMON G., MEJEAN V., JOURLIN C., CHIPPAUX M., PASCAL M.-C.;
RL J. BACTERIOL. 176:5601-5606(1994).

-1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM TORS/TORR.
-1- PROBABLY ACTIVATES TORR BY PHOSPHORYLATION.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
(POTENTIAL).
-1- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
KINASES.
CC EMBL; X94231; E214041; -.
DR EMBL; AE000201; G1787227; -.
DR ECOGENE; EG12617; TORS.
KW SENSORY TRANSDUCTION; TRANSFERASE; KINASE; PHOSPHORYLATION;
RN TRANSMEMBRANE; INNER MEMBRANE.
FT TRANSMEM 323 343 POTENTIAL.
FT MOD_RES 443 443 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 761 762 QR -> HG (IN REF. 1).
SQ SEQUENCE 904 AA; 99738 MW; 6F733AB3 CRC32;

Query Match 64.6%; Score 53; DB 1; Length 904;
Best Local Similarity 54.5%; Pred. No. 1.89e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 766 LFRGIIPKVP 776
QY 1 LFRVITKKVA 11
1:1:1:1:1:1:

RESULT 6
ID YGM1_YEAST STANDARD; PRT; 126 AA.
AC P53130;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE HYPOTHETICAL 14.9 KD PROTEIN IN NAB2-ABC1 INTERGENIC REGION.
GN YGL121C.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RA LAQUIN G.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; 272643; E243349; -.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 126 AA; 14922 MW; 61575BF2 CRC32;

Query Match 63.4%; Score 52; DB 1; Length 126;
Best Local Similarity 33.3%; Pred. No. 3.13e+00;
Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 82 LYRDVLSMKSE 93
QY 1 LFRVITKKVAD 12
1:1:1:1:1:1:

RESULT 7
ID MAG4_HUMAN STANDARD; PRT; 317 AA.
AC P43358;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 4 (MAGE-4 ANTIGEN) (MAGE-X2) (MAGE-41).
GN MAGE4 OR MAGE4.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENEE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE=SKIN;
 RX MEDLINE; 94311935.
 RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95369706.
 RA IMAI Y., SHICHIJO S., YAMADA A., KATAYAMA T., YANO H., ITOH K.;
 RL GENE 160:287-290(1995).
 CC -1- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
 CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
 CC PROGRESSION.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
 CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 CC FOR TESTES AND PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY WITH
 CC MAGE-1.
 DR EMBL; U10687; G533515; -;
 DR EMBL; U10688; G533517; -;
 DR EMBL; U10340; G499124; -;
 DR EMBL; D32077; G1125018; -;
 KW ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.
 FT DOMAIN 41 44 POLY-SER.
 FT VARIANT 173 173 T -> A.
 FT CONFLICT 307 307 E -> Q (IN REF. 2).
 SQ SEQUENCE 317 AA; 34929 MW; 3CE38AF9 CRC32;

 Query Match 63.4%; Score 52; DB 1; Length 317;
 Best Local Similarity 41.7%; Pred. No. 3.13e+00;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

 Db 105 LFRALSNKYDE 116
 ||| :||| :
 QY 1 LFRAVITKKVAD 12

 RESULT 8
 ID YN21 CAEEL STANDARD; PRT; 489 AA.
 AC P34580;
 DT 01-FEB-1994 (REL. 28, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.
 GN T26G10.1.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
 RA FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
 RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
 RA LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
 RA SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
 RA WATSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROUT J.,
 RA WOHLDMAN P.;
 RL NATURE 368:32-38(1994).
 CC -1- FUNCTION: PROBABLE ATP-BINDING RNA HELICASE.
 CC -1- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
 DR EMBL; Z29115; G439260; -;
 DR PIR; S40731; S40731.
 DR WORMPEP; T26G10.1; CE00337.
 DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
 KW HYPOTHETICAL PROTEIN; HELICASE; ATP-BINDING; RNA-BINDING.
 FT DOMAIN 31 40 ASP/GLU-RICH (ACIDIC).
 FT NP_BIND 88 95 ATP (BY SIMILARITY).
 FT SITE 194 197 DEAD BOX.

FT DOMAIN 471 482 GLY-RICH.
 SQ SEQUENCE 489 AA; 54227 MW; B9EFF81A CRC32;

 Query Match 63.4%; Score 52; DB 1; Length 489;
 Best Local Similarity 63.6%; Pred. No. 3.13e+00;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

 Db 223 LFSATMTKKVS 233
 ||| :||| :
 QY 1 LFRAVITKKVA 11

 RESULT 9
 ID MAG8 HUMAN STANDARD; PRT; 234 AA.
 AC P43361;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).
 GN MAGE8 OR MAGE8.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUETHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95012457.
 RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
 RA DE SMET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,
 RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENEE W., BOON T.;
 RL IMMUNOGENETICS 40:360-369(1994).
 CC -1- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
 CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
 CC PROGRESSION.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
 CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 CC FOR TESTES AND PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE MAGE FAMILY.
 DR EMBL; U10693; G533526; -;
 KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
 FT DOMAIN 40 43 POLY-SER.
 SQ SEQUENCE 234 AA; 25197 MW; D4931BC3 CRC32;

 Query Match 62.2%; Score 51; DB 1; Length 234;
 Best Local Similarity 50.0%; Pred. No. 5.14e+00;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

 Db 107 LFRALDEKVAE 118
 ||| :||| :
 QY 1 LFRAVITKKVAD 12

 RESULT 10
 ID CC24 YEAST STANDARD; PRT; 854 AA.
 AC P11433;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE CELL DIVISION CONTROL PROTEIN 24 (CALCIUM REGULATORY PROTEIN).
 GN CDC24 OR CLS4 OR YAL041W.
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87277425.
 RA MIYAMOTO S., OHYA Y., OHSUMI Y., ANRAKU Y.;
 RL GENE 54:125-132(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE; 95249563.
 RA BUSSEY H., KABACK D.B., ZHONG W., VO D.T., CLARK M.W., FORTIN N.,
 RA HALL J., OUELLETTE B.F.F., KENG T., BARTON A.B., SU Y., DAVIES C.K.,

RA STORMS R.K.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 92:3809-3813(1995).
 RN [3]
 RP SIMILARITY TO CDC24 FAMILY.
 RX MEDLINE; 92095962.
 RA MIYAMOTO S., OHYA Y., SANO Y., SAKAGUCHI S., IIDA H., ANRAKU Y.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 181:604-610(1991).
 CC -!- FUNCTION: PROMOTES THE EXCHANGE OF CDC42-BOUND GDP BY GTP.
 CC CONTROL THE CALCIUM REGULATORY PROCESS OF BUD EMERGENCE. CDC24 MAY
 CC BE INVOLVED IN THE INITIAL SELECTION AND ORGANIZATION OF THE
 CC BUDDING SITE.
 CC -!- SIMILARITY: TO OTHER GUANINE-NUCLEOTIDE RELEASING FACTORS OF THE
 CC CDC24 FAMILY.
 CC -!- SIMILARITY: CONTAINS A PH DOMAIN.
 DR EMBL; M16809; G1100997; -.
 DR EMBL; U12980; G1101003; -.
 DR PIR; A27477; A27477.
 DR SGD; L0000262; CDC24.
 DR PROSITE; PS00741; GDS_CDC24; 1.
 DR GUANINE-NUCLEOTIDE RELEASING FACTOR.
 KW DOMAIN 478 668 PH.
 FT DOMAIN 494 600 SER/THR-RICH.
 FT DOMAIN 681 778 SER/THR-RICH.
 SQ SEQUENCE 854 AA; 96939 MW; E74FC7DC CRC32;

Query Match 62.2%; Score 51; DB 1; Length 854;
 Best Local Similarity 63.6%; Pred. No. 5.14e+00;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 517 LFSEVTKKSA 527
 QY 1 LFRVITKKVA 11

RESULT 11
 ID BOB1_YEAST STANDARD; PRT; 980 AA.
 AC P38041;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE BOB1 PROTEIN (BEM1-BINDING PROTEIN).
 GN BOB1 OR BOI1 OR YBL085W OR YBL0717.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BENDER A., BENDER L., KOKOJAN V.;
 RL SUBMITTED (APR-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE; 96076635.
 RA OBERMAIER B., GASSENHUBER J., PIRAVANDI E., DOMDEY H.;
 RL YEAST 11:1103-1112(1995).
 CC -!- FUNCTION: BINDS TO THE BEM1 PROTEIN.
 CC -!- SIMILARITY: CONTAINS A COPY OF THE SH3 DOMAIN.
 CC -!- SIMILARITY: CONTAINS A PH DOMAIN.
 DR EMBL; L31406; G466436; -.
 DR EMBL; X79489; G496694; -.
 DR EMBL; Z35846; G536138; -.
 DR PIR; S45444; S45444.
 DR SGD; L0000191; BOI1.
 DR PROSITE; PS50002; SH3; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 KW SH3 DOMAIN.
 FT DOMAIN 13 77 SH3.
 FT DOMAIN 776 895 PH.
 SQ SEQUENCE 980 AA; 109295 MW; 9987E197 CRC32;

Query Match 62.2%; Score 51; DB 1; Length 980;
 Best Local Similarity 54.5%; Pred. No. 5.14e+00;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 66 LYPAVETKRIA 76
 QY 1 LFRVITKKVA 11

RESULT 12
 ID RRP5_YEAST STANDARD; PRT; 1729 AA.
 AC Q05022;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE RNA BIOGENESIS PROTEIN RRP5.
 GN RRP5 OR FM11 OR YMR229C OR YMR959.11C.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA SKELTON J., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE; 97051828.
 RA VENEMA J., TOLLERVEY D.;
 RL EMBO J. 15:5701-5714(1996).
 CC -!- FUNCTION: INVOLVED IN THE BIOGENESIS OF RNA. REQUIRED FOR THE
 CC FORMATION OF 18S AND 5.8S RNA.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
 DR EMBL; Z49939; G887610; -.
 DR SGD; L0003232; FM11.
 KW NUCLEAR PROTEIN; RNA PROCESSING.
 SQ SEQUENCE 1729 AA; 193133 MW; F8DOB338 CRC32;

Query Match 62.2%; Score 51; DB 1; Length 1729;
 Best Local Similarity 54.5%; Pred. No. 5.14e+00;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1674 LFERITKKIT 1684
 QY 1 LFRVITKKVA 11

RESULT 13
 ID MAM2_SCHPO STANDARD; PRT; 348 AA.
 AC Q00619;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PHEROMONE P-FACTOR RECEPTOR.
 GN MAM2.
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=975;
 RX MEDLINE; 92037537.
 RA KITAMURA K., SHIMODA C.;
 RL EMBO J. 10:3743-3751(1991).
 CC -!- FUNCTION: RECEPTOR FOR THE PEPTIDE PHEROMONE P-FACTOR, A MATING
 CC OF MEIOSIS IN S.POMBE. PHEROMONE SIGNALING IS ESSENTIAL FOR INITIATION
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 4 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; X61672; G4978; -.
 DR PIR; S18521; S18521.
 DR GCRDB; GCR_0252; -.
 KW TRANSMEMBRANE; G-PROTEIN COUPLED RECEPTOR; PHEROMONE RESPONSE.
 FT TRANSMEM 46 69 POTENTIAL.
 FT TRANSMEM 79 103 POTENTIAL.
 FT TRANSMEM 125 141 POTENTIAL.
 FT TRANSMEM 162 180 POTENTIAL.
 FT TRANSMEM 207 225 POTENTIAL.


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FT TRANSMEM 249 267 POTENTIAL.
FT TRANSMEM 283 301 POTENTIAL.
SQ SEQUENCE 348 AA; 39285 MW; 68E94E15 CRC32;

Query Match 61.0%; Score 50; DB 1; Length 348;
Best Local Similarity 55.6%; Pred. No. 8.37e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 229 LFRAILIRK 237
||||:|
Qy 1 LFRAVITKK 9

RESULT 14
ID FMDH_BACNO STANDARD; PRT; 394 AA.
AC P17421.
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE POSSIBLE FIBRILLAR ASSEMBLY PROTEIN F1MD (SEROGROUP H1).
GN F1MD.
OS BACTEROIDES NODOSUS (DICHELOBACTER NODOSUS).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; ANAEROBIC RODS;
CC BACTEROIDACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SEROGROUP H1 ISOLATE VCS1215;
RX MEDLINE; 91260439.
RA HOBBS M., DALRYMPLE B.P., COX P.T., LIVINGSTONE S.P., DELANEY S.F.,
RA MATTICK J.S.;
RL MOL. MICROBIOL. 5:543-560(1991).
DR EMBL; X52390; G580812; -.
DR PIR; S15255; Y0BZDH
DR PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN1.
KW FIMBRIA.
SQ SEQUENCE 394 AA; 45105 MW; 1310A727 CRC32;

Query Match 61.0%; Score 50; DB 1; Length 394;
Best Local Similarity 72.7%; Pred. No. 8.37e+00;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 365 FRAASTKKTAD 375
|||||
Qy 2 FRAVITKKVAD 12

RESULT 15
ID BPL1_YEAST STANDARD; PRT; 690 AA.
AC P48445;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE BIOTIN--PROTEIN LIGASE (EC 6.3.4.-) (BIOTIN APO-PROTEIN LIGASE)
DE (BIOTIN--[METHYLMALONYL-COA-CARBOXYLTRANSFERASE] LIGASE (EC 6.3.4.9) /
DE BIOTIN--[PROPIONYL-COA-CARBOXYLASE (ATP-HYDROLYSING)] LIGASE
DE (EC 6.3.4.10) (HOLOCARBOXYLASE SYNTHETASE) (HCS) / BIOTIN--
DE [METHYLCROTONOYL-COA-CARBOXYLASE] LIGASE (EC 6.3.4.11) / BIOTIN--
DE [ACETYL-COA-CARBOXYLASE] LIGASE (EC 6.3.4.15)).
GN BPL1 OR ACC2 OR YDL141W OR D2140.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
CC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RX MEDLINE; 95377607.
RA CRONAN J.E. JR., WALLACE J.C.;
RL FEMS MICROBIOI. LETT. 130:221-230(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / FY1679;
RX MEDLINE; 97127826.
RA WOELFL S., HANEMAN V., SALUZ H.P.;
RL YEAST 12:1549-1554(1996).

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RN [3]
RP SEQUENCE OF 1-291 FROM N.A.
RA BARON L., LEGROS Y., BITEAU N., MONNET A., GRANOTIER C.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC FUNCTION: POSTTRANSLATIONAL MODIFICATION OF SPECIFIC PROTEIN BY
CC ATTACHMENT OF BIOTIN. ACTS ON VARIOUS CARBOXYLASES SUCH AS ACETYL-
CC COA-CARBOXYLASE, PYRUVATE CARBOXYLASE, PROPIONYL COA CARBOXYLASE,
CC AND 3-METHYLCROTONYL COA CARBOXYLASE.
CC CATALYTIC ACTIVITY: ATP + BIOTIN + APO-[METHYLMALONYL-COA:PYRUVATE
CC CARBOXYLTRANSFERASE] - AMP + DIPHOSPHATE + [METHYLMALONYL-
CC COA:PYRUVATE CARBOXYLTRANSFERASE].
CC CATALYTIC ACTIVITY: ATP + BIOTIN + APO-[PROPANOYL-COA:CARBON-
CC DIOXIDE LIGASE (ADP-FORMING)] - AMP + DIPHOSPHATE + [PROPANOYL-
CC COA:CARBON-DIOXIDE LIGASE (ADP-FORMING)].
CC CATALYTIC ACTIVITY: ATP + BIOTIN + APO-[3-METHYLCROTONOYL-
CC COA:CARBON-DIOXIDE LIGASE (ADP-FORMING)] - AMP + DIPHOSPHATE + [3-
CC METHYLCROTONOYL-COA:CARBON-DIOXIDE LIGASE (ADP-FORMING)].
CC CATALYTIC ACTIVITY: ATP + BIOTIN + APO-[ACETYL-COA:CARBON-DIOXIDE
CC LIGASE (ADP FORMING)] - AMP + DIPHOSPHATE + [ACETYL-COA:CARBON-
CC DIOXIDE LIGASE (ADP FORMING)].
CC SUBUNIT: MONOMER (BY SIMILARITY).
CC SIMILARITY: WITH E. COLI BIRA AND OTHER EUKARYOTIC BIOTIN--PROTEIN
CC LIGASES.
CC EMBL; U27182; G886081; -.
DR EMBL; X96876; E239063; -.
DR EMBL; Z74189; E253238; -.
DR SGD; L0002771; BPL1.
KW LIGASE.
SQ SEQUENCE 690 AA; 76363 MW; AA6F29D3 CRC32;

Query Match 61.0%; Score 50; DB 1; Length 690;
Best Local Similarity 50.0%; Pred. No. 8.37e+00;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 679 IPKSLIAKKV 688
:|::|:|
Qy 1 LFRAVITKKV 10

RESULT 16
ID YOUN_ECOLI STANDARD; PRT; 890 AA.
AC P39838; P47725; P47726; P76456;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PROBABLE SENSOR PROTEIN YOUN (EC 2.7.3.-).
GN YOUN.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
CC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RA BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 97251358.
RA ITOH T., AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T.,
RA ISONO K., KASAI H., KIMURA S., KITAKAWA M., KITAGAWA M.,
RA MAKINO K., MIKI T., MIZOBUCHI K., MORI H., MORI T., MOTOMURA K.,
RA NAKADE S., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T.,
RA SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H.,
RA TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.;
RL DNA RES. 3:379-392(1996).
RN [3]
RP SEQUENCE OF 1-596 FROM N.A.
RC STRAIN-K12 / EMG2;
RA ROBISON K., ESTEP P.E., O'KEEFE T., CHURCH G.M.;
RL SUBMITTED (OCT-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE OF 593-890 FROM N.A.

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RC STRAIN-K12;
RX MEDLINE: 90130299.
RA STOUT V., GORTESMAN S.;
RL J. BACTERIOL. 172:659-669(1990).
RN [5]
RP IDENTIFICATION.
RX MEDLINE: 95075659.
RA BORODOVSKY M., RUDD K.E., KOONIN E.V.;
RL NUCLEIC ACIDS RES. 22:4756-4767(1994).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (PROBABLY).
CC -!- PTM: ACTIVATION PROBABLY REQUIRES A TRANSFER OF A PHOSPHATE GROUP
CC BETWEEN A HIS IN THE TRANSMITTER DOMAIN AND A ASP OF THE RECEIVER
CC DOMAIN (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
CC KINASES.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
CC IN POSITIONS 145 AND 488.
CC -!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
CC IN POSITIONS 597 AND 702.
DR EMBL; AE000310; G1788545; -.
DR EMBL; D90850; G1736857; -.
DR EMBL; U38659; G1054951; ALT_FRAME.
DR EMBL; U38659; G1054952; ALT_FRAME.
DR EMBL; U38659; G1054953; ALT_FRAME.
DR EMBL; M28242; -; NOT_ANNOTATED_CDS.
DR ECGENE; EG12385; YOUN.
KW HYPOTHETICAL PROTEIN; SENSORY TRANSDUCTION; TRANSFERASE; KINASE;
FT PHOSPHORYLATION; TRANSMEMBRANE; INNER MEMBRANE.
FT DOMAIN 1 21
CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 22 42
POTENTIAL.
FT DOMAIN 43 308
PERIPLASMIC (POTENTIAL).
FT TRANSMEM 309 329
POTENTIAL.
FT DOMAIN 330 890
CYTOPLASMIC (POTENTIAL).
FT CONFLICT 61 61
Q -> L (IN REF. 3).
FT CONFLICT 164 164
K -> E (IN REF. 3).
FT CONFLICT 174 174
T -> A (IN REF. 3).
FT CONFLICT 176 176
S -> N (IN REF. 3).
FT CONFLICT 179 179
V -> G (IN REF. 3).
FT CONFLICT 184 184
A -> T (IN REF. 3).
FT CONFLICT 267 267
T -> A (IN REF. 3).
FT CONFLICT 598 599
ES -> DA (IN REF. 4).
SQ SEQUENCE 890 AA; 100372 MW; 6D5BF6A8 CRC32;

Query Match 61.0%; Score 50; DB 1; Length 890;
Best Local Similarity 60.0%; Pred. No. 8.37e+00;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 377 RTVISNKIAD 386

Qy 3 RAVITKKVAD 12

1:|||||

RESULT 17
ID PPS2_BACSU STANDARD; PRT; 2560 AA.
AC P39846;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PEPTIDE SYNTHETASE 2.
GN PPSB OR PPS2.
OS BACILLUS SUBTILIS.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE; 95227362.
RA TOGNONI A., FRANCHI E., MAGISTRELLI C., COLOMBO E., COSMINA P.,
RA GRANDI G.;
RL MICROBIOLOGY 141:645-648(1995).
CC -!- COFACTOR: CONTAINS A COVALENTLY BOUND PHOSPHOPANTHETHEINE
CC (POTENTIAL).
CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT

CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
DR EMBL; 234883; G509469; -.
DR SUBTILIST; BG10971; PPSB.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
DR PROSITE; PS00455; AMP_BINDING; 2.
DR PROSITE; PS00075; ACP_DOMAIN; 2.
KW MULTIFUNCTIONAL ENZYME; LIGASE; REPEAT; PHOSPHOPANTHETHEINE.
FT BINDING 2041 2041 PHOSPHOPANTHETHEINE (POTENTIAL).
SQ SEQUENCE 2560 AA; 290161 MW; 9BAA32F6 CRC32;

Query Match 61.0%; Score 50; DB 1; Length 2560;
Best Local Similarity 41.7%; Pred. No. 8.37e+00;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 63 IFRITFIKEVPD 74

Qy 1 LFRAVITKKVAD 12

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RESULT 18
ID VGLL_HSV2H STANDARD; PRT; 224 AA.
AC P28278;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN L PRECURSOR.
GN GL OR ULL.
OS HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92113549.
RA MCGEOCH D.J., CUNNINGHAM C., MCINTYRE G., DOLAN A.;
RL J. GEN. VIROL. 72:3057-3075(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA DOLAN A.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: ASSOCIATED WITH GLYCOPROTEIN H (GH) TO FORM A COMPLEX
CC IMPORTANT FOR INFECTION AND CELL FUSION (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN L.
DR EMBL; D10470; G221792; -.
DR EMBL; 286099; E304262; -.
DR PIR; JQ1494; WMBHG.
KW GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 ?
FT CHAIN ? 224
GLYCOPROTEIN L.
FT CARBOHYD 170 170
POTENTIAL.
SQ SEQUENCE 224 AA; 25192 MW; 943BCE65 CRC32;

Query Match 59.8%; Score 49; DB 1; Length 224;
Best Local Similarity 50.0%; Pred. No. 1.35e+01;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 27 VLRSVIAKEVGD 38

Qy 1 LFRAVITKKVAD 12

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RESULT 19
ID DAPD_ACTPL STANDARD; PRT; 274 AA.
AC P41396;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE 2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE
DE (EC 2.3.1.117) (TETRAHYDRODIPICOLINATE N-SUCCINYLTRANSFERASE)
DE (THP SUCCINYLTRANSFERASE) (TETRAHYDRODIPICOLINATE SUCCINYLASE).
GN DAPD.
OS ACTINOBACILLUS PLEUROPSAUMONIAE (HAEMOPHILUS PLEUROPSAUMONIAE).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURACEAE.
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-4074;
 RX MEDLINE; 94224145.
 RA LALONDE G., O'HANLEY P.D., STOCKER B.A., DENICH K.;
 RL MOL. MICROBIOL. 11:273-280(1994).
 CC -1- CATALYTIC ACTIVITY: SUCCINYL-COA + 2,3,4,5-TETRAHYDROPYRIDINE-
 CC 2-CARBOXYLATE = COA + N-SUCCINYL-L-2-AMINO-6-OXOHEPTANEDIOATE.
 CC -1- PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF DIAMINOPIMELATE AND
 CC LYSINE FROM ASPARTATE SEMIALDEHYDE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 DR EMBL; X63201; G38947; -.
 DR PROSITE; PS00101; HEXAPEP TRANSFERASES; 1.
 KW TRANSFERASE; ACYLTRANSFERASE; REPEAT; LYSINE BIOSYNTHESIS;
 KW DIAMINOPIMELATE BIOSYNTHESIS.
 SQ SEQUENCE 274 AA; 29761 MW; 80E49D1C CRC32;
 Query Match 59.8%; Score 49; DB 1; Length 274;
 Best Local Similarity 70.08; Pred. No. 1.35e+01;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 246 LYCAVITKVV 255
 I: ||| |||
 QY 1 LFRVITKVV 10
 RESULT 20
 ID DAPD.ECOLI STANDARD; PRT; 274 AA..
 AC P03948;
 DT 23-OCT-1986 (REL. 02, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE 2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE
 DE (EC 2.3.1.117) (TETRAHYDRODIPICOLINATE N-SUCCINYLTRANSFERASE)
 DE (THP SUCCINYLTRANSFERASE) (TETRAHYDRODIPICOLINATE SUCCINYLASE).
 GN DAPD.
 OS ESCHERICHIA COLI.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85054973.
 RA RICHARD C., RICHARD F., MARTIN C., HAZIZA C., PATTE J.-C.;
 RL J. BIOL. CHEM. 259:14824-14828(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / W3110;
 RX MEDLINE; 94261430.
 RA FUJITA N., MORI H., YURA T., ISHIHAMA A.;
 RL NUCLEIC ACIDS RES. 22:1637-1639(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RA BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA SCHRAMM S., DUNCAN M., ALLEN E., ARAUJO R., APARICIO A., CHUNG E.,
 RA DAVIS K., FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O.,
 RA LASHKARI D., LEW H., LIN D., NAMATH A., OEFNER P., ROBERTS D.,
 RA DAVIS R.W.;
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [5]
 RP SEQUENCE OF 1-15 FROM N.A.
 RC STRAIN-K12 / W3110;
 RX MEDLINE; 94018640.
 RA VAN HEESWIJK W.C., RABENBERG M., WESTERHOFF H.V., KAHN D.D.;
 RL MOL. MICROBIOL. 9:443-458(1993).
 RN [6]
 RP SEQUENCE OF 1-11.
 RC* STRAIN-K12 / W3110;
 RA PASQUALI C., SANCHEZ J.-C., RAVIER F., GOLAZ O., HUGHES G.J.,

RA FRUTIGER S., PAQUET N., WILKINS M., APPEL R.D., BAIRIOCH A.,
 RA HOCHSTRASSER D.F.;
 RL SUBMITTED (SEP-1994) TO THE SWISS-PROT DATA BANK.
 RN [7]
 RP SEQUENCE OF 1-12.
 RC STRAIN-K12 / EMG2;
 RA LINK A.J.;
 RL SUBMITTED (OCT-1994) TO THE SWISS-PROT DATA BANK.
 CC -1- CATALYTIC ACTIVITY: SUCCINYL-COA + 2,3,4,5-TETRAHYDROPYRIDINE-
 CC 2-CARBOXYLATE = COA + N-SUCCINYL-L-2-AMINO-6-OXOHEPTANEDIOATE.
 CC -1- PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF DIAMINOPIMELATE AND
 CC LYSINE FROM ASPARTATE SEMIALDEHYDE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 DR EMBL; K02970; G145712; -.
 DR EMBL; D26562; G473821; -.
 DR EMBL; AE000126; G1786362; -.
 DR EMBL; U70214; G1552743; -.
 DR EMBL; Z21842; G49394; -.
 DR PIR; A00601; XNECSD.
 DR SWISS-2DPAGE; P03948; COLI.
 DR ECGENE; EG10207; DAPD.
 DR PROSITE; PS00101; HEXAPEP TRANSFERASES; 1.
 KW TRANSFERASE; ACYLTRANSFERASE; REPEAT; LYSINE BIOSYNTHESIS;
 KW DIAMINOPIMELATE BIOSYNTHESIS.
 FT CONFLICT 31 31 V -> D (IN REF. 1).
 FT CONFLICT 163 163 G -> R (IN REF. 1).
 FT CONFLICT 177 177 I -> M (IN REF. 1).
 FT CONFLICT 190 190 V -> L (IN REF. 1).
 SQ SEQUENCE 274 AA; 29892 MW; 4C9DF5CE CRC32;
 Query Match 59.8%; Score 49; DB 1; Length 274;
 Best Local Similarity 70.08; Pred. No. 1.35e+01;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 247 LYCAVITKVV 256
 I: ||| |||
 QY 1 LFRVITKVV 10
 RESULT 21
 ID DAPD.HAEIN STANDARD; PRT; 275 AA..
 AC P45284;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE 2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE
 DE (EC 2.3.1.117) (TETRAHYDRODIPICOLINATE N-SUCCINYLTRANSFERASE)
 DE (THP SUCCINYLTRANSFERASE) (TETRAHYDRODIPICOLINATE SUCCINYLASE).
 GN DAPD OR H1634.
 OS HAEMOPHILUS INFLUENZAE.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC PASTEURILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20;
 RX MEDLINE; 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T.T., HEDBLUM E., COTTON M.D.,
 RA UTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RL SCIENCE 269:496-512(1995).
 CC -1- CATALYTIC ACTIVITY: SUCCINYL-COA + 2,3,4,5-TETRAHYDROPYRIDINE-
 CC 2-CARBOXYLATE = COA + N-SUCCINYL-L-2-AMINO-6-OXOHEPTANEDIOATE.
 CC -1- PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF DIAMINOPIMELATE AND
 CC LYSINE FROM ASPARTATE SEMIALDEHYDE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 DR EMBL: U32836; G1574480; ALT INIT.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 DR TIGR: H11634; -.
 KW TRANSFERASE; ACYLTRANSFERASE; REPEAT; LYSINE BIOSYNTHESIS;
 KW DIAMINOPIMELATE BIOSYNTHESIS.
 SQ SEQUENCE 275 AA; 29723 MW; E5F6024D CRC32;

Query Match 59.88; Score 49; DB 1; Length 275;
 Best Local Similarity 70.0%; Pred. No. 1.35e+01;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 247 LYCAVIVKKV 256
 I: ||| |||
 QY 1 LFRVITKKV 10

RESULT 22
 ID GBALCRYN STANDARD; PRT; 432 AA.
 AC P54853;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA SUBUNIT.
 GN GPAL.
 OS CRYPTOCOCCUS NEOFORMANS (FILOBASIDIELLA NEOFORMANS).
 OC EUKARYOTA; FUNGI; BASIDIOMYCOTINA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 42163;
 RX MEDLINE: 94274301.
 RA TOLKACHEVA T., MCNAMARA P., PIEKARZ E., COURCHESNE W.;
 RL INFECT. IMMUN. 62:2849-2856(1994).
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
 CC INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
 CC SIGNALING SYSTEMS. INVOLVED IN THE MATING PATHWAY.
 CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
 CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
 CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY.
 DR EMBL: U09372; G53374; -.
 KW GTP-BINDING; TRANSDUCER; MYRISTYLATION.
 FT INIT MET 0 0 BY SIMILARITY.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT NP_BIND 118 125 GTP (BY SIMILARITY).
 FT NP_BIND 279 283 GTP (BY SIMILARITY).
 FT NP_BIND 348 351 GTP (BY SIMILARITY).
 SQ SEQUENCE 432 AA; 47848 MW; 7650F9E0 CRC32;

Query Match 59.88; Score 49; DB 1; Length 432;
 Best Local Similarity 63.6%; Pred. No. 1.35e+01;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 147 FRGVYKVVLD 157
 I: ||| |||
 QY 2 FRVITKKVAD 12

RESULT 23
 ID ECHB RAT STANDARD; PRT; 475 AA.
 AC Q60587;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE MITOCHONDRIAL TRIFUNCTIONAL ENZYME BETA SUBUNIT PRECURSOR (CONTAINS:
 DE 3-KETOACYL-COA THIOLASE (EC 2.3.1.16) (ACETYL-COA ACYLTRANSFERASE)
 DE (BETA-KETOTHIOLASE)) (TP-BETA).
 GN HADHB.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-WISTAR;
 RX MEDLINE: 94075334.
 RA KAMIJO T., AOYAMA T., MIYAZAKI J., HASHIMOTO T.;
 RL J. BIOL. CHEM. 268:26452-26460(1993).
 CC -!- CATALYTIC ACTIVITY: ACYL-COA + ACETYL-COA - COA + 3-OXOACYL-COA.
 CC -!- PATHWAY: THIRD STEP OF THE FATTY ACID BETA-OXIDATION CYCLE.
 CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 CC -!- SIMILARITY: BELONGS TO THE THIOLASE FAMILY.
 DR EMBL: D16479; G510110; -.
 DR PROSITE: PS00098; THIOLASE_1; 1.
 DR PROSITE: PS00099; THIOLASE_3; 1.
 DR PROSITE: PS00737; THIOLASE_2; 1.
 KW FATTY ACID METABOLISM; TRANSFERASE; ACYLTRANSFERASE; MITOCHONDRION;
 TRANSIT PEPTIDE.
 FT TRANSIT 1 34 MITOCHONDRION (POTENTIAL).
 FT CHAIN 35 475 3-KETOACYL-COA THIOLASE BETA-SUBUNIT OF
 FT TRIFUNCTIONAL PROTEIN.
 FT ACT_SITE 139 139 SUBSTRATE BINDING (BY SIMILARITY).
 FT ACT_SITE 459 459 BASE (BY SIMILARITY).
 SQ SEQUENCE 475 AA; 51414 MW; BEBF9109 CRC32;

Query Match 59.8%; Score 49; DB 1; Length 475;
 Best Local Similarity 50.0%; Pred. No. 1.35e+01;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 89 LYRTNIPKDVVD 100
 I: | | | | |
 QY 1 LFRVITKKVAD 12

RESULT 24
 ID CTK1 YEAST STANDARD; PRT; 528 AA.
 AC Q03957;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE CTD KINASE ALPHA SUBUNIT (EC 2.7.1.-) (CTD KINASE 58 KD SUBUNIT)
 DE (CTDK-I ALPHA SUBUNIT).
 GN CTK1 OR YKL139W.
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92314702.
 RA LEE J.M., GREENLEAF A.L.;
 RL GENE EXPR. 1:149-167(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA RAD M.R., XU G., KIRCHRATH L., FRITZ C., KEUCHEL H., HOLLENBERG C.P.;
 RL SUBMITTED (MAR-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- FUNCTION: CTDK-I HYPERPHOSPHORYLATES THE CARBOXYL-TERMINAL REPEAT
 CC DOMAIN (CTD) OF RNA POLYMERASE II LARGEST SUBUNIT. THIS PROTEIN IS
 CC THE CATALYTIC SUBUNIT.
 CC -!- SUBUNIT: CONSISTS OF THREE SUBUNITS (ALPHA, BETA, GAMMA) OF 58,
 CC 38, AND 32 KD, RESPECTIVELY.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- SIMILARITY: BELONGS TO THE CDC2/CDC28 SUBFAMILY OF SER/THR
 CC PROTEIN KINASES.
 DR EMBL: M69024; G171328; -.
 DR EMBL: Z28139; G486235; -.
 DR PIR: S32593; S32593.
 DR SGD: L0000432; CTK1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
 NUCLEAR PROTEIN; PHOSPHORYLATION.
 FT DOMAIN 37 44 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 183 469 PROTEIN KINASE.
 FT NP_BIND 189 197 ATP (BY SIMILARITY).
 FT BINDING 212 212 ATP (BY SIMILARITY).
 FT ACT_SITE 306 306 BY SIMILARITY.

FT DOMAIN 506 528 ASN/ASP-RICH.
FT MOD_RES 14 14 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 528 AA; 60501 MW; 48629C3C CRC32;

Query Match 59.8%; Score 49; DB 1; Length 528;
Best Local Similarity 66.7%; Pred. No. 1.35e+01;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 162 RSVIAKVP 170
|:|:|:|:|:
Qy 3 RAVITKKVA 11

RESULT 25
ID KML2CHICK STANDARD; PRT; 1906 AA.
AC P19038;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE (BC 2.7.1.117).
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96033976.
RA WATTESON D.M., COLLINGE M., LUKAS T.J., VAN ELDIK L.J.,
RA BRUKOV K.G., STEPANOVA O.V., SHIRINSKY V.P.;
RL FEBS LETT. 373:217-220(1995).
RN [2]
RP SEQUENCE FROM N.A. (MLCK-108).
RX MEDLINE: 90192792.
RA OLSON N.J., PEARSON R.B., NEEDLEMAN D.S., HURWITZ M.J., KEMP B.E.,
RA MEANS A.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2284-2288(1990).
RN [3]
RP SEQUENCE OF 649-1906 FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE-FIBROBLAST;
RX MEDLINE: 90361738.
RA SHOEMAKER M.O., LAU W., SHATTUCK R.L., KWIATKOWSKI A.P.,
RA MATRISIAN P.E., GUERRA-SANTOS L., WILSON E., LUKAS T.J.,
RA VAN ELDIK L.J., WATTESON D.M.;
RL J. CELL BIOL. 111:1107-1125(1990).
CC -!- FUNCTION: MLCK PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS
OF A MYOSIN LIGHT CHAIN, WHICH LEADS TO THE FORMATION CALMODULIN/
MLCK SIGNAL TRANSDUCTION COMPLEXES WHICH ALLOW SELECTIVE
TRANSDUCTION OF CALCIUM SIGNALS.
CC -!- CATALYTIC ACTIVITY: ATP + [MYOSIN LIGHT-CHAIN] = ADP + [MYOSIN
LIGHT-CHAIN] PHOSPHATE.
CC -!- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS
BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING
FRAME.
CC EMBL: X52876; G992993; -.
DR EMBL: X52876; G992994; -.
DR EMBL: M31048; G212661; -.
DR PIR: A37099; A37099.
DR PIR: S11652; S11652.
DR HSP: P02593; ICDL.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; CALMODULIN-BINDING;
KW ATP-BINDING; PHOSPHORYLATION; REPEAT; ALTERNATIVE INITIATION.
FT CHAIN 1 1906 MLCK-210.
FT CHAIN 935 1906 MLCK-108.
FT DOMAIN 1453 1708 PROTEIN KINASE.
FT NP_BIND 1459 1467 ATP (BY SIMILARITY).
FT BINDING 1482 1482 ATP (BY SIMILARITY).
FT ACT_SITE 1574 1574 BY SIMILARITY.
FT DOMAIN 1716 1728 CALMODULIN AUTOINHIBITION (AM13) REGION
(POTENTIAL).
FT* DOMAIN 1730 1749 CALMODULIN RECOGNITION (RS20) REGION
(POTENTIAL).
FT

FT DOMAIN 1317 1364 MOTIF IA.
FT DOMAIN 1385 1402 MOTIF IB.
FT DOMAIN 560 1833 4 X REPEATS, MOTIF IIA.
FT REPEAT 560 576 IIA-1.
FT REPEAT 758 774 IIA-2.
FT REPEAT 1107 1123 IIA-3.
FT REPEAT 1817 1833 IIA-4.
FT DOMAIN 693 1866 5 X REPEATS, MOTIF IIB.
FT REPEAT 693 708 IIB-1.
FT REPEAT 791 807 IIB-2.
FT REPEAT 1140 1156 IIB-3.
FT REPEAT 1281 1297 IIB-4.
FT REPEAT 1851 1866 IIB-5.
FT DOMAIN 970 1226 4 X REPEATS, MOTIF III.
FT REPEAT 970 987 III-1.
FT REPEAT 999 1016 III-2.
FT REPEAT 1061 1078 III-3.
FT REPEAT 1209 1226 III-4.
FT MOD_RES 1748 1748 PHOSPHORYLATION.
FT MOD_RES 1762 1762 PHOSPHORYLATION.
SQ SEQUENCE 1906 AA; 210445 MW; 0D2515AE CRC32;

Query Match 59.8%; Score 49; DB 1; Length 1906;
Best Local Similarity 50.0%; Pred. No. 1.35e+01;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 909 FRDILGKKVS 918
|:|:|:|:|:
Qy 2 FRVITKKVA 11

RESULT 26
ID Y226_METJA STANDARD; PRT; 193 AA.
AC Q57679;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN MJ0226.
CN MJ0226.
OS METHANOCOCCUS JANNASCHII.
OC ARCHAEABACTERIA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96337999.
RA BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.F., ADAMS M.D., REICH C.I.,
RA OVERBEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
RA SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
RA COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESSE C.R., VENTER J.C.;
RL SCIENCE 273:1058-1073(1996).
CC -!- SIMILARITY: TO YEAST HAM1.
DR EMBL: U67478; G1590963; -.
DR TIGR: MJ0226; -.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 193 AA; 22202 MW; DF81189B CRC32;

Query Match 58.5%; Score 48; DB 1; Length 193;
Best Local Similarity 25.0%; Pred. No. 2.16e+01;
Matches 3; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 129 LFKGIVGRVSE 140
|:|:|:|:|:
Qy 1 LFRVITKKVAD 12

RESULT 27
ID FLIP_CAUCR STANDARD; PRT; 266 AA.
AC Q45980;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE FLAGELLAR BIOSYNTHETIC PROTEIN FLIP.
 GN FLIP.
 OS CAULOBACTER CRESCENTUS.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; BUDDING AND/OR APPENDAGED.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CB15;
 RX MEDLINE: 95325304.
 RA GOBER J.W., BOYD C.H., JARVIS M., MANGAN E.K., RIZZO M.F.,
 RA WINGROVE J.A.;
 RL J. BACTERIOL. 177:3656-3667(1995).
 CC -!- FUNCTION: PLAYS A ROLE IN THE FLAGELLUM-SPECIFIC TRANSPORT SYSTEM
 CC (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
 DR EMBL: U20387; G841253; -.
 DR PROSITE: PS01060; FLIP_1; 1.
 DR PROSITE: PS01061; FLIP_2; 1.
 KW FLAGELLA; TRANSMEMBRANE.
 FT TRANSMEM 20 40 POTENTIAL.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 102 122 POTENTIAL.
 FT TRANSMEM 202 222 POTENTIAL.
 FT TRANSMEM 226 246 POTENTIAL.
 SQ SEQUENCE 266 AA; 28527 MW; C506FCD8 CRC32;

 Query Match 58.5%; Score 48; DB 1; Length 266;
 Best Local Similarity 50.0%; Pred. No. 2.16e+01;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

 Db 5 LFKSVIGAKAED 16
 QY 1 LFRVITKKVAD 12

 RESULT 28
 ID TH14_FUSOX STANDARD; PRT; 320 AA.
 AC P23618;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE THIAZOLE BIOSYNTHETIC ENZYME (STRESS-INDUCIBLE PROTEIN STI35).
 GN STI35.
 OS FUSARIUM OXYSPORUM.
 OC EUKARYOTA; FUNGI; DEUTEROMYCOTINA (IMPERFECT FUNGI).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SP. CUCUMERINUM OWEN, ISOLATE B1-GK;
 RX MEDLINE: 90330561.
 RA CHOI G.H., MAREK E.T., SCHARDL C.L., RICHEY M.G., CHANG S.,
 RA SMITH D.A.;
 RL J. BACTERIOL. 172:4522-4528(1990).
 CC -!- FUNCTION: INVOLVED IN BIOSYNTHESIS OF THE THIAMINE PRECURSOR
 CC THIAZOLE (BY SIMILARITY).
 CC -!- INDUCTION: BY ETHANOL, COPPER(II) CHLORIDE AND HEAT.
 CC -!- SIMILARITY: BELONGS TO THE TH14 FAMILY OF ENZYMES.
 DR EMBL: M33643; G168164; -.
 DR PIR: B37767; B37767.
 KW THIAMIN BIOSYNTHESIS; HEAT SHOCK.
 SQ SEQUENCE 320 AA; 34579 MW; 94180D07 CRC32;

 Query Match 58.5%; Score 48; DB 1; Length 320;
 Best Local Similarity 58.3%; Pred. No. 2.16e+01;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

 Db 118 LFSAMIMRKPAD 129
 QY 1 LFRVITKKVAD 12

 RESULT 29
 ID B3AR_CAVPO STANDARD; PRT; 351 AA.

AC Q60483;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE BETA-3 ADRENERGIC RECEPTOR (FRAGMENT).
 GN ADRE3.
 OS CAVIA PORCELLUS (GUINEA PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 97151378.
 RX TISSUE=LIVER;
 RA ATGIE C., TAVERNIER G., D'ALLAIRE F., BENGTSSON T., MARTI L.,
 RA CARPENE C., LAFONTAN M., BUKOWIECKI L.J., LANGIN D.;
 RL AM. J. PHYSIOL. 271:R179-R1738(1996).
 CC -!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
 CC PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
 CC THERMOGENESIS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: WHITE AND BROWN ADIPOSE TISSUES.
 CC -!- THE GUINEA PIG DIFFERS FROM OTHER RODENTS BY AN ABSENCE OF BETA-3
 CC ADRENERGIC EFFECTS AND BY LOW EXPRESSION IN BROWN AND WHITE
 CC ADIPOSE TISSUES. IT IS CLOSER TO HUMAN OR PRIMATE THAN RODENT
 CC BETA-3.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: U51098; G1256416; -.
 DR PROSITE: PS02337; G-PROTEIN_RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KW MULTIGENE FAMILY.
 FT DOMAIN 1 36 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 37 60 1 (POTENTIAL).
 FT DOMAIN 61 69 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 70 88 2 (POTENTIAL).
 FT DOMAIN 89 108 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 109 130 3 (POTENTIAL).
 FT DOMAIN 131 152 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 153 175 4 (POTENTIAL).
 FT DOMAIN 176 200 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 201 222 5 (POTENTIAL).
 FT DOMAIN 223 290 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 291 312 6 (POTENTIAL).
 FT DOMAIN 313 324 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 325 345 7 (POTENTIAL).
 FT DOMAIN 346 >351 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 107 186 BY SIMILARITY.
 FT CARBOHYD 8 8 POTENTIAL.
 FT CARBOHYD 26 26 POTENTIAL.
 FT NON_TER 351 351
 SQ SEQUENCE 351 AA; 37364 MW; 72E17433 CRC32;

 Query Match 58.5%; Score 48; DB 1; Length 351;
 Best Local Similarity 62.5%; Pred. No. 2.16e+01;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

 Db 142 YRAVYTKR 149
 QY 2 FRAVITKK 9

 RESULT 30
 ID FADH_METMR STANDARD; PRT; 424 AA.
 AC P47734;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1) (FDH)
 DE (FALDH).
 OS METHYLOBACTER MARINUS.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
 OC METHYLOCOCCACEAE.

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RN  SEQUENCE FROM N.A.
RP  STRAIN=A45;
RX  MEDLINE: 95011501.
RA  SPER B.S., CHISTOSEROVA L., LIDSTROM M.E.;
RL  FEMS MICROBIOL. LETT. 121:349-355(1994).
CC  -1- CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NAD(+) =
CC  S-FORMYLGLUTATHIONE + NADH.
CC  -1- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (POTENTIAL).
CC  -1- COFACTOR: EQUALLY ACTIVE ON NAD AND NADP.
CC  -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC  -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC  FAMILY. BELONGS TO THE ADH CLASS-III SUBFAMILY.
DR  EMBL: L33464; G496118; -.
DR  PROSITE: PS00059; ADH_ZINC; 1.
KW  OXIDOREDUCTASE; ZINC; NAD; NADP.
FT  METAL 72 72 ZINC (CATALYTIC) (BY SIMILARITY).
FT  METAL 94 94 ZINC (CATALYTIC) (BY SIMILARITY).
FT  METAL 124 124 ZINC (SECOND ATOM) (BY SIMILARITY).
FT  METAL 127 127 ZINC (SECOND ATOM) (BY SIMILARITY).
FT  METAL 130 130 ZINC (SECOND ATOM) (BY SIMILARITY).
FT  METAL 138 138 ZINC (SECOND ATOM) (BY SIMILARITY).
SQ  SEQUENCE 424 AA; 46033 MW; 5DAB3AD0 CRC32;

Query Match 58.5%; Score 48; DB 1; Length 424;
Best Local Similarity 62.5%; Pred. No. 2.16e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 LFRSVVVK 36
QY 1 LFRAVITK 8

RESULT 31
ID RSP3_CHLRE STANDARD; PRT; 516 AA.
AC P12759;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE RADIAL SPOKE PROTEIN 3.
GN RSP3.
OS CHLAMYDOMONAS REINHARDTII.
OC EUKARYOTA; PLANTA; PHYCOPHYTA; CHLOROPHYTA (GREEN ALGAE);
OC CHLOROPHYCEAE; VOLVOCALES; CHLAMYDOMONADACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89308863.
RA WILLIAMS B.D., VELLECA M.A., CURRY A.M., ROSENBAUM J.L.;
RL J. CELL BIOL. 109:235-245(1989).
CC -1- FUNCTION: PROTEIN 3 MAY ATTACH THE RADIAL SPOKE TO THE OUTER
CC DOUBLET MICROTUBULE OR IS REQUIRED TO FORM A STABLE SPOKE
CC STRUCTURE.
CC -1- FUNCTION: FLAGELLAR RADIAL SPOKES CONTRIBUTE TO THE REGULATION
CC OF DYNEIN ARM ACTIVITY AND THUS THE PATTERN OF FLAGELLAR BENDING.
CC THEY CONSIST OF A THIN STALK, WHICH IS ATTACHED TO THE A SUBRIBER
CC OF THE OUTER DOUBLET MICROTUBULE, AND A BULBOUS HEAD, WHICH IS
CC ATTACHED TO THE STALK AND APPEARS TO INTERACT WITH THE
CC PROJECTIONS FROM THE CENTRAL PAIR OF MICROTUBULES.
CC -1- SUBCELLULAR LOCATION: RADIAL SPOKE.
CC -1- PTM: PROTEIN 3 IS ONE OF THE 5 RADIAL SPOKE PROTEINS THAT ARE
CC PHOSPHORYLATED.
CC -1- PTM: THE ISOFORM PROTEIN 3A MIGHT BE SIMPLY THE UNPHOSPHORYLATED
CC POLYPEPTIDE.
DR EMBL: X14549; G18218; -.
DR PIR: S05962; S05962.
DR PIR: A31270; A31270.
KW FLAGELLA; PHOSPHORYLATION.
SQ SEQUENCE 516 AA; 56784 MW; 9768D176 CRC32;

Query Match 58.5%; Score 48; DB 1; Length 516;
Best Local Similarity 41.7%; Pred. No. 2.16e+01;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Db 290 LARGWARRVVD 301
QY 1 LFRAVITK 12

RESULT 32
ID AMYM_BACLI STANDARD; PRT; 578 AA.
AC Q04977;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE MALTOGENIC ALPHA-AMYLASE PRECURSOR (EC 3.2.1.133) (GLUCAN 1,4-ALPHA-
DE MALTOHYDROLASE).
GN BLMA.
OS BACILLUS LICHENIFORMIS.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27811;
RX MEDLINE: 93054487.
RA KIM I.C., CHA J.H., KIM J.R., JANG S.Y., SEO B.C., CHEONG T.K.,
RA LEE D.S., CHOI Y.D., PARK K.H.;
RL J. BIOL. CHEM. 267:22108-22114(1992).
CC -1- FUNCTION: CONVERTS STARCH INTO MALTOSE. IN CONTRARY TO OTHER
CC MALTOGENIC ALPHA-AMYLASES BLMA CANNOT HYDROLYSE 1,4-ALPHA-
CC GLUCOSIDIC LINKAGE NEXT TO 1,6-ALPHA-GLUCOSIDIC LINKAGES.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-ALPHA-D-GLUCOSIDIC LINKAGES
CC IN POLYSACCHARIDES SO AS TO REMOVE SUCCESSIVE ALPHA-MALTOSE UNITS
CC FROM THE NON-REDUCING ENDS OF THE CHAINS.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
DR EMBL: X67133; G39564; -.
DR PIR: A44326; A44326.
KW HYDROLASE; GLYCOSIDASE; CARBOHYDRATE METABOLISM; SIGNAL.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN ? 578 MALTOGENIC ALPHA-AMYLASE.
SQ SEQUENCE 578 AA; 66924 MW; E5888900 CRC32;

Query Match 58.5%; Score 48; DB 1; Length 578;
Best Local Similarity 50.0%; Pred. No. 2.16e+01;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 221 LFRVTVSR 228
QY 1 LFRAVITK 8

RESULT 33
ID YAJ3_SCHPO STANDARD; PRT; 754 AA.
AC Q09903;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.
GN SPAC30D11.03.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA PEARSON D., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: PUTATIVE ATP-DEPENDENT RNA HELICASE.
CC -1- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.
DR EMBL: Z67961; E209203; -.
DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
KW HYPOTHETICAL PROTEIN; ATP-BINDING; RNA-BINDING; HELICASE.
FT NP_BIND 303 310 ATP (POTENTIAL).
FT SITE 412 415 DEAD BOX.
SQ SEQUENCE 754 AA; 85452 MW; 5D3AA652 CRC32;

Query Match 58.5%; Score 48; DB 1; Length 754;

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Best Local Similarity 58.3%; Pred. No. 2.16e+01;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 441 LFSATMTDKVDD 452
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QY 1 LFRVITKKVAD 12

RESULT 34
ID RM39_YEAST STANDARD; PRT; 69 AA.
AC P36533;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L39 (YML39).
GN MRPL39 OR YML009C OR YN9571.09C.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA GENTLES S., BOWMAN S., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 1-49.
RX MEDLINE: 91285106.
RA GROHMANN L., GRAACK H.-R., KRUFFT V., CHOLI T., GOLDSCHMIDT-REISIN S.,
RA KITAKAWA M.;
RL FEBS LETT. 284:51-56(1991).
DR EMBL; 249810; G854481; -.
DR PIR; S17278; S17278.
DR SGD; L0002695; MRPL39.
KW RIBOSOMAL PROTEIN; MITOCHONDRION.
FT INIT_MET 0
FT CONFLICT 28 K -> R (IN REF. 2).
FT CONFLICT 37 R -> K (IN REF. 2).
FT CONFLICT 46 V -> R (IN REF. 2).
SQ SEQUENCE 69 AA; 7841 MW; 3BAFE480 CRC32;

Query Match 57.3%; Score 47; DB 1; Length 69;
Best Local Similarity 41.7%; Pred. No. 3.43e+01;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 47 LFKKAKKVAE 58
|||:| | | |
QY 1 LFRVITKKVAD 12

RESULT 35
ID RL9_HAEIN STANDARD; PRT; 149 AA.
AC P44349;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE 50S RIBOSOMAL PROTEIN L9.
GN RPL1 OR RPL5 OR H10544.
OS HAEMOPHILUS INFLUENZAE.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURELLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RD / KW20;
RX MEDLINE: 95350630.
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOW E., COTTON M.D.,
RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
RA VENTER J.C.;
RL SCIENCE 269:496-512(1995).

CC -!- FUNCTION: BINDS TO THE 23S RRNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L9P FAMILY OF RIBOSOMAL PROTEINS.
DR EMBL; U32736; G1573529; -.
DR PROSITE; PS00651; RIBOSOMAL_L9; 1.
DR TIGR; H10544; -.
KW RIBOSOMAL PROTEIN; RRNA-BINDING.
SQ SEQUENCE 149 AA; 15636 MW; 30C08516 CRC32;

Query Match 57.3%; Score 47; DB 1; Length 149;
Best Local Similarity 50.0%; Pred. No. 3.43e+01;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 90 LFGAITTRDVAE 101
|||:| | | |
QY 1 LFRVITKKVAD 12

Search completed: Tue Apr 7 08:39:41 1998
Job time : 9 secs.

 W O R L D
 (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:39:59 1998; MasPar time 4.83 Seconds
 Tabular output not generated. 104.542 Million cell updates/sec

Title: >US-08-190-411A-3
 Description: (1-12) from 5541104.pep
 Perfect Score: 82
 Sequence: 1 LFRVITKRVAD 12

Scoring table:
 PAM 150
 Gap 15

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
 Listing first 100 summaries

Database:
 1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
 5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
 13:sp_unclassified

Statistics: Mean 25.051; Variance 28.357; scale 0.883

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	61	74.4	953	3	Q19753	4.55e-02
2	55	67.1	875	9	P95949	1.09e+00
3	54	65.9	693	12	Q18890	1.82e+00
4	54	65.9	701	12	Q18890	1.82e+00
5	53	64.6	362	3	Q22897	3.00e+00
6	52	63.4	317	2	Q14798	4.92e+00
7	52	63.4	663	3	Q16057	4.92e+00
8	51	62.2	380	3	Q20049	8.02e+00
9	49	59.8	201	8	Q32469	2.08e+01
10	49	59.8	224	11	Q69112	2.08e+01
11	49	59.8	236	9	Q38415	2.08e+01
12	49	59.8	287	9	Q24963	2.08e+01
13	49	59.8	446	3	P91320	2.08e+01
14	49	59.8	447	3	Q23501	2.08e+01
15	49	59.8	481	3	Q19905	2.08e+01
16	49	59.8	522	2	Q2573	2.08e+01
17	49	59.8	660	10	Q45923	2.08e+01
18	49	59.8	813	10	Q63315	2.08e+01
19	49	59.8	851	8	Q23524	2.08e+01
20	49	59.8	1454	1	Q06164	2.08e+01

21	49	59.8	1509	10	Q61194	2.08e+01
22	49	59.8	1658	10	Q61182	2.08e+01
23	49	59.8	1686	2	O00443	2.08e+01
24	49	59.8	1807	1	O13661	2.08e+01
25	48	58.5	131	12	Q98914	3.31e+01
26	48	58.5	133	9	Q53037	3.31e+01
27	48	58.5	167	11	P87594	3.31e+01
28	48	58.5	167	11	Q66247	3.31e+01
29	48	58.5	281	6	O21267	3.31e+01
30	48	58.5	319	9	O28219	3.31e+01
31	48	58.5	336	9	Q58293	3.31e+01
32	48	58.5	458	9	O26038	3.31e+01
33	48	58.5	478	9	O32912	3.31e+01
34	48	58.5	624	8	O04130	3.31e+01
35	48	58.5	793	9	P73465	3.31e+01
36	48	58.5	1253	3	Q19523	3.31e+01
37	48	58.5	2165	11	O09721	3.31e+01
38	48	58.5	2165	11	Q82027	3.31e+01
39	47	57.3	87	9	O27942	5.23e+01
40	47	57.3	94	10	Q63229	5.23e+01
41	47	57.3	266	3	Q18669	5.23e+01
42	47	57.3	268	9	Q58489	5.23e+01
43	47	57.3	309	3	Q27083	5.23e+01
44	47	57.3	353	3	O15975	5.23e+01
45	47	57.3	353	3	Q17386	5.23e+01
46	47	57.3	359	2	O15108	5.23e+01
47	47	57.3	359	2	O15109	5.23e+01
48	47	57.3	359	10	Q61939	5.23e+01
49	47	57.3	367	10	Q60942	5.23e+01
50	47	57.3	399	9	O27322	5.23e+01
51	47	57.3	437	2	O99764	5.23e+01
52	47	57.3	457	3	O01907	5.23e+01
53	47	57.3	610	2	Q92732	5.23e+01
54	47	57.3	627	9	Q59455	5.23e+01
55	47	57.3	679	10	Q62430	5.23e+01
56	47	57.3	706	10	Q08679	5.23e+01
57	47	57.3	722	10	Q08679	5.23e+01
58	47	57.3	745	2	Q15524	5.23e+01
59	47	57.3	991	2	Q14844	5.23e+01
60	47	57.3	998	11	Q66929	5.23e+01
61	47	57.3	1037	2	O15397	5.23e+01
62	47	57.3	1147	4	O28729	5.23e+01
63	47	57.3	1176	4	Q28824	5.23e+01
64	47	57.3	1687	10	Q35651	5.23e+01
65	47	57.3	1706	10	P97790	5.23e+01
66	47	57.3	1719	10	P97789	5.23e+01
67	47	57.3	1914	2	Q15746	5.23e+01
68	46	56.1	112	9	Q58983	8.19e+01
69	46	56.1	123	1	P87267	8.19e+01
70	46	56.1	131	3	O18236	8.19e+01
71	46	56.1	175	9	O07562	8.19e+01
72	46	56.1	215	9	Q59805	8.19e+01
73	46	56.1	215	9	Q59436	8.19e+01
74	46	56.1	237	3	Q17116	8.19e+01
75	46	56.1	238	3	Q18773	8.19e+01
76	46	56.1	273	1	Q07505	8.19e+01
77	46	56.1	279	8	O04361	8.19e+01
78	46	56.1	330	9	Q45263	8.19e+01
79	46	56.1	331	9	Q44602	8.19e+01
80	46	56.1	346	8	Q41641	8.19e+01
81	46	56.1	350	1	O03130	8.19e+01
82	46	56.1	357	9	O29920	8.19e+01
83	46	56.1	412	8	Q42761	8.19e+01
84	46	56.1	475	4	O18757	8.19e+01
85	46	56.1	482	2	O92879	8.19e+01
86	46	56.1	509	9	O58485	8.19e+01
87	46	56.1	551	10	P70459	8.19e+01
88	46	56.1	658	11	O41288	8.19e+01
89	46	56.1	696	9	O07651	8.19e+01
90	46	56.1	728	9	O55262	8.19e+01
91	46	56.1	732	9	P95869	8.19e+01
92	46	56.1	907	12	Q98850	8.19e+01
93	46	56.1	1203	3	O17720	8.19e+01

P170 PHOSPHATIDYLINOSI
 PHOSPHOINOSITIDE 3-KIN
 PHOSPHOINOSITIDE 3-KIN
 HYPOHETICAL 229,9KD P
 CHICK OLFACTORY RECEPT
 4.6KDA PROTEIN.
 P346, 54-KDA RNA DEPEND
 P18, P13, P20, AND P23
 ATP SYNTHASE F1 SUBUNIT
 ACTIVATOR 1, REPLICATI
 HYPOHETICAL PROTEIN M
 FERRODOXIN-LIKE PROTEI
 INOSINE-5'-MONOPHOSPHA
 PHOSPHOGLYCERATE DEHYD
 DNA HELICASE II.
 F17C8.1.
 POLYMERASE (L).
 RNA POLYMERASE LARGE S
 CONSERVED HYPOHETICAL
 GUANINE NUCLEOTIDE REG
 HYPOHETICAL PROTEIN C
 HYPOHETICAL PROTEIN M
 CLOTTING FACTOR G BETA
 GTP-BINDING PROTEIN Q
 EGL-30.
 GTP-BINDING PROTEIN AL
 GUANINE NUCLEOTIDE BIN
 GUANINE NUCLEOTIDE BIN
 POTASSIUM VOLTAGE GATE
 .ARGINOSUCCINATE SYNT
 HYPOHETICAL 48.5 KD P
 SIMILAR TO ALPHA TUBUL
 RNA HELICASE.
 PYRUVATE SYNTHASE (EC
 MMRE11B.
 PUTATIVE ENDO/EXONUCLE
 SERINE/THREONINE KINAS
 SERINE/THREONINE PROTE
 MYOSIN LIGHT CHAIN KIN
 PROTEIN A.
 RANBP8.
 SMOOTH MUSCLE MYOSIN L
 155 KDA MYOSIN LIGHT C
 DHM2 PROTEIN.
 5'-3' EXONUCLEASE.
 5'-3' EXONUCLEASE.
 MYOSIN LIGHT CHAIN KIN
 HYPOHETICAL 12.8 KD P
 YDR417CP.
 Y57G11C.12.
 HYPOHETICAL 20.4 KD P
 CHLORAMPHENICOL ACETYL
 CHLORAMPHENICOL ACETYL
 F39E9.1 PROTEIN.
 SIMILAR TO RAS-RELATED
 CHROMOSOME IV READING
 PROHIBITIN.
 MODULATION PROTEIN.
 PHOSPHORIBOSYL ANTHRAN
 FERRODOXIN-NADP+ REDUC
 O3635P (FRAGMENT).
 CONSERVED HYPOHETICAL
 SQUALENE SYNTHASE (EC
 PEROXISOMAL CA-DEPEND
 CUG-BP/HNAB50.
 HYPOHETICAL PROTEIN M
 ETS-DOMAIN TRANSCRIPTI
 GAG PROTEIN.
 FERRIC RECEPTOR CFRA.
 GLYCOSYLTRANSFERASE-PROD
 ALPHA-AMYLASE.
 NEURONAL MYOSIN LIGHT
 C55A6.2.

94 46 56.1 1242 3 Q18033 8.19e+01
95 46 56.1 1265 10 Q61992 8.19e+01
96 46 56.1 1283 3 Q94887 8.19e+01
97 46 56.1 1313 1 P87141 8.19e+01
98 46 56.1 1365 11 O37174 8.19e+01
99 46 56.1 1365 11 Q65005 8.19e+01
100 46 56.1 4131 3 Q19542 8.19e+01

ALIGNMENTS

RESULT 1
ID Q19753 PRELIMINARY; PRT; 953 AA.
AC Q19753;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE F23B12.7.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RA WILD A.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., McMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SHALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLDMAN P.,
RL NATURE 368:32-38(1994).
DR EMBL; Z77659; E255897;
SQ SEQUENCE 953 AA; 108423 MW; 080348D8 CRC32;

Query Match 74.4%; Score 61; DB 3; Length 953;
Best Local Similarity 41.7%; Pred. No. 4.55e-02;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 388 LFRVITKKITD 399
|||::: ||::||
QY 1 LFRVITKKVAD 12

RESULT 2
ID P95949 PRELIMINARY; PRT; 875 AA.
AC P95949;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE ATP-DEPENDENT HELICASE.
OS SULFOLOBUS SOLFATARICUS.
OC ARCHAEABACTERIA; CRENARCHAEOTA; SULFOLOBALES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P2;
RA SENSEN C.W., KLENK H.P., SINGH R.K., ALLARD G., CHAN C.C.Y.,
RA LIU Q.Y., PENNY S.L., YOUNG F., SCHENK M.E., GAASTERLAND T.,
RA DOOLITTLE W.F., RAGAN M.A., CHARLEBOIS R.L.;
RL MOL. MICROBIOL. 22:175-191(1996).
DR EMBL; Y08257; E283825;
KW HELICASE.
SQ SEQUENCE 875 AA; 100392 MW; 5508D4B1 CRC32;

Query Match 67.1%; Score 55; DB 9; Length 875;
Best Local Similarity 77.8%; Pred. No. 1.09e+00;
Matches *7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 193 LFRNLITKK 201
|||:||||
QY 1 LFRVITKK 9
RESULT 3
ID Q91889 PRELIMINARY; PRT; 693 AA.
AC Q91889;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE UBIQUITIN-LIKE FUSION PROTEIN.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93292985.
RA LINNEN J.M., BAILEY C.P., WEEKS D.L.;
RL GENE 128:181-188(1993).
DR EMBL; L08474; G214866;
SQ SEQUENCE 693 AA; 76862 MW; 3C04F5C3 CRC32;

Query Match 65.9%; Score 54; DB 12; Length 693;
Best Local Similarity 50.0%; Pred. No. 1.82e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 474 LFRSVEVRNIAD 485
|||::: ||::||
QY 1 LFRVITKKVAD 12

RESULT 4
ID Q91890 PRELIMINARY; PRT; 701 AA.
AC Q91890;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE UBIQUITIN-LIKE FUSION PROTEIN.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93292985.
RA LINNEN J.M., BAILEY C.P., WEEKS D.L.;
RL GENE 128:181-188(1993).
DR EMBL; L08475; G214868;
SQ SEQUENCE 701 AA; 78581 MW; 369C8F29 CRC32;

Query Match 65.9%; Score 54; DB 12; Length 701;
Best Local Similarity 50.0%; Pred. No. 1.82e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 481 LFRSVEVRNIAD 492
|||:|:::|
QY 1 LFRVITKKVAD 12

RESULT 5
ID Q22897 PRELIMINARY; PRT; 362 AA.
AC Q22897;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE COSMID C16D9.
GN C16D9.3.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
RA COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
RA FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
RA LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B.,
RA O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A.,
RA SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E.,
RA STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M.,
RA VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
RA WILKINSON-SPROAT J., WOHLDMAN P.,
RA NATURE 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U64858; G1465843; -.
SQ SEQUENCE 362 AA; 42771 MW; 33408B5C CRC32;

Query Match 64.6%; Score 53; DB 3; Length 362;
Best Local Similarity 33.3%; Pred. No. 3.00e+00;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 223 LFKELASKRISD 234
||: : ||:::
QY 1 LFRVITKKVAD 12

RESULT 6
ID Q14798 PRELIMINARY; PRT; 317 AA.
AC Q14798;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE MAGE-4 PROTEIN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95369706.
RA IMAI Y., SHICHIJO S., YAMADA A., KATAYAMA T., YANO H., ITOH K.;
RL GENE 160:287-290(1995).
DR EMBL: D32075; G1125014; -.
SQ SEQUENCE 317 AA; 35044 MW; 982E1AC9 CRC32;

Query Match 63.4%; Score 52; DB 2; Length 317;
Best Local Similarity 41.7%; Pred. No. 4.92e+00;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 105 LFRALSNKVD 116
||: : ||:::
QY 1 LFRVITKKVAD 12

RESULT 7
ID Q16057 PRELIMINARY; PRT; 663 AA.
AC Q16057;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE LIM DOMAIN PROTEIN.
GN ANON2D9.
OS DROSOPHILA YAKUBA (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97420753.

RA SCHMID K.J., TAUTZ D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 94:9746-9750(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA SCHMID K.J., TAUTZ D.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF005862; G2459922; -.
SQ SEQUENCE 663 AA; 76060 MW; 8F370705 CRC32;

Query Match 63.4%; Score 52; DB 3; Length 663;
Best Local Similarity 50.0%; Pred. No. 4.92e+00;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 65 LFRSTITEKLEN 76
||: : ||:::
QY 1 LFRVITKKVAD 12

RESULT 8
ID Q20049 PRELIMINARY; PRT; 380 AA.
AC Q20049;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE F35G12.2.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RA CHUI C.;
RL SUBMITTED (OCT-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
RA COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
RA FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
RA LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B.,
RA O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A.,
RA SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E.,
RA STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M.,
RA VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
RA WILKINSON-SPROAT J., WOHLDMAN P.;
RL NATURE 368:32-38(1994).
DR EMBL: 246242; G559425; -.
SQ SEQUENCE 380 AA; 41659 MW; BEADFCFB CRC32;

Query Match 62.2%; Score 51; DB 3; Length 380;
Best Local Similarity 40.0%; Pred. No. 8.02e+00;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 354 LFRVLVDKRI 363
||: : ||:::
QY 1 LFRVITKKV 10

RESULT 9
ID Q23469 PRELIMINARY; PRT; 201 AA.
AC Q23469;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE SMILARITY TO MYROSINASE-ASSOCIATED PROTEIN - BRASSICA.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC CAPPARALE; CRUCIFERAE.
RN [1]
RP SEQUENCE FROM N.A.
RA BEVAN M., STIEKEMA W., MURPHY G., WAMBUTT R., POHL T., TERRY N.,
RA KREIS M., KAVANAGH T., ENTIAN K.D., RIEGER M., JAMES R.,
RA PUIGDOMENECH P., HATZPOULOS P., OBERMAIER B., DUESTERHOFT A., JONES J.,

RA PALME K., ANSORGE W., DELSENY M., BANCROFT I., MEWES H.W., SCHUELLER C.,
RA CHALWATZIS N.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.

RA EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Z97340; E326980; -;
SQ SEQUENCE 201 AA; 22098 MW; 5F30ABCE CRC32;

Query Match 59.8%; Score 49; DB 8; Length 201;
Best Local Similarity 45.5%; Pred. No. 2.08e+01;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 125 LYROIKAKEVA 135
|:|:|:|:|:|
QY 1 LFRVITKKA 11

RESULT 10
ID Q69112 PRELIMINARY; PRT; 224 AA.
AC Q69112;
DT 01-NOV-1996 (TREMREL. 01, CREATED)
DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMREL. 01, LAST ANNOTATION UPDATE)
DE ULLORE.
GN ULLORE.
OS HERPES SIMPLEX VIRUS.
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89037371.
RA WOPRAD D.M., CARADONNA S.J.;
RL J. VIROL. 62:4774-4777(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA WOPRAD D.M., CARADONNA S.;
RL SUBMITTED (FEB-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RA WOPRAD D.M.;
RL SUBMITTED (FEB-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: M87011; G330304; -;
SQ SEQUENCE 224 AA; 25128 MW; BBCA07B0 CRC32;

Query Match 59.8%; Score 49; DB 11; Length 224;
Best Local Similarity 50.0%; Pred. No. 2.08e+01;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 27 VLRSVIAKEVD 38
|:|:|:|:|:|
QY 1 LFRVITKKA 12

RESULT 11
ID Q58415 PRELIMINARY; PRT; 236 AA.
AC Q58415;
DT 01-JAN-1998 (TREMREL. 05, CREATED)
DT 01-JAN-1998 (TREMREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMREL. 05, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN M1009.
GN M1009.
OS METHANOCOCCUS JANNASCHII.
OC ARCHAEABACTERIA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9637999.
RA BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
RA OVERBEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
RA SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

RA COTTON M.D., ROBERTS K.M., HURST M.A., KATNE B.P., BORODOVSKY M.,
RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESSE C.R., VENTER J.C.;
RL SCIENCE 273:1058-1073(1996).
CC -!- SIMILARITY: TO E.COLI PHOSPHATE TRANSPORT SYSTEM REGULATORY
CC PROTEIN.
DR EMBL: U67543; G1591668; -;
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 236 AA; 27426 MW; OD3453CA CRC32;

Query Match 59.8%; Score 49; DB 9; Length 236;
Best Local Similarity 33.3%; Pred. No. 2.08e+01;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 161 LYRSMISKIEN 172
|:|:|:|:|:|
QY 1 LFRVITKKA 12

RESULT 12
ID Q24963 PRELIMINARY; PRT; 287 AA.
AC Q24963;
DT 01-JAN-1998 (TREMREL. 05, CREATED)
DT 01-JAN-1998 (TREMREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMREL. 05, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 32.9 KD PROTEIN.
GN HP0152.
OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
OC AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695;
RA TOMB, WHITE, KERLAVAGE, CLAYTON, SUTTON, FLEISCHMANN, KETCHUM, KLENK,
RA GILL, DOUGHERTY, NELSON, QUACKENBUSH, ZHOU, KIRKNESS, PETERSON, LOFTUS,
RA RICHARDSON, DODSON, KHALAK, GLODEK, MCKENNEY, FITZGERALD, LEE, ADAMS,
RA HICKEY, BERG, GOCAYNE, UTTERBACK, PETERSON, KELLEY, COTTON, WEIDMAN,
RA FUJII, BOWMAN, WATTHEY, WALLIN, HAYES, BORODOVSKY, KARP, SMITH,
RA FRASER VENTER.;
RL NATURE 388:539-547(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=26695;
RA TOMB, WHITE, KERLAVAGE, CLAYTON, SUTTON, FLEISCHMANN, KETCHUM, KLENK,
RA GILL, DOUGHERTY, NELSON, QUACKENBUSH, ZHOU, KIRKNESS, PETERSON, LOFTUS,
RA RICHARDSON, DODSON, KHALAK, GLODEK, MCKENNEY, FITZGERALD, LEE, ADAMS,
RA HICKEY, BERG, GOCAYNE, UTTERBACK, PETERSON, KELLEY, COTTON, WEIDMAN,
RA FUJII, BOWMAN, WATTHEY, WALLIN, HAYES, BORODOVSKY, KARP, SMITH,
RA FRASER VENTER.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AE000536; G2313242; -;
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 287 AA; 32948 MW; 81AA2EBE CRC32;

Query Match 59.8%; Score 49; DB 9; Length 287;
Best Local Similarity 55.6%; Pred. No. 2.08e+01;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 189 LYRAILIKK 197
|:|:|:|:|
QY 1 LFRVITKKA 9

RESULT 13
ID P91320 PRELIMINARY; PRT; 446 AA.
AC P91320;
DT 01-MAY-1997 (TREMREL. 03, CREATED)
DT 01-MAY-1997 (TREMREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMREL. 03, LAST ANNOTATION UPDATE)
DE SIMILAR TO ACETYLCHOLINE RECEPTOR PROTEIN.
GN F5310.2.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RL NATURE 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA BECK C., WAMSLEY P.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U88177; G1825676; -.
SQ SEQUENCE 446 AA; 52054 MW; 3317B8AC CRC32;

Query Match 59.8%; Score 49; DB 3; Length 446;
Best Local Similarity 85.7%; Pred. No. 2.08e+01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 140 LFRATIT 146
QY 1 LFRAVIT 7
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RESULT 14
ID Q23501 PRELIMINARY; PRT; 447 AA.
AC Q23501;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE ZK455.8.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACLOELOMATES; NEMATODA; SECERNENTEIA; RHABDITIDA.
RN [1]
RA WHITE S.;
RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RL NATURE 368:32-38(1994).
DR EMBL; Z66567; G1051350; -.
SQ SEQUENCE 447 AA; 50790 MW; 3DE8B3B0 CRC32;

Query Match 59.8%; Score 49; DB 3; Length 447;
Best Local Similarity 66.7%; Pred. No. 2.08e+01;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 259 RSVTRKVG 267
QY 3 RAVITKVA 11
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RESULT 15
ID Q19905 PRELIMINARY; PRT; 481 AA.
AC Q19905;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE F29F11.1.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACLOELOMATES; NEMATODA; SECERNENTEIA; RHABDITIDA.
RN [1]
RA GARDNER A.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
DR EMBL; Z73974; E248315; -.
SQ SEQUENCE 481 AA; 52755 MW; 4D9F8CBE CRC32;

Query Match 59.8%; Score 49; DB 3; Length 481;
Best Local Similarity 54.5%; Pred. No. 2.08e+01;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 329 LFNTVTDKKA 339
QY 1 LFRAVITKVA 11
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|:|:|:|

RESULT 16
ID Q92573 PRELIMINARY; PRT; 522 AA.
AC Q92573;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE MYELOBLAST KIAA0241 (FRAGMENT).
GN KIAA0241.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
RN [1]
RA EUTHERIA; PRIMATES.
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RX MEDLINE; 97191544.
RA NAGASE T., SEKI N., ISHIKAWA K., OHIRA M., KAWARABAYASI Y., OHARA O.,
RA TANAKA A., KOTANI H., MIYAJIMA N., NOMURA N.;
RL DNA RES. 3:321-329(1996).
DR EMBL; D87682; D1014125; -.
FT NON_TER 1
SQ SEQUENCE 522 AA; 57659 MW; EC0B5136 CRC32;

Query Match 59.8%; Score 49; DB 2; Length 522;
Best Local Similarity 46.2%; Pred. No. 2.08e+01;
Matches 6; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Db 456 LFRIVNVAKKIGN 468
QY 1 LFRAV-ITKVKAD 12
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|:|:|:|

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RESULT 17

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ID Q45923      PRELIMINARY; PRT; 660 AA.
AC Q45923;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE SIMILAR TO TNPB OF TRANSPOSON TN554 FROM STAPHYLOCOCCUS AUREUS.
OS CLOSTRIDIUM BUTYRICUM.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RA HESSLINGER C., MULLER N., KAISER M., SAWERS G.;
RL SUBMITTED (DEC-1993) TO EMBL/GENBANK/DBDJ DATA BANKS.
DR EMBL; Z29084; G436133; -
SQ SEQUENCE 660 AA; 78996 MW; B9D4CCFC CRC32;

Query Match      59.8%; Score 49; DB 9; Length 660;
Best Local Similarity 62.5%; Pred. No. 2.08e+01;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 210 FRVITKK 217
   || :|||
QY 2 FRVITKK 9

RESULT 18
ID Q63315      PRELIMINARY; PRT; 813 AA.
AC Q63315;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE LONG TYPE PB-CADHERIN.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=BRAIN;
RX MEDLINE; 96212232.
RA SUGIMOTO K., HONDA S., YAMAMOTO T., UEKI T., MONDEN M., KAJI A.,
RA MATSUMOTO K., NAKAMURA T.;
RL J. BIOL. CHEM. 271:11548-11556(1996).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; D83348; G1398906; -
DR PROSITE; PS00232; CADHERIN; 2.
KW CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; CALCIUM-BINDING; REPEAT.
SQ SEQUENCE 813 AA; 87978 MW; 6E4D9F1D CRC32;

Query Match      59.8%; Score 49; DB 10; Length 813;
Best Local Similarity 54.5%; Pred. No. 2.08e+01;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 731 VFRDFISRKVA 741
   || |::|||
QY 1 LFRVITKKVA 11

RESULT 19
ID Q23524      PRELIMINARY; PRT; 851 AA.
AC Q23524;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 96.8 KD PROTEIN.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC CAPPARALES; CRUCIFERAE.
RN [1]
RP SEQUENCE FROM N.A.
RA BEVAN M., STIEREMA W., MURPHY G., WAMBUIT R., POHL T., TERRY N.,
RA KREIS M., KAVANAGH T., ENTIAN K.D., RIEGER M., JAMES R.,
RA PUIGDOMENECH P., HATZIOPOULOS P., OBERMAIER B., DUESTERHOFT A.,
RA JONES J., PALME K., ANSORGE W., DELSENY M., BANCROFT I., MEWES H.W.,
RA SCHUELLER C., CHALWATZIS N.;

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RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBDJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBDJ DATA BANKS.
DR EMBL; Z97342; E327517; -
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 851 AA; 96849 MW; 23B0FD66 CRC32;

Query Match      59.8%; Score 49; DB 8; Length 851;
Best Local Similarity 50.0%; Pred. No. 2.08e+01;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 346 LFRVIMDKI 355
   ||| :| :|
QY 1 LFRVITKKV 10

RESULT 20
ID Q06164      PRELIMINARY; PRT; 1454 AA.
AC Q06164;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE CHROMOSOME XII COSMID 8543.
GN L8543.13.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA DU Z.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBDJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
RA FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J.,
RA KUCABA T., HALLSWORTH K., HAWKINS J., HILLIER L., JIER M.,
RA JOHNSON D., JOHNSTON L., LANGSTON Y., LATREILLE P., LE T.,
RA MARDIS E., MEIZES S., MILLER N., NHAN M., PAULEY A., PELUSO D.,
RA RIFKIN L., RILES L., TAICH A., TREVASKIS E., VIGNATI D.,
RA WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBDJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA WATERSTON R.;
RL SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBDJ DATA BANKS.
DR EMBL; U20618; G662137; -
SQ SEQUENCE 1454 AA; 167682 MW; 7C4BD4F7 CRC32;

Query Match      59.8%; Score 49; DB 1; Length 1454;
Best Local Similarity 41.7%; Pred. No. 2.08e+01;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 623 IFRVIIDKGITD 634
   || :| :| :|
QY 1 LFRVITKKVAD 12

RESULT 21
ID Q61194      PRELIMINARY; PRT; 1509 AA.
AC Q61194;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE P170 PHOSPHATIDYLINOSITOL 3-KINASE.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.

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RA VIRBASIUS J.V., GUILHERME A., CZECH M.P.;
RL J. BIOL. CHEM. 271:13304-13307(1996).
DR EMBL: U55772; G1305538; -.
SQ SEQUENCE 1509 AA; 170777 MW; E404092B CRC32;

Query Match          59.8%; Score 49; DB 10; Length 1509;
Best Local Similarity 45.5%; Pred. No. 2.08e+01;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 545 LFKPIOSKKVG 555
||::: |||:
QY 1 LFRVITKKVA 11

RESULT 22
ID Q61182 PRELIMINARY; PRT; 1658 AA.
AC Q61182;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE PHOSPHOINOSITIDE 3-KINASE.
GN CPK-M.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB C.
RA MOLZ L.M., CHEN Y.W., HIRANO M., WILLIAMS L.T.;
RL J. BIOL. CHEM. 271:13892-13899(1996).
DR EMBL: U52193; G1272422; -.
SQ SEQUENCE 1658 AA; 187439 MW; D29F37A0 CRC32;

Query Match          59.8%; Score 49; DB 10; Length 1658;
Best Local Similarity 45.5%; Pred. No. 2.08e+01;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 692 LFKPIOSKKVG 702
||::: |||:
QY 1 LFRVITKKVA 11

RESULT 23
ID O00443 PRELIMINARY; PRT; 1686 AA.
AC O00443;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE PHOSPHOINOSITIDE 3-KINASE.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA DOMIN J., PAGES F., VOLINIA S., RITTENHOUSE S.E., ZVELEBIL M.J.,
RA STEIN R.C., WATERFIELD M.D.;
RL BIOCHEM. J. 326:139-147(1997).
DR EMBL: Y13367; E1188595; -.
SQ SEQUENCE 1686 AA; 190736 MW; 8BA83E82 CRC32;

Query Match          59.8%; Score 49; DB 2; Length 1686;
Best Local Similarity 45.5%; Pred. No. 2.08e+01;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 720 LFKPIOSKKVG 730
||::: |||:
QY 1 LFRVITKKVA 11

RESULT 24
ID O13661 PRELIMINARY; PRT; 1807 AA.
AC O13661;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
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DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE HYPOTHEICAL 229.9KD PROTEIN IN NUC1-PRP21 INTERGENIC REGION.
GN P1070.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972 H-.
RA KUSHIDA N., YAMAZAKI S., TANAKA T., JINNO K., HAIKAWA Y., YAMAZAKI J.,
RA YAMAMOTO S., SEKINE M., OGUCHI A., NAGAI Y., SAKAI M., AOKI K.,
RA OGURA K., OTSUKA R., KUDOH Y., YANAGIDA M., MACHIDA M., ZHANG M.Q.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AB004539; D1022298; -.
SQ SEQUENCE 1807 AA; 204620 MW; F5887D03 CRC32;

Query Match          59.8%; Score 49; DB 1; Length 1807;
Best Local Similarity 55.6%; Pred. No. 2.08e+01;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 249 LFRDVIGRR 257
||| ||:
QY 1 LFRVITKK 9

RESULT 25
ID Q98914 PRELIMINARY; PRT; 131 AA.
AC Q98914;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DE CHICK OLFACTORY RECEPTOR 9 (FRAGMENT).
GN COR9.
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RA NEF S., ALLAMAN I., FIUMELLI H., DE CASTRO E., NEF P.;
RL MECH. DEV. 55:65-77(1996).
DR EMBL: Z79592; E262005; -.
KW G-PROTEIN COUPLED RECEPTOR.
FT NON_TER 1 1
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14274 MW; 5FA99425 CRC32;

Query Match          58.5%; Score 48; DB 12; Length 131;
Best Local Similarity 50.0%; Pred. No. 3.31e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 8 LYSTVMTKRV 17
|: |:|:|:
QY 1 LFRVITKKV 10

RESULT 26
ID Q53037 PRELIMINARY; PRT; 133 AA.
AC Q53037;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 4.6KDA PROTEIN.
GN NHHE.
OS RHODOCOCCUS RHODOCHROUS.
OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; NOCARDIOFORM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-J1;
RA KOMEDA H., KOBAYASHI M., SHIMIZU S.;
RL PROC. NATL. ACAD. SCI. U.S.A. 93:4267-4272(1996).
DR EMBL: D67027; G1402519; -.
SQ SEQUENCE 133 AA; 14610 MW; 2AE0B4E6 CRC32;
```

Query Match 58.5%; Score 48; DB 9; Length 133;
Best Local Similarity 41.7%; Pred. No. 3.31e+01;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 3 VFRPVTTRSSD 14
:|:|:|:|:|:
QY 1 LFRAVITKKVAD 12

RESULT 27
ID P87594 PRELIMINARY; PRT; 167 AA.
AC P87594;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE P346, 54-KDA RNA DEPENDENT RNA POLYMERASE,
DE P33, P6, P65, P61, P27, 25-KDA COAT PROTEIN (CPG), P18, P13, P20,
DE AND P23 GENES, COMPLETE CDS.
OS CITRUS TRISTEZA VIRUS (CTV).
OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; CAPILLOVIRIDAE.
RN [1]
RP SEQUENCE OF 1-11 FROM N.A.
RC STRAIN=VT;
RX MEDLINE; 94106113.
RA MAWASSI M., GAFNY R., BAR-JOSEPH M.;
RL VIRUS GENES 7:265-275(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VT;
RX MEDLINE; 95205086.
RA MAWASSI M., GAFNY R., GAGLIARDI D., BAR-JOSEPH M.;
RL J. GEN. VIROL. 76:651-659(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=VT;
RX MAWASSI M., MIETKIEWSKA E., GOFMAN R., YANG G., BAR-JOSEPH M.;
RL J. GEN. VIROL. 77:2359-2364(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA BAR-JOSEPH M.;
RL SUBMITTED (APR-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U56902; G1732502; -.
SQ SEQUENCE 167 AA; 18266 MW; CF2C717B CRC32;

Query Match 58.5%; Score 48; DB 11; Length 167;
Best Local Similarity 41.7%; Pred. No. 3.31e+01;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 124 LFKVIIGTNVDD 135
:|:|:|:|:|:
QY 1 LFRVITKKVAD 12

RESULT 28
ID Q66247 PRELIMINARY; PRT; 167 AA.
AC Q66247;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE P18, P13, P20, AND P23.5 GENES, COMPLETE CDS,
DE AND COAT PROTEIN.
OS CITRUS TRISTEZA VIRUS (CTV).
OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; CAPILLOVIRIDAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VT;
RX MEDLINE; 95205086.
RA MAWASSI M., GAFNY R., GAGLIARDI D., BAR-JOSEPH M.;
RL J. GEN. VIROL. 76:651-659(1995).
DR EMBL; U17265; G596063; -.
SQ SEQUENCE 167 AA; 18292 MW; 93BD9214 CRC32;

Query Match 58.5%; Score 48; DB 11; Length 167;
Best Local Similarity 41.7%; Pred. No. 3.31e+01;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 124 LFKVIIGTNVDD 135
:|:|:|:|:|:
QY 1 LFRVITKKVAD 12

RESULT 29
ID O21267 PRELIMINARY; PRT; 281 AA.
AC O21267;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE ATP SYNTHASE F1 SUBUNIT ALPHA.
GN ATP3.
OS RECLINOMONAS AMERICANA.
OC MITOCHONDRION.
OC EUKARYOTA; NOT YET CLASSIFIED.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC50394;
RX MEDLINE; 97311393.
RA LANG B.F., BURGER G., O'KELLY C.J., CEDERGREN R., GOLDING G.B.,
RA LEMIEUX C., SANKOFF D., TURMEL M., GRAY M.W.;
RL NATURE 387:493-497(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC50394;
RA LANG B.F., BURGER G.;
RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF007261; G2258360; -.
RW MITOCHONDRION.
SQ SEQUENCE 281 AA; 31195 MW; 87B481F4 CRC32;

Query Match 58.5%; Score 48; DB 6; Length 281;
Best Local Similarity 45.5%; Pred. No. 3.31e+01;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 166 FRSVLTQNVIE 176
:|:|:|:|:|:
QY 2 FRVITKKVAD 12

RESULT 30
ID O28219 PRELIMINARY; PRT; 319 AA.
AC O28219;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE ACTIVATOR 1, REPLICATION FACTOR C, 35 KD SUBUNIT.
GN AF2060.
OS ARCHAEoglobus fulgidus.
OC ARCHAEABACTERIA; EURYARCHAEOTA; ARCHAEoglobales; ARCHAEoglobaceae.
RN [1]
RP SEQUENCE FROM N.A.
RA KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA OVERBECK R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA VENTER J.C.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
 RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
 RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
 RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
 RA OVERBECK R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
 RA COTTON M.D., SPRIGGS T., ARTIACH P., KATNE B.P., STOKES S.M.,
 RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
 RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
 RA VENTER J.C.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AE000961; G2648471; -;
 SQ SEQUENCE 319 AA; 35993 MW; BC82CD7C CRC32;

 Query Match 58.5%; Score 48; DB 9; Length 319;
 Best Local Similarity 41.7%; Pred. No. 3.31e+01;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

 Db 268 LFEIISMPKD 279
 ||| :|| :|
 QY 1 LFRVITKKVAD 12

 RESULT 31
 ID Q58293 PRELIMINARY; PRT; 336 AA.
 AC Q58293;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL PROTEIN MJ0883.
 GN MJ0883.
 OS METHANOCOCCLUS JANNASCHII.
 OC ARCHAEBACTERIA; EURYARCHAEOTA; METHANOCOCCELES; METHANOCOCCEACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96377999.
 RA SUTTON G.G., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
 RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
 RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.F., ADAMS M.D., REICH C.I.,
 RA OVERBECK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
 RA SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
 RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
 RA COTTON M.D., ROBERTS K.M., HURST M.A., KATNE B.P., BORODOVSKY M.,
 RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
 RL SCIENCE 273:1058-1073(1996).
 CC -!- SIMILARITY: STRONG IN THE C-TERMINAL, OF M.JANNASCHII M1557.
 DR EMBL; U67532; G1499713; -;
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; UNKNOWN_1.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 336 AA; 39000 MW; 7F372A03 CRC32;

 Query Match 58.5%; Score 48; DB 9; Length 336;
 Best Local Similarity 62.5%; Pred. No. 3.31e+01;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 Db 76 FREIISK 83
 || :|| :||
 QY 2 FRAVITKK 9

 RESULT 32
 ID O26038 PRELIMINARY; PRT; 458 AA.
 AC O26038;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE FERRODOXIN-LIKE PROTEIN.
 GN HP1508
 OS HELICOBACTER PYLORI (CAMPHYLOBACTER PYLORI).
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
 OC AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-26695;

RA TOMB, WHITE, KERLAVAGE, CLAYTON, SUTTON, FLEISCHMANN, KETCHUM, KLENK,
 RA GILL, DOUGHERTY, NELSON, QUACKENBUSH, ZHOU, KIRKNESS, PETERSON,
 RA LOFTUS, RICHARDSON, DODSON, KHALAK, GLODEK, MCKENNEY, FITZGERALD,
 RA LEE, ADAMS, HICKEY, BERG, GOCAYNE, UTTERBACK, PETERSON, KELLEY,
 RA COTTON, WEIDMAN, FUJII, BOWMAN, WATTHEY, WALLIN, HAYES, BORODOVSKY,
 RA KARP, SMITH, FRASER VENTER.;
 RL NATURE 388:539-547(1997).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN-26695;
 RA TOMB, WHITE, KERLAVAGE, CLAYTON, SUTTON, FLEISCHMANN, KETCHUM, KLENK,
 RA GILL, DOUGHERTY, NELSON, QUACKENBUSH, ZHOU, KIRKNESS, PETERSON,
 RA LOFTUS, RICHARDSON, DODSON, KHALAK, GLODEK, MCKENNEY, FITZGERALD,
 RA LEE, ADAMS, HICKEY, BERG, GOCAYNE, UTTERBACK, PETERSON, KELLEY,
 RA COTTON, WEIDMAN, FUJII, BOWMAN, WATTHEY, WALLIN, HAYES, BORODOVSKY,
 RA KARP, SMITH, FRASER VENTER.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AE000649; G2314689; -;
 DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
 KW IRON-SULFUR.
 SQ SEQUENCE 458 AA; 52651 MW; 80152970 CRC32;

 Query Match 58.5%; Score 48; DB 9; Length 458;
 Best Local Similarity 50.0%; Pred. No. 3.31e+01;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

 Db 100 LYRDVIETKI 109
 ||| :|| :|
 QY 1 LFRVITKKV 10

 RESULT 33
 ID O32912 PRELIMINARY; PRT; 478 AA.
 AC O32912;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
 GN GUAB.
 OS MYCOBACTERIUM LEPRAE.
 OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SKELTON J., CHURCHER C.M.;
 RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
 RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EIGLMEIER K., HONORE N., WOODS S.A., CAUDRON B., COLE S.T.;
 RL MOL. MICROBIOL. 7:197-206(1993).
 DR EMBL; AL008609; E1168632; -;
 SQ SEQUENCE 478 AA; 50383 MW; B8FC1940 CRC32;

 Query Match 58.5%; Score 48; DB 9; Length 478;
 Best Local Similarity 60.0%; Pred. No. 3.31e+01;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

 Db 390 RAVVARTVAD 399
 ||| :|| :||
 QY 3 RAVITKKVAD 12

 RESULT 34
 ID O04130 PRELIMINARY; PRT; 624 AA.
 AC O04130;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
 DE PHOSPHOGLYCERATE DEHYDROGENASE.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
 OC APPARAELES; CRUCIFERAE.

RN [1]
 RP SEQUENCE FROM N.A.
 RA HO C., NOJI M., SAITO K.;
 RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AB003280; D1021238; -
 SQ SEQUENCE 624 AA; 66453 MW; 598FBAC6 CRC32;

Query Match 58.5%; Score 48; DB 8; Length 624;
 Best Local Similarity 50.0%; Pred. No. 3.31e+01;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 450 LFRVITKGVAD 12
 QY 1 LFRVITKGVAD 12

RESULT 35
 ID P73465 PRELIMINARY; PRT; 793 AA.
 AC P73465;
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
 DT 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
 DE DNA HELICASE II.
 GN UVRD.
 OS SYNECHOCYSTIS SP.
 OC EUBACTERIA; CYANOBACTERIA; CHROCOCCOCCALES; SYNECHOCYSTIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RA TABATA S.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 RL DNA RES. 3:109-136(1996).
 DR EMBL; D90906; G1652584; -
 KW HELICASE.
 SQ SEQUENCE 793 AA; 90395 MW; 47FD4B3F CRC32;

Query Match 58.5%; Score 48; DB 9; Length 793;
 Best Local Similarity 40.0%; Pred. No. 3.31e+01;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 160 LFRVITKGVAD 169
 QY 1 LFRVITKGVAD 10

Search completed: Tue Apr 7 08:40:13 1998
 Job time : 14 secs.

MSRPH

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:42:04 1998; MasPar time 6.36 Seconds
Tabular output not generated. 79.499 Million cell updates/sec

Title: >US-08-190-411A-4
Description: (1-12) from 5541104.pep
Perfect Score: 81
Sequence: 1 DVREADPTGHSY 12

Scoring table: PAM 150
Gap 15

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mmc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 22.764; Variance 22.337; scale 1.019

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	63	77.8	347	2	000601 DAM10-DSS-AHC CRITICAL	1.78e-04
2	59	72.8	317	2	014798 MAGE-4 PROTEIN	2.52e-03
3	58	71.6	330	10	060762 MELANOMA ANTIGEN, RELA	4.83e-03
4	58	71.6	330	10	060763 MELANOMA ANTIGEN, RELA	4.83e-03
5	58	71.6	330	10	060761 MELANOMA ANTIGEN, RELA	4.83e-03
6	54	66.7	346	2	015481 MAGE-B4	6.07e-02
7	53	65.4	277	3	017687 C06A6.3 PROTEIN	1.12e-01
8	51	63.0	334	9	029369 SIGNAL-TRANSDUCING HIS	3.77e-01
9	48	59.3	90	4	028835 COMP-GATED RETINAL PHO	2.18e+00
10	48	59.3	308	2	092788 RAD GTPASE	2.18e+00
11	48	59.3	309	9	044483 NIFU2	2.18e+00
12	48	59.3	450	9	007752 HYPOTHETICAL 46.7 KD P	2.18e+00
13	48	59.3	875	9	031978 YOMG PROTEIN	2.18e+00
14	48	59.3	4340	9	030764 POLYKETIDE SYNTHASE MO	2.18e+00
15	47	58.0	215	1	009717 RAN/SPIL BINDING PROTE	3.84e+00
16	47	58.0	313	2	015479 MAGE-B2	3.84e+00
17	46	56.8	108	9	P74837 NAPHTHALENESULFONIC AC	6.72e+00
18	46	56.8	198	9	P95779 DTDP-4-KETO-L-RHAMNOSE	6.72e+00
19	46	56.8	272	3	017311 20S PROTEASOME BETA2 S	6.72e+00
20	46	56.8	272	3	017312 20S PROTEASOME BETA2 S	6.72e+00

21	46	56.8	317	8	Q41681	1-AMINOCYCLOPROPANE-1-
22	46	56.8	382	9	P92966	SPLICING FACTOR.
23	46	56.8	356	9	Q51532	PILU.
24	46	56.8	439	8	Q40565	RIBULOSE BIPHOSPHATE
25	46	56.8	526	3	Q24044	FIZZY (FZY).
26	46	56.8	543	1	Q05684	TRANSCRIPTION FACTOR.
27	46	56.8	551	1	Q08224	CHROMOSOME XV READING
28	46	56.8	551	1	Q08975	ORF YPL258C.
29	46	56.8	597	10	Q63615	VACUOLAR PROTEIN SORTI
30	46	56.8	628	7	Q38231	UNIDENTIFIED ORF34.
31	46	56.8	702	3	Q33539	F20D1.7.
32	46	56.8	1187	2	Q12866	CELLULAR PROTO-ONCOGEN
33	46	56.8	1187	2	Q12866	ENDOXYLANASE (EC 3.2.1
34	45	55.6	46	9	Q34568	YBBU PROTEIN.
35	45	55.6	86	10	Q61740	INTEGRIN ALPHA 4 (CD49
36	45	55.6	125	9	Q46451	RIBOSOMAL PROTEIN S11.
37	45	55.6	199	9	Q32481	GRPE.
38	45	55.6	353	11	Q88626	ORFIV.
39	45	55.6	477	9	Q32354	GLUTAMINE SYNTHETASE (
40	45	55.6	503	11	Q10400	P57 (FRAGMENT).
41	45	55.6	503	11	Q10399	P57 (FRAGMENT).
42	45	55.6	503	11	Q10397	P57 (FRAGMENT).
43	45	55.6	503	11	Q10403	P57 (FRAGMENT).
44	45	55.6	503	11	Q10394	P57 (FRAGMENT).
45	45	55.6	503	11	Q89857	GLYCOPROTEIN.
46	45	55.6	503	11	Q65459	GLYCOPROTEIN.
47	45	55.6	581	9	Q51317	PENICILLIN-BINDING PRO
48	45	55.6	582	9	Q50960	PENICILLIN-BINDING PRO
49	45	55.6	644	9	P77391	FBP BASES 1860594 TO
50	45	55.6	770	9	Q33622	PBP PROTEIN.
51	45	55.6	1032	10	Q61989	INTEGRIN ALPHA 4 (CD49
52	45	55.6	1078	10	Q08995	MYELIN TRANSCRIPTION F
53	45	55.6	1288	2	Q15038	KIAA0324 (FRAGMENT).
54	45	55.6	1518	3	Q21850	SIMILAR TO LDL RECEPTO
55	44	54.3	61	9	Q54538	M TYPE 15 (EMML) (FRAG
56	44	54.3	221	12	Q90685	AGRIN (FRAGMENT).
57	44	54.3	377	9	Q53475	EMML15.
58	44	54.3	438	11	Q66640	VIRION PROTEIN KINASE.
59	44	54.3	449	9	P95692	GLUTAMINE SYNTHETASE T
60	44	54.3	467	9	P73043	GLUTAMATE DECARBOXYLAS
61	44	54.3	608	11	Q41253	PNS7.
62	44	54.3	608	9	Q28171	SIGNAL-TRANSDUCING HIS
63	44	54.3	775	11	P89057	RNA FOR VP4, COMPLETE
64	44	54.3	2044	3	P91620	STILL LIFE TYPE 2.
65	44	54.3	2457	11	Q41965	TEGUMENT PROTEIN.
66	43	53.1	67	3	Q26797	PROTEIN KINASE (FRAGME
67	43	53.1	156	3	Q23961	AMYLASE (FRAGMENT).
68	43	53.1	272	10	Q35830	LECITHIN-CHOLESTEROL A
69	43	53.1	330	10	P97269	SPERAD-B.
70	43	53.1	337	10	P97268	SPERAD-A.
71	43	53.1	341	3	Q25028	CYSTEINE PROTEINASE.
72	43	53.1	370	12	Q91904	FORK HEAD PROTEIN.
73	43	53.1	390	9	Q28032	ARGININOSUCCINATE SYNT
74	43	53.1	506	3	Q17381	CE-FKH-1.
75	43	53.1	564	2	Q14111	MATRIX METALLOPROTEINA
76	43	53.1	615	7	Q21976	GP49.
77	43	53.1	621	11	Q66196	PEPLOMERIC POLYPROTEIN
78	43	53.1	762	10	Q64595	CGMP DEPENDENT PROTEIN
79	43	53.1	767	3	Q15882	POLO-LIKE PROTEIN KINA
80	43	53.1	2509	2	Q16702	FATTY ACID SYNTHASE (E
81	43	53.1	3224	2	Q15280	RANBP2 (EC 5.2.1.8) (R
82	42	51.9	156	11	Q84828	17 KD PROTEIN.
83	42	51.9	156	11	Q84839	ORF 5.
84	42	51.9	288	9	Q51323	MOLYBDENUM-CONTAINING
85	42	51.9	307	9	Q24828	CATECHOL 2,3-DIOXYGENA
86	42	51.9	349	9	Q59575	TUNGSTEN FORMYLMETHANO
87	42	51.9	381	3	Q94399	ZK265.2.
88	42	51.9	401	13	Q36039	ELONGATION FACTOR-1 AL
89	42	51.9	444	3	Q21861	R09D1.5.
90	42	51.9	445	9	P94491	XYLOSE ISOMERASE (EC 5
91	42	51.9	446	8	Q23175	HYPOTHETICAL 50.3 KD P
92	42	51.9	461	9	P71984	HYPOTHETICAL 49.4 KD P
93	42	51.9	493	2	Q92772	P56 KIAKRE PROTEIN KI

94 42 51.9 503 9 033360 HYPOTHETICAL 54.2 KD P 5.68e+01
95 42 51.9 627 11 065811 (STRAIN DRAPER) P125 (5.68e+01
96 42 51.9 691 3 001477 CODED FOR BY C. ELEGAN 5.68e+01
97 42 51.9 859 3 021401 COSMID K09E3. 5.68e+01
98 42 51.9 1358 11 065814 (STRAIN SINGER) P125 (5.68e+01
99 42 51.9 1358 11 065813 (STRAIN OREGON) P125 (5.68e+01
100 42 51.9 1608 7 003937 MINOR CAPSID PROTEIN. 5.68e+01

ALIGNMENTS

RESULT 1
ID O00601 PRELIMINARY; PRT; 347 AA.
AC O00601;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DE DAM10-DSS-AHC CRITICAL INTERVAL MAGE SUPERFAMILY GENE 10.
GN DAM10.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96081328.
RA DABOVIC B., ZANARIA E., BARDONI B., LISA A., BORDIGNON C., RUSSO V.,
RA MATESSI C., TRAVERSARI C., CAMERINO G.;
RL MAMM. GENOME 6.571-580(1995).
DR EMBL; S80936; E323784; -.
SQ SEQUENCE 347 AA; 39049 MW; AB96D5B5B CRC32;

Query Match 77.8%; Score 63; DB 2; Length 347;
Best Local Similarity 58.3%; Pred. No. 1.78e-04;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 164 DLKEDNPSTGHSY 175
::: |||::: |||
Qy 1 DVKEADPTGHSY 12

RESULT 2
ID Q14798 PRELIMINARY; PRT; 317 AA.
AC Q14798;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE MAGE-4 PROTEIN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95369706.
RA IMAI Y., SHICHIJO S., YAMADA A., KATAYAMA T., YANO H., ITOH K.;
RL GENE 160.287-290(1995).
DR EMBL; D32075; G1125014; -.
SQ SEQUENCE 317 AA; 35044 MW; 982B1AC9 CRC32;

Query Match 72.8%; Score 59; DB 2; Length 317;
Best Local Similarity 58.3%; Pred. No. 2.52e-03;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 166 DVKEVDPSNTY 177
||| |||::: |||
Qy 1 DVKEADPTGHSY 12

RESULT 3
ID Q60762 PRELIMINARY; PRT; 330 AA.
AC Q60762;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DE MELANOMA ANTIGEN, RELATED SEQUENCE 2 (SMAGE-2 PROTEIN).
GN MAGE-RS2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2; TISSUE-KIDNEY;
RX MEDLINE; 96070435.
RA DE BACKER O., VERHEYDEN A.M., MARTIN B., GODELAINE D., DE PLAEN E.,
RA BRASSEUR R., AVNER P., BOON T.;
RL GENOMICS 28:74-83(1995).
DR EMBL; U19032; G1165172; -.
DR MGD; MGI:105117; MAGE-RS2.
SQ SEQUENCE 330 AA; 35936 MW; 36D760C5 CRC32;

Query Match 71.6%; Score 58; DB 10; Length 330;
Best Local Similarity 58.3%; Pred. No. 4.83e-03;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 158 ELKEIDPSTHSY 169
::: |||::: |||
Qy 1 DVKEADPTGHSY 12

RESULT 4
ID Q60763 PRELIMINARY; PRT; 330 AA.
AC Q60763;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE MELANOMA ANTIGEN, RELATED SEQUENCE 2 (SMAGE-3 PROTEIN).
GN MAGE-RS2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2; TISSUE-KIDNEY;
RX MEDLINE; 96070435.
RA DE BACKER O., VERHEYDEN A.M., MARTIN B., GODELAINE D.,
RA DE PLAEN E., BRASSEUR R., AVNER P., BOON T.;
RL GENOMICS 28:74-83(1995).
DR EMBL; U19033; G1165174; -.
DR MGD; MGI:105117; MAGE-RS2.
SQ SEQUENCE 330 AA; 35985 MW; 83AD4246 CRC32;

Query Match 71.6%; Score 58; DB 10; Length 330;
Best Local Similarity 58.3%; Pred. No. 4.83e-03;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 158 ELKEIDPSTHSY 169
::: |||::: |||
Qy 1 DVKEADPTGHSY 12

RESULT 5
ID Q60761 PRELIMINARY; PRT; 380 AA.
AC Q60761;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE MELANOMA ANTIGEN, RELATED SEQUENCE 2 (SMAGE-1 PROTEIN).
GN MAGE-RS2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2; TISSUE-KIDNEY;
RX MEDLINE; 96070435.
RA DE BACKER O., VERHEYDEN A.M., MARTIN B., GODELAINE D., DE PLAEN E.,
RA BRASSEUR R., AVNER P., BOON T.;

RL GENOMICS 28:74-83(1995).
 DR EMBL; U19031; G1165170; -.
 DR MGD; MGI:105117; MAGE-RS2.
 SQ SEQUENCE 380 AA; 41317 MW; AD78F38E CRC32;

Query Match 71.6%; Score 58; DB 10; Length 380;
 Best Local Similarity 58.3%; Pred. No. 4.83e-03;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 208 ELKEIDPSTHSY 219
 :||| ||: |||
 QY 1 DVKEADPTGHSY 12

RESULT 6
 ID O15481 PRELIMINARY; PRT; 346 AA.
 AC O15481;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DE MAGE-B4.
 GN MAGE-B4.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA LORQUIN C.;
 RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U93163; G2459682; -.
 SQ SEQUENCE 346 AA; 38923 MW; C6A5A407 CRC32;

Query Match 66.7%; Score 54; DB 2; Length 346;
 Best Local Similarity 63.8%; Pred. No. 6.07e-02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 166 LKEVNPTTHSY 176
 :||: ||| |||
 QY 2 VKREADPTGHSY 12

RESULT 7
 ID Q17687 PRELIMINARY; PRT; 277 AA.
 AC Q17687;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DE C06A6.3 PROTEIN.
 GN C06A6.3.
 OS CAENORHABDITIS ELIGANS.
 OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEIA; RHABDITIDA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WU X.; GATTUNG S.;
 RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U41012; G1086626; -.
 SQ SEQUENCE 277 AA; 30379 MW; D0A604DF CRC32;

Query Match 65.4%; Score 53; DB 3; Length 277;
 Best Local Similarity 54.5%; Pred. No. 1.12e-01;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 87 VRESDPPIPHGY 97
 :||| ||: |||
 QY 2 VKREADPTGHSY 12

RESULT 8
 ID O29369 PRELIMINARY; PRT; 334 AA.
 AC O29369;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE SIGNAL-TRANSDUCING HISTIDINE KINASE.
 GN AF0893.
 OS ARCHAEoglobus fulgidus.
 OC ARCHAEABACTERIA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA KLENK H.P.; CLAYTON R.A.; TOMB J.; WHITE O.; NELSON K.E.; KETCHUM K.A.;
 RA DODSON R.J.; GWINN M.; HICKEY E.K.; PETERSON J.D.; RICHARDSON D.L.;
 RA KERLAVAGE A.R.; GRAHAM D.E.; KYRPIDES N.C.; FLEISCHMANN R.D.;
 RA QUACKENBUSH J.; LEE N.H.; SUTTON G.G.; GILL S.; KIRKNESS E.F.;
 RA DOUGHERTY B.A.; MCKENNEY K.; ADAMS M.D.; LOFTUS B.; PETERSON S.;
 RA REICH C.I.; MCNEIL L.K.; BADGER J.H.; GLODEK A.; ZHOU L.; OVERBECK R.;
 RA GOCAYNE J.D.; WEIDMAN J.F.; MCDONALD L.; UTTERBACK T.; COTTON M.D.;
 RA SPRIGGS T.; ARTIACH P.; KATNE B.P.; SYKES S.M.; SADOW P.W.;
 RA D'ANDREA K.P.; BOWMAN C.; FUJII C.; GARLAND S.A.; MASON T.M.;
 RA OLSEN G.J.; FRASER C.M.; SMITH H.O.; WOESE C.R.; VENTER J.C.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA KLENK H.P.; CLAYTON R.A.; TOMB J.; WHITE O.; NELSON K.E.; KETCHUM K.A.;
 RA DODSON R.J.; GWINN M.; HICKEY E.K.; PETERSON J.D.; RICHARDSON D.L.;
 RA KERLAVAGE A.R.; GRAHAM D.E.; KYRPIDES N.C.; FLEISCHMANN R.D.;
 RA QUACKENBUSH J.; LEE N.H.; SUTTON G.G.; GILL S.; KIRKNESS E.F.;
 RA DOUGHERTY B.A.; MCKENNEY K.; ADAMS M.D.; LOFTUS B.; PETERSON S.;
 RA REICH C.I.; MCNEIL L.K.; BADGER J.H.; GLODEK A.; ZHOU L.; OVERBECK R.;
 RA GOCAYNE J.D.; WEIDMAN J.F.; MCDONALD L.; UTTERBACK T.; COTTON M.D.;
 RA SPRIGGS T.; ARTIACH P.; KATNE B.P.; SYKES S.M.; SADOW P.W.;
 RA D'ANDREA K.P.; BOWMAN C.; FUJII C.; GARLAND S.A.; MASON T.M.;
 RA OLSEN G.J.; FRASER C.M.; SMITH H.O.; WOESE C.R.; VENTER J.C.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA KLENK H.P.; CLAYTON R.A.; TOMB J.; WHITE O.; NELSON K.E.; KETCHUM K.A.;
 RA DODSON R.J.; GWINN M.; HICKEY E.K.; PETERSON J.D.; RICHARDSON D.L.;
 RA KERLAVAGE A.R.; GRAHAM D.E.; KYRPIDES N.C.; FLEISCHMANN R.D.;
 RA QUACKENBUSH J.; LEE N.H.; SUTTON G.G.; GILL S.; KIRKNESS E.F.;
 RA DOUGHERTY B.A.; MCKENNEY K.; ADAMS M.D.; LOFTUS B.; PETERSON S.;
 RA REICH C.I.; MCNEIL L.K.; BADGER J.H.; GLODEK A.; ZHOU L.; OVERBECK R.;
 RA GOCAYNE J.D.; WEIDMAN J.F.; MCDONALD L.; UTTERBACK T.; COTTON M.D.;
 RA SPRIGGS T.; ARTIACH P.; KATNE B.P.; SYKES S.M.; SADOW P.W.;
 RA D'ANDREA K.P.; BOWMAN C.; FUJII C.; GARLAND S.A.; MASON T.M.;
 RA OLSEN G.J.; FRASER C.M.; SMITH H.O.; WOESE C.R.; VENTER J.C.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AE001042; G2649708; -.
 SQ SEQUENCE 334 AA; 38033 MW; 9E77911F CRC32;

Query Match 63.0%; Score 51; DB 9; Length 334;
 Best Local Similarity 41.7%; Pred. No. 3.77e-01;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 314 EVKDNEPTGVTF 325
 :||: ||| :
 QY 1 DVKEADPTGHSY 12

RESULT 9
 ID Q28835 PRELIMINARY; PRT; 90 AA.
 AC Q28835;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DE CGMP-GATED RETINAL PHOTORECEPTOR CHANNEL (FRAGMENT).
 OS ORYCTOLAGUS CUNICULUS (RABBIT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; LAGOMORPHA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HUNDAL S.P.; DI FRANCESCO D.; MANGONI M.; BRAMMAR W.J.; CONLEY E.C.;
 RL BIOCHEM. SOC. TRANS. 21:0-0(1993).
 DR EMBL; S65218; G410552; -.
 FT NON_TER 1
 SQ SEQUENCE 90 AA; 10981 MW; 98DBC53A CRC32;

Query Match 59.3%; Score 48; DB 4; Length 90;
 Best Local Similarity 41.7%; Pred. No. 2.18e+00;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 22 EVMIIDPSGNTY 33
 :||: ||: ||: ||
 QY 1 DVKEADPTGHSY 12

RESULT 10
 ID Q92788 PRELIMINARY; PRT; 308 AA.
 AC Q92788;

DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE RAD GTPASE.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94069319.
 RA REYNET C., KAHN C.R.;
 RL SCIENCE 262:1441-1444(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96375161.
 RA CALDWELL J.S., MOYERS J.S., DORIA A., REYNET C., KAHN R.C.;
 RL BIOCHIM. BIOPHYS. ACTA 1316:145-148(1996).
 DR EMBL; U46165; G1620563; -.
 SQ SEQUENCE 308 AA; 33220 MW; 487A3673 CRC32;

Query Match 59.3%; Score 48; DB 2; Length 308;
 Best Local Similarity 55.6%; Pred. No. 2.18e+00;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 119 EAEAGHTY 127
 ||::||:|
 QY 4 EADPTGHSY 12

RESULT 11
 ID Q44483 PRELIMINARY; PRT; 309 AA.
 AC Q44483;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
 DE NIFU2.
 GN NIFU2.
 OS ANABAENA VARIABILIS.
 OC PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
 OC CYANOBACTERIA (BLUE-GREEN ALGAE); NOSTOCALES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29413;
 RX MEDLINE; 96016168.
 RA THIEL T., LYONS E.M., ERKER J.C., ERNST A.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 92:9358-9362(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29413;
 RA THIEL T., LYONS E.M., ERKER J.C.;
 RL SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U49859; G1236928; -.
 SQ SEQUENCE 309 AA; 33028 MW; 4899DDAA CRC32;

Query Match 59.3%; Score 48; DB 9; Length 309;
 Best Local Similarity 54.5%; Pred. No. 2.18e+00;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 194 IKESAPVGTST 204
 ||:| | | |
 QY 2 VKADPTGHSY 12

RESULT 12
 ID O07752 PRELIMINARY; PRT; 450 AA.
 AC O07752;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 46.7 KD PROTEIN.
 GN MTCY180.40C.
 OS MYCOBACTERIUM TUBERCULOSIS.
 OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA OLIVER K., HARRIS D.;
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA BARRELL B.G., RAJANDREAM M.A., PARKHILL J.;
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE; 96181548.
 RA PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
 DR EMBL; Z97193; E324883; -.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 450 AA; 46720 MW; 1606486B CRC32;

Query Match 59.3%; Score 48; DB 9; Length 450;
 Best Local Similarity 41.7%; Pred. No. 2.18e+00;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 337 EVKVVDPANPY 348
 :|| |::|
 QY 1 DVKEADPTGHSY 12

RESULT 13
 ID O31978 PRELIMINARY; PRT; 875 AA.
 AC O31978;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE YONG PROTEIN.
 GN YONG.
 OS BACILLUS SUBTILIS.
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
 RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
 RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
 RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
 RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
 RA DENIZOT F., DEVINE K.M., DUSTERHOPT A., EHRLICH S.D., EMERSON P.T.,
 RA ENJIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D., FRITZ C.,
 RA FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N., GHIM S.Y.,
 RA GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPPI G., GUY B.J.,
 RA HAGA K., HATIECH J., HARWOOD C.R., HENAUT A., HILBERT H., HOLSAPPEL S.,
 RA HOSONO S., HULLO M.F., ITAYA M., JONES L., JORIS B., KARAMATA D.,
 RA KASAHARA Y., KLAER-BLANCHARD M., KLEIN C., KOBAYASHI Y., KOETTER P.,
 RA KONINGSTEIN G., KROGH S., KUMANO M., KURITA K., LAPIDUS A., LIU H.,
 RA LARDINOIS S., LAUBER J., LAZAREVIC V., LEE S.M., LEVINE A., LIU H.,
 RA MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M.,
 RA MOESTL D., NAKAI S., NOBACK M., NOONE D., O'REILLY M., OGAWA K.,
 RA OGIIWARA A., OUDEGA B., PARK S.H., PARRO V., POHL T.M., PORTETELLE D.,
 RA PORWOLLIK S., PRESCOTT A.M., PRESCAN E., PUJIC P., PURNELLE B.,
 RA RAPOPORT G., REY M., REYNOLDS S., RIEGER M., RIVOLTA C., ROCHA E.,
 RA ROCHE B., ROSE M., SADAIE Y., SATO T., SCANLAN E., SCHLEICH S.,
 RA SCHROETER R., SCOFFONE F., SEKIGUCHI J., SEKOWSKA A., SEROR S.J.,
 RA SERROR P., SHIN B.S., SORDO B., SOROKIN A., TACCONI E., TAKAGI T.,
 RA TAKAHASHI H., TAKEMARU K., TAKEUCHI M., TAMAKOSHI A., TANAKA T.,
 RA TERPSTRA P., TOGNONI A., TOSATO V., UCHIYAMA S., VANDENBOL M.,
 RA VANNIER F., VASSAROTTI A., VIARI A., WAMBUIT R., WEDLER H.,
 RA WEITZENEGGER T., WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K.,
 RA YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E.,
 RA YOSHIKAWA H., DANCHIN A.;
 RL NATURE 390:249-256(1997).

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; Z99115; E1183584; -.
SQ SEQUENCE 875 AA; 98885 MW; C0AD7428 CRC32;

Query Match 59.3%; Score 48; DB 9; Length 875;
Best Local Similarity 45.5%; Pred. No. 2.18e+00;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 231 INSNPTGQSY 241
QY 2 VKREADPTGHSY 12

RESULT 14
ID O30764 PRELIMINARY; PRT; 4340 AA.
AC O30764;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE POLYKETIDE SYNTHASE MODULES 1 AND 2.
GN NIDAL.
OS STREPTOMYCES CAELESTIS.
OC EUBACTERIA; FIRMICUTES; ACTINOMYCETES; STREPTOMYCETES;
OC STREPTOMYCETACEAE; STREPTOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NRRL-2821;
RA KAKAVAS S.J., KATZ L., STASSI D.;
RL J. BACTERIOL. 179:7515-7522(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-NRRL-2821;
RA KAKAVAS S., STASSI D.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF016585; G2559838; -.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
KW TRANSFERASE.
SQ SEQUENCE 4340 AA; 457589 MW; 659B2ECB CRC32;

Query Match 59.3%; Score 48; DB 9; Length 4340;
Best Local Similarity 60.0%; Pred. No. 2.18e+00;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 3618 VRAADPAGHP 3627
QY 2 VKREADPTGHS 11

RESULT 15
ID Q09717 PRELIMINARY; PRT; 215 AA.
AC Q09717;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE RAN/SP11 BINDING PROTEIN.
GN SBP1.
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMICETES.
RN [1]
RP SEQUENCE FROM N.A.
RA HAYASHI N., SAZER S., NISHIMOTO T.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; D86381; G1408521; -.
SQ SEQUENCE 215 AA; 24150 MW; 1D19BCB7 CRC32;

Query Match 58.0%; Score 47; DB 1; Length 215;
Best Local Similarity 41.7%; Pred. No. 3.84e+00;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 173 DVSEGEPTAETF 184
QY 1 DVKREADPTGHSY 12

RESULT 16
ID O15479 PRELIMINARY; PRT; 313 AA.
AC O15479;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE MAGE-B2.
GN MAGE-B2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA LURQUIN C.;
RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U93163; G2459680; -.
SQ SEQUENCE 313 AA; 34739 MW; 9543930D CRC32;

Query Match 58.0%; Score 47; DB 2; Length 313;
Best Local Similarity 33.3%; Pred. No. 3.84e+00;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 167 ELKNVPNGHTY 178
QY 1 DVKREADPTGHSY 12

RESULT 17
ID P74837 PRELIMINARY; PRT; 108 AA.
AC P74837;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE NAPHTHALENESULFONIC ACID DIOXYGENASE FERREDOXIN SUBUNIT.
OS SPHINGOMONAS SP.
OC EUBACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; ZYMONONAS GROUP;
OC SPHINGOMONAS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BN6;
RA CONRADT D., KLEIN J., MATTES R.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U65001; G1513105; -.
KW DIOXYGENASE.
SQ SEQUENCE 108 AA; 11595 MW; 5B7478FD CRC32;

Query Match 56.8%; Score 46; DB 9; Length 108;
Best Local Similarity 55.6%; Pred. No. 6.72e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 12 DVKDGEPVG 20
QY 1 DVKREADPTG 9

RESULT 18
ID P95779 PRELIMINARY; PRT; 198 AA.
AC P95779;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE DTDp-4-KETO-L-RHAMNOSE REDUCTASE.
GN RMLC.
OS STREPTOCOCCUS MUTANS.
OC PROKARYOTA; FIRMICUTES; COCCI; STREPTOCOCCACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-XC;
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RA TSUKIOKA Y., YAMASHITA Y., NAKANO Y., OHNO T., KOGA T.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-XC;
RA TSUKIOKA Y., YAMASHITA Y., NAKANO Y., OHNO T., KOGA T.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; D78182; G1813346; -.
SQ SEQUENCE 198 AA; 22364 MW; 8C148392 CRC32;

Query Match 56.8%; Score 46; DB 9; Length 198;
Best Local Similarity 50.0%; Pred. No. 6.72e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 99 DLREGDSFGHYV 110
|:|:|:|:|
Qy 1 DVKEADPTGHSY 12

RESULT 19
ID O17311 PRELIMINARY; PRT; 272 AA.
AC O17311;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE 205 PROTEASOME BETA2 SUBUNIT (EC 3.4.99.46).
GN BETA2.DM.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN [1]
RA SMYTH K.A., BELOTE J.M.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF025791; G2582504; -.
DR PROSITE; PS00854; PROTEASOME_B; 1.
KW PROTEASOME; HYDROLASE; PROTEASE.
SQ SEQUENCE 272 AA; 29895 MW; 3B6F291D CRC32;

Query Match 56.8%; Score 46; DB 3; Length 272;
Best Local Similarity 75.0%; Pred. No. 6.72e+00;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 194 VRDADPTG 201
|:|:|:|:|
Qy 2 VKEADPTG 9

RESULT 20
ID O17312 PRELIMINARY; PRT; 272 AA.
AC O17312;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE 205 PROTEASOME BETA2 SUBUNIT (EC 3.4.99.46).
GN BETA2.DM.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN [1]
RA SMYTH K.A., BELOTE J.M.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF025792; G2582506; -.
DR PROSITE; PS00854; PROTEASOME_B; 1.
KW PROTEASOME; HYDROLASE; PROTEASE.
SQ SEQUENCE 272 AA; 29883 MW; 5688BBDA CRC32;

Query Match 56.8%; Score 46; DB 3; Length 272;
Best Local Similarity 75.0%; Pred. No. 6.72e+00;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 194 VRDADPTG 201
|:|:|:|:|
Qy 2 VKEADPTG 9

RESULT 21
ID O41681 PRELIMINARY; PRT; 317 AA.
AC O41681;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE
DE OXIDASE HOMOLOG.
OS PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
OC FABACEAE.
RN [1]
RA SEQUENCE FROM N.A.
RC TISSUE-HYPOCOTYL;
RX MEDLINE; 94339795.
RA KIM W.T., YANG S.F.;
RL PLANTA 194:223-229(1994).
DR EMBL; U06046; G458338; -.
SQ SEQUENCE 317 AA; 35773 MW; F02E6272 CRC32;

Query Match 56.8%; Score 46; DB 8; Length 317;
Best Local Similarity 54.5%; Pred. No. 6.72e+00;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 266 VKESDETQVY 276
|:|:|:|:|
Qy 2 VKEADPTGHSY 12

RESULT 22
ID P92966 PRELIMINARY; PRT; 356 AA.
AC P92966;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
DE SPLICING FACTOR.
GN RSP41
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC CAPPARALES; CRUCIFERAE.
RN [1]
RA LOPATO S., WAGHMAN E., BARTA A.;
RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; X99436; E258268; -.
SQ SEQUENCE 356 AA; 41297 MW; 7F090666 CRC32;

Query Match 56.8%; Score 46; DB 8; Length 356;
Best Local Similarity 45.5%; Pred. No. 6.72e+00;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 166 VKDDDSRGNGY 176
|:|:|:|:|
Qy 2 VKEADPTGHSY 12

RESULT 23
ID Q51532 PRELIMINARY; PRT; 382 AA.
AC Q51532;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE PILU.
GN PILU.
OS PSEUDOMONAS AERUGINOSA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC PSEUDOMONADACEAE.
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN-PAOL;
RX MEDLINE; 91285432.

RA WHITCHURCH C.B., HOBBS M., LIVINGSTON S.P., KRISHNAPILLAI V.,
RA MATTICK J.S.;
RL GENE 101:33-44(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RA WHITCHURCH C.B., MATTICK J.S.;
RL SUBMITTED (MAR-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; L27667; G443686;-;
SQ SEQUENCE 382 AA; 42533 MW; 6F4A16C2 CRC32;

Query Match 56.8%; Score 46; DB 9; Length 382;
Best Local Similarity 25.0%; Pred. No. 6.72e+00;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 370 EITDDDPAGRRF 381
::: |||:::
QY 1 DVKEADPTGHSY 12

RESULT 24
ID Q40565 PRELIMINARY; PRT; 439 AA.

AC Q40565;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE RIBULOSE BISPHOSPHATE CARBOXYLASE ACTIVASE.
GN RCA.
OS NICOTIANA TABACUM (COMMON TOBACCO).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC SOLANALES; SOLANACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SRI; TISSUE=LEAF;
RA RODERMEYER S., QIAN J.;
RL SUBMITTED (AUG-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; 214980; G19990;-;
SQ SEQUENCE 439 AA; 48343 MW; 0E004E3C CRC32;

Query Match 56.8%; Score 46; DB 8; Length 439;
Best Local Similarity 41.7%; Pred. No. 6.72e+00;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 60 EEKDADPKKQTY 71
: |||:::
QY 1 DVKEADPTGHSY 12

RESULT 25
ID Q24044 PRELIMINARY; PRT; 526 AA.

AC Q24044;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE FIZZY (FZY).
GN FZY.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95247821.
RA DAWSON I.A., ROTH S., ARTAVANIS-TSAKONAS S.;
RL J. CELL BIOL. 129:725-737(1995).
DR EMBL; U22419; G1109772;-;
DR FLYBASE; FBgn0001086; fzy.
SQ SEQUENCE 526 AA; 57080 MW; 122FC6EB CRC32;

Query Match 56.8%; Score 46; DB 3; Length 526;
Best Local Similarity 70.0%; Pred. No. 6.72e+00;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 461 VKQADLTGHT 470
||: |||:

QY 2 VKEADPTGHS 11

RESULT 26
ID Q05664 PRELIMINARY; PRT; 543 AA.

AC Q05664;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE TRANSCRIPTION FACTOR.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ALPHA S288;
RA MANNHAUPT G., VETTER I., SCHWARZLOSE C., MITZEL S., FELDMANN H.;
RL YEAST 0:0-0(0).
DR EMBL; X91067; G984187;-;
SQ SEQUENCE 543 AA; 60305 MW; 25845EE2 CRC32;

Query Match 56.8%; Score 46; DB 1; Length 543;
Best Local Similarity 45.5%; Pred. No. 6.72e+00;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db 285 VKDNGPINHVY 295
||: |||:
QY 2 VKEADPTGHSY 12

RESULT 27
ID Q08224 PRELIMINARY; PRT; 551 AA.

AC Q08224;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE CHROMOSOME XV READING FRAME ORF YOLO55C.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RA FELDMANN H., MANNHAUPT G., VETTER I.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA ANSORGE W., BENES V., RECHMANN S., SCHWAGER C., TEODORU C., VOSS H.,
RA WIEMANN S.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RA MIPS;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; 274797; E251864;-;
SQ SEQUENCE 551 AA; 61269 MW; DDAD22AB CRC32;

Query Match 56.8%; Score 46; DB 1; Length 551;
Best Local Similarity 45.5%; Pred. No. 6.72e+00;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db 285 VKDNGPINHVY 295
||: |||:
QY 2 VKEADPTGHSY 12

RESULT 28
ID Q08975 PRELIMINARY; PRT; 551 AA.

AC Q08975;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE ORF YPL258C.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]

RP SEQUENCE FROM N.A.
 RA MESSENGUY F., DUBOIS E., VIERENDELS F., SCHERENS B.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 273614; E246962; -;
 SQ SEQUENCE 551 AA; 61334 MW; E3E8364D CRC32;

Query Match 56.8%; Score 46; DB 1; Length 551;
 Best Local Similarity 45.5%; Pred. No. 6.72e+00;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db 285 VKDNGPINHVY 295
 ||: || ||
 Qy 2 VKADPTGHSY 12

RESULT 29
 ID Q63615 PRELIMINARY; PRT; 597 AA.
 AC Q63615;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
 DE VACUOLAR PROTEIN SORTING HOMOLOG R-VPS33A.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PEYSNER J., HSU S.C., HYDE P.S., SCHELLER R.H.;
 RL GENE 183:7-14(1996).
 DR EMBL: U35244; G1477468; -;
 SQ SEQUENCE 597 AA; 67513 MW; 7469FB50 CRC32;

Query Match 56.8%; Score 46; DB 10; Length 597;
 Best Local Similarity 58.3%; Pred. No. 6.72e+00;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 477 DVNEQNPTDISY 488
 ||: || ||
 Qy 1 DVKEADPTGHSY 12

RESULT 30
 ID Q38231 PRELIMINARY; PRT; 628 AA.
 AC Q38231;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
 DE UNIDENTIFIED ORF34.
 OS BACTERIOPHAGE BIL67.
 CC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; SIPHOVIRIDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95111629.
 RA SCHOULER C., EHRLICH S.D., CHOPIN M.C.;
 RL MICROBIOLOGY 140:3061-3069(1994).
 DR EMBL: L33769; G522256; -;
 SQ SEQUENCE 628 AA; 72844 MW; 7292CDBD CRC32;

Query Match 56.8%; Score 46; DB 7; Length 628;
 Best Local Similarity 36.4%; Pred. No. 6.72e+00;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 596 IKDENPQNSY 606
 ||: || ||
 Qy 2 VKADPTGHSY 12

RESULT 31
 ID Q93539 PRELIMINARY; PRT; 702 AA.

AC Q93539;
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
 DT 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
 DE F20D1.7.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; ACLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BURTON J.;
 RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
 RA COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
 RA FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
 RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
 RA LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B.,
 RA O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A.,
 RA SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E.,
 RA STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M.,
 RA VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
 RA WILKINSON-SPROAT J., WOHLDMAN P.;
 RL NATURE 368:32-38(1994).
 DR EMBL: 278542; E259712; -;
 SQ SEQUENCE 702 AA; 79995 MW; 8818ED6B CRC32;

Query Match 56.8%; Score 46; DB 3; Length 702;
 Best Local Similarity 36.4%; Pred. No. 6.72e+00;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 413 IRQTATVGHSHY 423
 ||: || || ||
 Qy 2 VKADPTGHSY 12

RESULT 32
 ID Q12866 PRELIMINARY; PRT; 999 AA.
 AC Q12866;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR (C-MER).
 GN C-MER.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD LEUKOCYTES;
 RX MEDLINE; 94368701.
 RA GRAHAM D.K., DAWSON T.L., MULLANEY D.L., SNODGRASS H.R., EARP H.S.;
 RL CELL GROWTH DIFFER. 5:647-657(1994).
 RN [2]
 RP ERRATUM.
 RA GRAHAM D.K., DAWSON T.L., MULLANEY D.L., SNODGRASS H.R., EARP H.S.;
 RL CELL GROWTH DIFFER. 5:1022-1022(1994).
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE
 CC EXTRACELLULAR DOMAINS CONTAINS 2 IG-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 DR EMBL: U08023; G505665; -;
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW PROTO-ONCOGENE; TRANSMEMBRANE; REPEAT; IMMUNOGLOBULIN FOLD; SIGNAL.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 999 CELLULAR PROTO-ONCOGENE (C-MER).
 FT DOMAIN 19 501 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 502 518 POTENTIAL.
 FT DOMAIN 519 999 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 90 182 IG-LIKE DOMAIN.
 FT DOMAIN 198 266 IG-LIKE DOMAIN.

FT DOMAIN 283 372 FIBRONECTIN TYPE-III.
 FT DOMAIN 376 480 FIBRONECTIN TYPE-III.
 SQ SEQUENCE 999 AA: 110391 MW; 20274ED6 CRC32;

Query Match 56.8%; Score 46; DB 2; Length 999;
 Best Local Similarity 63.6%; Pred. No. 6.72e+00;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 320 QVKEADPLNG 330
 QY :|||||:;
 1 DVKEADPTGHS 11

RESULT 33

ID Q59278 PRELIMINARY; PRT; 1187 AA.

AC Q59278;

DT 01-NOV-1996 (TREMREL. 01, CREATED)

DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1996 (TREMREL. 01, LAST ANNOTATION UPDATE)

DE ENDOXYLANASE (EC 3.2.1.8) (ENDO-1,4-BETA-XYLANASE)

DE (1,4-BETA-D-XLAN XYLANOXYDROLASE).

GN XINC.

OS CELLULOSONAS FIMI.

OC PROKARYOTA; FIRMICUTES; IRREGULAR ASPOROGENOUS RODS; CORYNEFORM GROUP.

RN [1]

RP SEQUENCE OF 1-352 FROM N.A.

RA CLARKE J.H., DAVIDSON K., GILBERT H.J., HAZLEWOOD G.P.;

RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [2]

RP SEQUENCE FROM N.A.

RA CLARKE J.H.;

RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC

CC LINKAGES IN XYLANS.

DR EMBL; 250866; E212269; -.

KW XLAN DEGRADATION; HYDROLASE; GLYCOSIDASE.

SQ SEQUENCE 1187 AA; 125378 MW; 92B3994A CRC32;

Query Match

Best Local Similarity 75.0%; Score 46; DB 9; Length 1187;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1046 TDPTGRSY 1053

QY :||||:|

5 ADPTGHSY 12

RESULT 34

ID Q34568 PRELIMINARY; PRT; 46 AA.

AC Q34568;

DT 01-JAN-1998 (TREMREL. 05, CREATED)

DT 01-JAN-1998 (TREMREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMREL. 05, LAST ANNOTATION UPDATE)

DE YBU PROTEIN.

GN YBU.

OS BACILLUS SUBTILIS.

OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-168;

RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,

RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,

RA BOURISS R., BOURSICHER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,

RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,

RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,

RA DENIZOT F., DEVINE K.M., DUSTERHOF A., EHRLICH S.D., EMERSON P.T.,

RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,

RA FRITZ C., FUJITA M., FUJITA Y., FUNA S., GALIZZI A., GALLERON N.,

RA GHIM S.Y., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,

RA GUISEPPI G., GUY B.J., HAGA K., HAECH J., HARWOOD C.R., HENAUT A.,

RA HILBERT H., HOLSHAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,

RA JORIS B., KARAWATA D., KASHARA Y., KLAERR-BLANCHARD M., KLEIN C.,

RA KOBAYASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,

RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
 RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
 RA MEDINA N., MELIADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
 RA NOONE D., O'REILLY M., OGAWA K., OGIMURA A., OUDEGA B., PARK S.H.,
 RA PARRO V., POHL T.M., PORTETELLE D., PORWOLLIK S., PRESCOTT A.M.,
 RA PRESECAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
 RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
 RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
 RA SEKIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., SHIN B.S., SOLDI B.,
 RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K.,
 RA TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
 RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
 RA VIARI A., WAMBUIT R., WEDLER E., WEDLER H., WEITZENEGGER T.,
 RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
 RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.,
 RL NATURE 390:249-256(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-168;

RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;

RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL; 299104; E1182112; -.

DR EMBL; 299105; E1182130; -.

SQ SEQUENCE 46 AA; 5370 MW; 60D493CA CRC32;

Query Match

Best Local Similarity 55.6%; Score 45; DB 9; Length 46;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 14 IKEVDGTGPDY 24

QY :||| | | |

2 VKEADPTGHSY 12

RESULT 35

ID Q61740 PRELIMINARY; PRT; 86 AA.

AC Q61740;

DT 01-NOV-1996 (TREMREL. 01, CREATED)

DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMREL. 05, LAST ANNOTATION UPDATE)

DE INTEGRIN ALPHA 4 (CD49D) (INTEGRIN ALPHA-4 SUBUNIT) (FRAGMENT).

GN ITGA4 OR VLA-4.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RX DE MEIRSMAN C., SCHOLLEN E., JASPERS M., ONGENA K., MATTHIJS G.,

RA MARYNEN P., CASSINAN J.J.;

RL DNA CELL BIOL. 13:743-754(1994).

DR EMBL; L20788; G309417; -.

DR MGD; MGI:96603; ITGA4.

KW INTEGRIN.

FT NON_TER

SQ SEQUENCE 86 AA; 9255 MW; C6D01AE6 CRC32;

Query Match

Best Local Similarity 100.0%; Score 45; DB 10; Length 86;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 PTGHSY 34

QY :|||||

7 PTGHSY 12

Search completed: Tue Apr 7 08:42:16 1998

Job time : 12 secs.

WQESRPH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:41:29 1998; MasPar time 2.18 Seconds
Tubular output not generated. 138.083 Million cell updates/sec

Title: >US-08-190-411A-4
Description: (1-12) from 5541104.pap
Perfect Score: 81
Sequence: 1 DVKEADPTGHSY 12

Scoring table: PAM 150
Gap 15

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 23.518; Variance 22.821; scale 1.031

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query %	Match	Length	DB	ID	Description	Pred. No.
1	81	100.0		309	1	MAG1_HUMAN		MELANOMA-ASSOCIATED AN	4.36e-10
2	74	91.4		234	1	MAG8_HUMAN		MELANOMA-ASSOCIATED AN	7.50e-08
3	74	91.4		315	1	MAG9_HUMAN		MELANOMA-ASSOCIATED AN	7.50e-08
4	72	88.9		369	1	MAGA_HUMAN		MELANOMA-ASSOCIATED AN	3.15e-07
5	71	87.7		319	1	MAGB_HUMAN		MELANOMA-ASSOCIATED AN	6.43e-07
6	62	76.5		317	1	MAGC_HUMAN		MELANOMA-ASSOCIATED AN	3.14e-04
7	57	70.4		347	1	MAGX_HUMAN		MELANOMA-ASSOCIATED AN	8.07e-03
8	53	65.4		411	1	MAG6_HUMAN		MELANOMA-ASSOCIATED AN	9.61e-02
9	52	64.2		417	1	F16P_ARATH		FRUCTOSE-1,6-BISPHOSPH	1.75e-01
10	50	61.7		314	1	MAG3_HUMAN		MELANOMA-ASSOCIATED AN	5.69e-01
11	50	61.7		407	1	F16P_PEA		FRUCTOSE-1,6-BISPHOSPH	5.69e-01
12	50	61.7		835	1	FASD_ECOLI		OUTER MEMBRANE USHER P	5.69e-01
13	49	60.5		411	1	F16P_BRANA		FRUCTOSE-1,6-BISPHOSPH	1.01e+00
14	49	60.5		417	1	CBPC_HUMAN		MAST CELL CARBOXYPEPTI	1.01e+00
15	49	60.5		3998	1	POLG_BVDVS		GENOME POLYPROTEIN.	1.01e+00
16	48	59.3		268	1	RAD_RAT		GTP-BINDING PROTEIN RA	1.79e+00
17	48	59.3		269	1	RAD_HUMAN		GTP-BINDING PROTEIN RA	1.79e+00
18	48	59.3		866	1	YCBS_ECOLI		HYPOTHETICAL OUTER MEM	1.79e+00
19	48	59.3		873	1	PC1_HUMAN		PLASMA-CELL MEMBRANE G	3.12e+00
20	47	58.0		197	1	KGVA_PIG		GUANYLATE KINASE (EC 2	3.12e+00
21	47	58.0		443	1	GLNA_BACCE		GLUTAMINE SYNTHETASE (3.12e+00
22	47	58.0		443	1	GLNA_BACSU		GLUTAMINE SYNTHETASE (3.12e+00
23	47	58.0		445	1	GLNA_LACDE		GLUTAMINE SYNTHETASE (3.12e+00

47	58.0	446	1	GLNA_STAUI	GLUTAMINE SYNTHETASE (3.12e+00
24	58.0	497	1	PEN3_ADEL2	PENTON PROTEIN (VIRION	3.12e+00
25	58.0	633	1	XRCX_HUMAN	DNA-REPAIR PROTEIN XRC	3.12e+00
26	58.0	147	1	PA24_BUNMU	PHOSPHOLIPASE A2, BETA	5.40e+00
27	56.8	147	1	PA24_BUNMU	PHOSPHOLIPASE A2, BETA	5.40e+00
28	56.8	583	1	ARAL2_ECOLI	ARSENICAL PUMP-DRIVING	5.40e+00
29	56.8	583	1	ARAL2_ECOLI	ARSENICAL PUMP-DRIVING	5.40e+00
30	55.6	503	1	VP57_BDV	57 KD PROTEIN (P57).	9.26e+00
31	55.6	581	1	PBP2_NEIGO	PENICILLIN-BINDING PRO	9.26e+00
32	55.6	581	1	PBP2_NEIGO	PENICILLIN-BINDING PRO	9.26e+00
33	55.6	581	1	MYT1_HUMAN	MYELIN TRANSCRIPTION F	9.26e+00
34	55.6	725	1	MYT1_HUMAN	MYELIN TRANSCRIPTION F	9.26e+00
35	55.6	1033	1	TIR1_ECOLI	TYPE 1 RESTRICTION ENZ	9.26e+00
36	54.3	22	1	YHV4_LACHE	HYPOTHETICAL PROTEIN I	1.57e+01
37	54.3	98	1	Y037_MYCTU	VERY HYPOTHETICAL 11.3	1.57e+01
38	54.3	222	1	THIE_BACSU	THIAMIN-PHOSPHATE PYRO	1.57e+01
39	54.3	261	1	143A_VICFA	14-3-3-LIKE PROTEIN A	1.57e+01
40	54.3	377	1	NUEM_HUMAN	NADH-UBIQUINONE OXIDOR	1.57e+01
41	54.3	469	1	GLN1_RHIMV	GLUTAMINE SYNTHETASE I	1.57e+01
42	54.3	469	1	GLN1_RHIMV	GLUTAMINE SYNTHETASE I	1.57e+01
43	54.3	488	1	SUOX_RAT	SULFITE OXIDASE PRECUR	1.57e+01
44	54.3	488	1	SUOX_RAT	SULFITE OXIDASE PRECUR	1.57e+01
45	54.3	539	1	CCMM_SYNP7	CARBON DIOXIDE CONCENT	1.57e+01
46	54.3	629	1	HDF2_YEAST	HIGH AFFINITY DNA-BIND	1.57e+01
47	54.3	789	1	ACOX_YEAST	PUTATIVE ACONITASE IN	1.57e+01
48	54.3	826	1	VIL1_HUMAN	VILLIN.	1.57e+01
49	54.3	826	1	VIL1_HUMAN	VILLIN.	1.57e+01
50	54.3	1173	1	TSPL_XENLA	THROMBOSPONDIN 1 PRECU	1.57e+01
51	53.1	176	1	RL5_HALMA	50S RIBOSOMAL PROTEIN	2.63e+01
52	53.1	228	1	RL1_THETH	50S RIBOSOMAL PROTEIN	2.63e+01
53	53.1	290	1	YG1D_YEAST	HYPOTHETICAL 31.7 KD P	2.63e+01
54	53.1	293	1	Y331_MYCTU	HYPOTHETICAL 33.0 KD P	2.63e+01
55	53.1	301	1	SC14_KLULA	SEC14 CYTOSOLIC FACTOR	2.63e+01
56	53.1	326	1	YKX2_CAEEL	HYPOTHETICAL 34.6 KD P	2.63e+01
57	53.1	362	1	YCHF_HAEIN	PROBABLE GTP-BINDING P	2.63e+01
58	53.1	416	1	CBPB_CANFA	CARBOXYPEPTIDASE B PRE	2.63e+01
59	53.1	506	1	Z157_HUMAN	ZINC FINGER PROTEIN 15	2.63e+01
60	53.1	559	1	PPBI_MOUSE	ALKALINE PHOSPHATASE,	2.63e+01
61	53.1	669	1	COGU_HUMAN	MATRIX METALLOPROTEINA	2.63e+01
62	53.1	684	1	CNG1_MOUSE	CGMP-GATED CATION CHAN	2.63e+01
63	53.1	686	1	CNG1_HUMAN	CGMP-GATED CATION CHAN	2.63e+01
64	53.1	690	1	CNG1_BOVIN	CGMP-GATED CATION CHAN	2.63e+01
65	53.1	691	1	CNG1_CANFA	CGMP-GATED CATION CHAN	2.63e+01
66	53.1	796	1	ABAA_EMENI	REGULATORY PROTEIN ABA	2.63e+01
67	53.1	878	1	YB9X_YEAST	HYPOTHETICAL TRP-ASP R	2.63e+01
68	53.1	2504	1	FAS_HUMAN	FATTY ACID SYNTHASE (E	2.63e+01
69	53.1	3224	1	N358_HUMAN	NUCLEAR PORE COMPLEX P	2.63e+01
70	51.9	3396	1	POLG_DENIS	GENOME POLYPROTEIN (CO	2.63e+01
71	51.9	145	1	ANG3_MOUSE	ANGIOGENIN-3 PRECURSOR	4.37e+01
72	51.9	150	1	RPB8_HUMAN	DNA-DIRECTED RNA POLYM	4.37e+01
73	51.9	156	1	YLSX_BACSU	HYPOTHETICAL 17.6 KD P	4.37e+01
74	51.9	156	1	VPG_PLRVW	PUTATIVE GENOME-LINKED	4.37e+01
75	51.9	156	1	VPG_PLRV	PUTATIVE GENOME-LINKED	4.37e+01
76	51.9	156	1	VPG_PLRV	PUTATIVE GENOME-LINKED	4.37e+01
77	51.9	197	1	KGUA_MOUSE	GUANYLATE KINASE (EC 2	4.37e+01
78	51.9	283	1	FOLD_BACSU	METHYLENETETRAHYDROFOL	4.37e+01
79	51.9	292	1	TF_RABIT	TISSUE FACTOR PRECURSO	4.37e+01
80	51.9	342	1	YN9A_YEAST	HYPOTHETICAL 37.9 KD P	4.37e+01
81	51.9	347	1	PYRC_SALTY	DIHYDROOATASE (EC 3.5	4.37e+01
82	51.9	363	1	YCHF_ECOLI	PROBABLE GTP-BINDING P	4.37e+01
83	51.9	379	1	ILEU_HORSE	LEUKOCYTE ELASTASE INH	4.37e+01
84	51.9	392	1	CGL_CAEEL	PUTATIVE CYSTATINONE	4.37e+01
85	51.9	417	1	PVR_HUMAN	POLIOVIRUS RECEPTOR PR	4.37e+01
86	51.9	516	1	ACHD_BOVIN	ACETYLCHOLINE RECEPTOR	4.37e+01
87	51.9	555	1	WETA_EMENI	REGULATORY PROTEIN WET	4.37e+01
88	51.9	621	1	VP40_HSVBC	CAPSID PROTEIN P40 (CO	4.37e+01
89	51.9	699	1	EEG_AGRU	ELONGATION FACTOR G (E	4.37e+01
90	51.9	700	1	EEG_AQUPI	ELONGATION FACTOR G (E	4.37e+01
91	51.9	747	1	GUND_CELFI	ENDOGALACTANASE D PRECU	4.37e+01
92	51.9	773	1	MAK5_YEAST	ATP-DEPENDENT RNA HELI	4.37e+01
93	51.9	799	1	ZFX1_MOUSE	ZINC FINGER X-CHROMOSO	4.37e+01
94	51.9	839	1	ZFX2_MOUSE	ZINC FINGER X-CHROMOSO	4.37e+01
95	51.9	991	1	BMPL_MOUSE	BONE MORPHOGENETIC PRO	4.37e+01
96	51.9	1073	1	RESA_PLAFF	RING-INFECTED ERYTHROC	4.37e+01

97 42 51.9 1132 1 YKKS_YEAST HYPOTHETICAL 125.6 KD 4.37e+01
 98 42 51.9 1139 1 HMW1_MYCE CYTADHERENCE HIGH MOLE 4.37e+01
 99 41 50.6 366 1 CD44_BOVIN CD44 ANTIGEN PRECURSOR 7.17e+01
 100 41 50.6 407 1 CGLE_CHICK GL/S-SPECIFIC CYCLIN E 7.17e+01

ALIGNMENTS

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RESULT 1
ID MAG1_HUMAN STANDARD; PRT; 309 AA.
AC P43355; Q00346;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 1 (MAGE-1 ANTIGEN) (ANTIGEN M22-E).
GN MAGE1 OR MAGE1 OR MAGE1A.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92086861.
RA VAN DER BRUGEN P., TRAVERSARI C., CHOMEZ P., LURQUIN C., DE PLAEN E.,
RA VAN DEN EYNDE B., KNUTH A., BOON T.;
RL SCIENCE 254:1643-1647(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-SKIN;
RX MEDLINE; 94311935.
RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA GLOCKNER G., RUMP A., NORDSTIEK G., HINZMANN B., KIOSCHIS P.,
RA HEISS N., POUSTRKA A., BAUER D., DRESCHER B., KNOB A., ROSENTHAL A.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP MUTAGENESIS.
RC TISSUE-BLOOD;
RX MEDLINE; 94157413.
RA GAUGLER B., VAN DEN EYNDE B., VAN DER BRUGEN P., ROMERO P.,
RA GAFORIO J.J., DE PLAEN E., LETHE B., BRASSEUR F., BOON T.;
RL J. EXP. MED. 179:921-930(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS
CC CYTOLYTIC T LYMPHOCYTES.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES. NEVER EXPRESSED IN KIDNEY TUMORS, LEUKEMIAS AND
CC LYMPHOMAS.
CC -!- POLYMORPHISM: THE VARIANT AT POSITION 32 LIKELY REPRESENTS A
CC POLYMORPHISM OF THE MAGE-1 GENE.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
DR EMBL; M77481; G416115; -
DR EMBL; U82672; G2078527; -
DR MM; 300016; -
DR KW ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.
FT VARIANT 32 32 T -> A.
FT DOMAIN 33 36 POLY-SER.
FT MUTAGEN 163 163 D->A: ABOLISHES HLA-A1 BINDING.
FT MUTAGEN 169 169 Y->A: ABOLISHES HLA-A1 BINDING.
FT CONFLICT 72 72 R -> Q (IN REF. 3).
SQ SEQUENCE 309 AA; 34342 MW; E5CB1300 CRC32;

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Query Match 100.0%; Score 81; DB 1; Length 309;
 Best Local Similarity 100.0%; Pred. No. 4.36e-10;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 158 DVKEADPTGHSY 169
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 QY 1 DVKEADPTGHSY 12

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RESULT 2
ID MAG8_HUMAN STANDARD; PRT; 234 AA.
AC P43361;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).
GN MAGE8 OR MAGE8.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
DR EMBL; U10693; G533526; -
KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
FT DOMAIN 40 43 POLY-SER.
SQ SEQUENCE 234 AA; 25197 MW; D4931BC3 CRC32;

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Query Match 91.4%; Score 74; DB 1; Length 234;
 Best Local Similarity 83.3%; Pred. No. 7.50e-08;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 168 DVKEVDPAGHSY 179
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 QY 1 DVKEADPTGHSY 12

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RESULT 3
ID MAG9_HUMAN STANDARD; PRT; 315 AA.
AC P43362; Q82910;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 9 (MAGE-9 ANTIGEN).
GN MAGE9 OR MAGE9.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA TIMMS K.M., BONDESON M.L., ANSARI-LARI M.A., LAGERSTEDT K.,
RA NELSON D.L., PETERSSON U., GIBBS R.A.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.

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DR EMBL; U10694; G533528; -.
DR EMBL; U66083; G1519285; -.
KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
FT DOMAIN 34 37 POLY-GLU.
FT DOMAIN 87 90 POLY-GLU.
SQ SEQUENCE 315 AA; 35088 MW; 7DC3228E CRC32;

Query Match 91.4%; Score 74; DB 1; Length 315;
Best Local Similarity 83.3%; Pred. No. 7.50e-08;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 164 DVKEVDPTGHSY 175
QY 1 DVKEADPTGHSY 12

RESULT 4
ID MAG4_HUMAN STANDARD; PRT; 369 AA.
AC P43363;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 10 (MAGE-10 ANTIGEN).
GN MAGEA10 OR MAGE10.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENEE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
DR EMBL; U10685; G533511; -.
KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
FT DOMAIN 54 62 POLY-SER.
SQ SEQUENCE 369 AA; 40766 MW; D1E1870 CRC32;

Query Match 88.9%; Score 72; DB 1; Length 369;
Best Local Similarity 83.3%; Pred. No. 3.15e-07;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 190 DVKEVDPTGHSF 201
QY 1 DVKEADPTGHSY 12

RESULT 5
ID MAG5_HUMAN STANDARD; PRT; 319 AA.
AC P43364;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 11 (MAGE-11 ANTIGEN).
GN MAGEA11 OR MAGE11.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENEE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).

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CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
DR EMBL; U10686; G533513; -.
KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
SQ SEQUENCE 319 AA; 35536 MW; E3DBEDEF CRC32;

Query Match 87.7%; Score 71; DB 1; Length 319;
Best Local Similarity 83.3%; Pred. No. 6.43e-07;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 168 DVKEVDPTSHSY 179
QY 1 DVKEADPTGHSY 12

RESULT 6
ID MAG4_HUMAN STANDARD; PRT; 317 AA.
AC P43358;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 4 (MAGE-4 ANTIGEN) (MAGE-X2) (MAGE-41).
GN MAGEA4 OR MAGE4.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SMET C., BRASSEUR F., VAN DER BRUGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVEENEE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95369706.
RA IMAI Y., SHICHIGO S., YAMADA A., KATAYAMA T., YANO H., ITOH K.;
RL GENE 160:287-290(1995).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY WITH
CC MAGE-1.
DR EMBL; U10687; G533515; -.
DR EMBL; U10688; G533517; -.
DR EMBL; U10340; G499124; -.
DR EMBL; D32077; G1125018; -.
KW ANTIGEN; MULTIGENE FAMILY; POLYMORPHISM; TUMOR ANTIGEN.
FT DOMAIN 41 44 POLY-SER.
FT VARIANT 173 173 T -> A.
FT CONFLICT 307 307 E -> Q (IN REF. 2).
SQ SEQUENCE 317 AA; 34929 MW; 3CE38AF9 CRC32;

Query Match 76.5%; Score 62; DB 1; Length 317;
Best Local Similarity 66.7%; Pred. No. 3.14e-04;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 166 DVKEVDPTSNTY 177
QY 1 DVKEADPTGHSY 12

RESULT 7
ID MAGX_HUMAN STANDARD; PRT; 347 AA.
AC P43366;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN XP (MAGE-XP ANTIGEN).
GN MAGEB1 OR MAGEB1 OR MAGEXP.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE; 95281581.
RA MUSCATELLI F., WALKER A.P., DE PLAEN E., STAFFORD A.N., MONACO A.P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 92:4987-4991(1995).
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN TESTIS.
CC -1- SIMILARITY: BELONGS TO THE MAGE FAMILY.
DR EMBL; X82539; G608993; -.
DR MIM; 600619; -.
KW ANTIGEN; MULTIGENE FAMILY.
SQ SEQUENCE 347 AA; 39152 MW; A041BAB2 CRC32;

Query Match 70.4%; Score 57; DB 1; Length 347;
Best Local Similarity 50.0%; Pred. No. 8.07e-03;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 164 DLKEDNPSSHTY 175
QY 1 DVKEADPTGHSY 12

RESULT 8
ID MAG6_HUMAN STANDARD; PRT; 314 AA.
AC P43360;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MELANOMA-ASSOCIATED ANTIGEN 6 (MAGE-6 ANTIGEN) (MAGE3B).
GN MAGEA6 OR MAGE6.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE; 95012457.
RA DE PLAEN E., ARDEN K., TRAVERSARI C., GAFORIO J.J., SZIKORA J.-P.,
RA DE SVET C., BRASSEUR F., VAN DER BRUGGEN P., LETHE B., LURQUIN C.,
RA BRASSEUR R., CHOMEZ P., DE BACKER O., CAVERNEE W., BOON T.;
RL IMMUNOGENETICS 40:360-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE; 94311935.
RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RX MEDLINE; 95369706.
RA IWAI Y., SHICHIGO S., YAMADA A., KATAYAMA T., YANO H., ITOH K.;
RL GENE 160:287-290(1995).
CC -1- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN TUMOR
CC OR ASPECTS OF TUMOR PROGRESSION.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT

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CC FOR TESTES.
CC -1- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY TO
CC MAGE-3.
DR EMBL; U10691; G533523; -.
DR EMBL; U10339; G499122; -.
DR EMBL; D32076; G1125016; -.
KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
FT DOMAIN 40 43 POLY-SER.
SQ SEQUENCE 314 AA; 34891 MW; B7125E97 CRC32;

Query Match 65.4%; Score 53; DB 1; Length 314;
Best Local Similarity 50.0%; Pred. No. 9.61e-02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 165 ELMEVDPIGHVY 176
QY 1 DVKEADPTGHSY 12

RESULT 9
ID F16P_ARATH STANDARD; PRT; 417 AA.
AC P25851;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (EC 3.1.3.11)
DE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE).
GN FBP.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC CAPPARALES; CRUCIFERAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91329733.
RA HORSNELL P.R., RAINES C.A.;
RL PLANT MOL. BIOL. 17:185-186(1991).
CC -1- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE + H(2)O =
CC D-FRUCTOSE 6-PHOSPHATE + ORTHOPHOSPHATE.
CC -1- PATHWAY: THE CHLOROPLAST ISOZYME TAKES PART IN THE REGENERATION OF
CC RIBULOSE BISPHOSPHATE IN THE PHOTOSYNTHETIC CARBON REDUCTION
CC CYCLE (CALVIN CYCLE).
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- INDUCTION: LIGHT ACTIVATION THROUGH PH CHANGES, MG(2+) LEVELS
CC AND ALSO BY LIGHT-MODULATED REDUCTION OF ESSENTIAL DISULPHIDE
CC GROUPS VIA THE FERREDOXIN-THIOREDOXIN F SYSTEM (BY SIMILARITY).
CC -1- IN PLANTS THERE ARE TWO FBPAE ISOZYMES: ONE IN THE CYTOSOL AND
CC THE OTHER IN THE CHLOROPLAST.
DR EMBL; X58148; G11242; -.
DR PIR; S16582; S16582.
DR HSSP; P00636; 1FBH.
DR PROSITE; PS00124; FBPAE; 1.
KW HYDROLASE; CARBOHYDRATE METABOLISM; MULTIGENE FAMILY; CHLOROPLAST;
KW TRANSIT PEPTIDE; CALVIN CYCLE.
FT TRANSIT 1 59 CHLOROPLAST (POTENTIAL).
FT CHAIN 60 417 FRUCTOSE-1,6-BISPHOSPHATASE.
FT ACT_SITE 359 359 BY SIMILARITY.
FT DISULFID 233 238 REDOX-ACTIVE (LIGHT-MODULATED) (BY
FT SIMILARITY).
SQ SEQUENCE 417 AA; 45178 MW; 9A30B20C CRC32;

Query Match 64.2%; Score 52; DB 1; Length 417;
Best Local Similarity 50.0%; Pred. No. 1.75e-01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 314 DLKDPGPTGKPY 325
QY 1 DVKEADPTGHSY 12

RESULT 10
ID MAG3_HUMAN STANDARD; PRT; 314 AA.
AC P43357;

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DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE MELANOMA-ASSOCIATED ANTIGEN 3 (MAGE-3 ANTIGEN) (ANTIGEN M22-D).
 GN MAGE3 OR MAGE3.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.
 RC TISSUE=BLOOD;
 RX MEDLINE: 94157413.
 RA GAUGLER B., VAN DEN EYNDE B., VAN DER BRUGGEN P., ROMERO P.,
 RA GAFORIO J.J., DE PLAIN E., LETHE B., BRASSEUR F., BOON T.;
 RL J. EXP. MED. 179:921-930(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN;
 RX MEDLINE: 94311935.
 RA DING M., BECK R.J., KELLER C.J., FENTON R.G.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:549-555(1994).
 CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
 CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
 CC PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS
 CC CYTOLYTIC T LYMPHOCYTES.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG,
 CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 CC FOR TESTES AND PLACENTA. NEVER EXPRESSED IN KIDNEY TUMORS,
 CC LEUKEMIAS AND LYMPHOMAS.
 CC -!- SIMILARITY: BELONGS TO THE MAGE FAMILY.
 DR EMBL: U03735; G468826; -;
 KW ANTIGEN; MULTIGENE FAMILY; TUMOR ANTIGEN.
 FT DOMAIN 40 43 POLY-SER.
 FT MUTAGEN 170 170 D->A: ABOLISHES HLA-A1 BINDING.
 FT MUTAGEN 176 176 Y->A: ABOLISHES HLA-A1 BINDING.
 SQ SEQUENCE 314 AA; 34747 MW; AC557A64 CRC32;

 Query Match 61.7%; Score 50; DB 1; Length 314;
 Best Local Similarity 50.0%; Pred. No. 5.69e-01;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

 Db 165 ELMEVDPIGHLY 176
 QY :::|||::|
 QY 1 DVKEADPTGHSY 12

 RESULT 11
 ID F16P_PEN STANDARD; PRT; 407 AA.
 AC P46275; Q37263;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (EC 3.1.3.11)
 DE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE).
 GN FBP.
 OS PISUM SATIVUM (GARDEN PEA).
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
 OC FABACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. GIANT; TISSUE=LEAF;
 RA HAHN T.R., DONG S.M., RHIM J.H.;
 RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE OF 27-407 FROM N.A.
 RC STRAIN=CV. LINCOLN; TISSUE=LEAF;
 RX MEDLINE: 94297517.
 RA CARRASCO J.L., CHUECA A., PRADO F.E., HERMOSO R., LAZARO J.J.,
 RA RAMOS J.L., SAHRAWY M., LOPEZ GORGE J.;
 RL PLANTA 193:494-501(1994).
 CC -!- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE + H(2)O =
 D-FRUCTOSE 6-PHOSPHATE + ORTHOPHOSPHATE.

CC -!- PATHWAY: THE CHLOROPLAST ISOZYME TAKES PART IN THE REGENERATION OF
 CC RIBULOSE BISPHOSPHATE IN THE PHOTOSYNTHETIC CARBON REDUCTION
 CC CYCLE (CALVIN CYCLE).
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
 CC -!- INDUCTION: LIGHT ACTIVATION THROUGH PH CHANGES, MG(2+) LEVELS
 CC AND ALSO BY LIGHT-MODULATED REDUCTION OF ESSENTIAL DISULFIDE
 CC GROUPS VIA THE FERREDOXIN-THIOREDOXIN F SYSTEM (BY SIMILARITY).
 CC -!- IN PLANTS THERE ARE TWO FBPAE ISOZYMES: ONE IN THE CYTOSOL AND
 CC THE OTHER IN THE CHLOROPLAST.
 DR EMBL: L34806; G609561; -;
 DR EMBL: X68826; G20717; -;
 DR PROSITE; PS00124; FBPAE; 1.
 KW HYDROLASE; CARBOHYDRATE METABOLISM; MULTIGENE FAMILY; CHLOROPLAST;
 KW TRANSIT PEPTIDE; CALVIN CYCLE.
 FT TRANSIT 1 50 CHLOROPLAST (POTENTIAL).
 FT CHAIN 51 407 FRUCTOSE-1,6-BISPHOSPHATASE.
 FT ACT_SITE 349 349 BY SIMILARITY.
 FT DISULFID 223 228 REDOX-ACTIVE (LIGHT-MODULATED) (BY
 FT SIMILARITY).
 FT CONFLICT 82 82 G -> P (IN REF. 2).
 FT CONFLICT 160 160 A -> P (IN REF. 2).
 FT CONFLICT 247 247 A -> I (IN REF. 2).
 FT CONFLICT 282 282 E -> K (IN REF. 2).
 SQ SEQUENCE 407 AA; 44511 MW; DD67CDEC CRC32;

 Query Match 61.7%; Score 50; DB 1; Length 407;
 Best Local Similarity 50.0%; Pred. No. 5.69e-01;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

 Db 304 DLKEPGPSGKPY 315
 QY :::|||::|
 QY 1 DVKEADPTGHSY 12

 RESULT 12
 ID FASD_ECOLI STANDARD; PRT; 835 AA.
 AC P46000;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE OUTER MEMBRANE USHER PROTEIN FASD PRECURSOR.
 GN FASD.
 OS ESCHERICHIA COLI.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=987;
 RX MEDLINE: 94148769.
 RA SCHIFFERLI D.M., ALRUTZ M.A.;
 RL J. BACTERIOL. 176:1099-1110(1994).
 CC -!- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF THE 987P
 CC FIMBRIAE SUBUNITS ACROSS THE OUTER MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 CC -!- SIMILARITY: TO OTHER FIMBRIAL EXPORT USHER PROTEINS.
 DR EMBL: L22659; G437336; -;
 DR EMBL: U50547; G1381551; -;
 DR PROSITE; PS01151; FIMBRIAL_USHER; 1.
 KW OUTER MEMBRANE; TRANSMEMBRANE; FIMBRIA; TRANSPORT; SIGNAL.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 835 OUTER MEMBRANE USHER PROTEIN FASD.
 FT DISULFID 810 834 POTENTIAL.
 SQ SEQUENCE 835 AA; 92354 MW; D8FBDD31 CRC32;

 Query Match 61.7%; Score 50; DB 1; Length 835;
 Best Local Similarity 50.0%; Pred. No. 5.69e-01;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

 Db 324 NIKEDAGSEHSF 335
 QY :::|||::|
 QY 1 DVKEADPTGHSY 12


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RESULT 13
ID F16P_BRANA STANDARD; PRT; 411 AA.
AC Q07204;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (EC 3.1.3.11)
DE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE).
GN FBP.
OS BRASSICA NAPUS (RAPE).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC EUPARALEAE; CRUCIFERAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94120014.
RA RODRIGUEZ-SUAZES R.J., WOLOSUK R.A.;
RL PLANT PHYSIOL. 103:1453-1454(1993).
CC -1- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE + H(2)O =
CC D-FRUCTOSE 6-PHOSPHATE + ORTHOPHOSPHATE.
CC -1- PATHWAY: THE CHLOROPLAST ISOZYME TAKES PART IN THE REGENERATION OF
CC RUBULOSE BISPHOSPHATE IN THE PHOTOSYNTHETIC CARBON REDUCTION
CC CYCLE (CALVIN CYCLE).
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
CC -1- INDUCTION: LIGHT ACTIVATION THROUGH PH CHANGES, MG(2+) LEVELS
CC AND ALSO BY LIGHT-MODULATED REDUCTION OF ESSENTIAL DISULFIDE
CC GROUPS VIA THE FERREDOXIN-THIOREDOXIN F SYSTEM (BY SIMILARITY).
CC -1- IN PLANTS THERE ARE TWO FBPAE ISOZYMES: ONE IN THE CYTOSOL AND
CC THE OTHER IN THE CHLOROPLAST.
DR EMBL; L15303; G289367; -.
DR HSP; P00636; 1FPP.
KW HYDROLASE; CARBOHYDRATE METABOLISM; MULTIGENE FAMILY; CHLOROPLAST;
KW TRANSIT PEPTIDE; CALVIN CYCLE.
FT TRANSIT 1 53 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 54 411 FRUCTOSE-1,6-BISPHOSPHATASE.
FT ACT_SITE 353 353 BY SIMILARITY.
FT DISULFID 227 232 REDOX-ACTIVE (LIGHT-MODULATED) (BY
FT SIMILARITY).
SQ SEQUENCE 411 AA; 44446 MW; BFBD2BCD CRC32;

Query Match 60.5%; Score 49; DB 1; Length 411;
Best Local Similarity 41.7%; Pred. No. 1.01e+00;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 308 DKDPGSGPKY 319
|:::|:|:|
Qy 1 DVKEADPTGHSY 12

RESULT 14
ID CBPC_HUMAN STANDARD; PRT; 417 AA.
AC P15088;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MAST CELL CARBOXYPEPTIDASE A PRECURSOR (EC 3.4.17.1) (MC-CPA)
DE (CARBOXYPEPTIDASE A3).
GN CPA3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-LUNG;
RX MEDLINE; 90083291.
RA REYNOLDS D.S., GURLEY D.S., STEVENS R.L., SUGARBAKER D.J.,
RA AUSTEN K.F., SERAFIN W.E.;
RL PROC. NATL. ACAD. SCI. U.S.A. 86:9480-9484(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-MAST CELLS;

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RX MEDLINE; 92105393.
RA REYNOLDS D.S., GURLEY D.S., AUSTEN K.F.;
RA J. CLIN. INVEST. 89:273-282(1992).
RN [3]
RP SEQUENCE OF 110-417 FROM N.A.
RX MEDLINE; 92333165.
RA NATUSAKI M., STEWART C.B., VANDERSLICE P., SCHWARTZ L.B.,
RA NATUSAKI M., WINTROUB B.U., RUTTER W.J., GOLDSTEIN S.M.;
RA J. INVEST. DERMATOL. 99:138-145(1992).
RN [4]
RP SEQUENCE OF 110-137.
RX MEDLINE; 89214692.
RA GOLDSTEIN S.M., KAEMPFER C.E., KEALEY J.T., WINTROUB B.U.;
RA J. CLIN. INVEST. 83:1630-1636(1989).
CC -1- CATALYTIC ACTIVITY: PEPTIDYL-L-AMINO ACID + H(2)O = PEPTIDE +
CC L-AMINO ACID.
CC -1- SUBCELLULAR LOCATION: SECRETORY GRANULES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M14; ALSO KNOWN AS THE
CC ZINC CARBOXYPEPTIDASE FAMILY.
DR EMBL; M27717; G179934; -.
DR EMBL; M73720; G187442; -.
DR EMBL; M73716; G187442; JOINED.
DR EMBL; M73717; G187442; JOINED.
DR EMBL; M73718; G187442; JOINED.
DR EMBL; M73719; G187442; JOINED.
DR EMBL; S40234; E65321; ALT_SEQ.
DR PIR; A43929; A43929.
DR HSP; P09555; 1PBA.
DR MIN; I14851; -.
DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
KW HYDROLASE; CARBOXYPEPTIDASE; ZINC; ZYMOGEN; SIGNAL.
FT SIGNAL 1 15
FT PROPEP 16 109 ACTIVATION PEPTIDE.
FT CHAIN 110 417 MAST CELL CARBOXYPEPTIDASE A.
FT METAL 176 176 ZINC (BY SIMILARITY).
FT METAL 179 179 ZINC (BY SIMILARITY).
FT METAL 304 304 ZINC (BY SIMILARITY).
FT ACT_SITE 378 378 NUCLEOPHILE (BY SIMILARITY).
FT DISULFID 173 186 BY SIMILARITY.
FT DISULFID 245 268 BY SIMILARITY.
SQ SEQUENCE 417 AA; 48700 MW; 848CEC99 CRC32;

Query Match 60.5%; Score 49; DB 1; Length 417;
Best Local Similarity 66.7%; Pred. No. 1.01e+00;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 105 DVKEDIPGRHSY 116
|||||:|:|
Qy 1 DVKEADPTGHSY 12

RESULT 15
ID POLG_BVDVS STANDARD; PRT; 3898 AA.
AC Q01499;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GENOME POLYPROTEIN.
OS BOVINE VIRAL DIARRHEA VIRUS (STRAIN SD-1) (BVDV) (MUCOSAL DISEASE
OS VIRUS).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
OC PESTIVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93079889.
RA DENG R., BROCK K.V.;
RL VIROLOGY 191:867-869(1992).
CC -1- FUNCTION: PESTIVIRUS P80 (P125) MAY BE A BIFUNCTIONAL PROTEIN
CC WITH HELICASE AND PROTEASE ACTIVITY.
CC -1- PTM: GP116 GIVES RISE TO GP62 AND GP53; GP62 IN TURN YIELDS GP48
CC AND GP25.
CC -1- SIMILARITY: TO THE HOG CHOLERA VIRUS GENOME POLYPROTEIN.

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CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S31.
DR EMBL: M96751; G289508; -;
DR PIR: A44217; A44217
DR PROSITE: PS00531; RNASE_T2.2; UNKNOWN_1.
KW POLYPEPTIDE; GLYCOPROTEIN; HELICASE; SERINE PROTEASE; HYDROLASE.
FT CHAIN 1 2270 P20 (30KD).
FT CHAIN ?271 ?1063 GP116/GP62-GP53 (GLYCOPROTEIN).
FT CHAIN ? GP125/GP54-GP80.
FT CHAIN ? GP133/GP58-GP75.
FT DOMAIN 690 755 CYS-RICH.
FT ACT_SITE 1658 1658 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1695 1695 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 1752 1752 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 272 272 POTENTIAL.
FT CARBOHYD 281 281 POTENTIAL.
FT CARBOHYD 296 296 POTENTIAL.
FT CARBOHYD 335 335 POTENTIAL.
FT CARBOHYD 365 365 POTENTIAL.
FT CARBOHYD 370 370 POTENTIAL.
FT CARBOHYD 413 413 POTENTIAL.
FT CARBOHYD 487 487 POTENTIAL.
FT CARBOHYD 597 597 POTENTIAL.
FT CARBOHYD 809 809 POTENTIAL.
FT CARBOHYD 878 878 POTENTIAL.
FT CARBOHYD 922 922 POTENTIAL.
FT CARBOHYD 990 990 POTENTIAL.
FT CARBOHYD 1357 1357 POTENTIAL.
FT CARBOHYD 1419 1419 POTENTIAL.
FT CARBOHYD 1451 1451 POTENTIAL.
FT CARBOHYD 1713 1713 POTENTIAL.
FT CARBOHYD 2134 2134 POTENTIAL.
FT CARBOHYD 2217 2217 POTENTIAL.
FT CARBOHYD 2494 2494 POTENTIAL.
FT CARBOHYD 2682 2682 POTENTIAL.
FT CARBOHYD 2751 2751 POTENTIAL.
FT CARBOHYD 2891 2891 POTENTIAL.
FT CARBOHYD 2988 2988 POTENTIAL.
FT CARBOHYD 3688 3688 POTENTIAL.
FT CARBOHYD 3777 3777 POTENTIAL.
FT CARBOHYD 3793 3793 POTENTIAL.
SQ SEQUENCE 3898 AA; 437800 MW; A562145C CRC32;

Query Match 60.5%; Score 49; DB 1: Length 3898;
Best Local Similarity 58.3%; Pred. No. 1.01e+00;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1132 DVVKADPGQGY 1143
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QY 1 DVKEADPTGHSY 12

RESULT 16
ID RAD_RAT STANDARD; PRT; 268 AA.
AC P55043;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE GTP-BINDING PROTEIN RAD (RAS ASSOCIATED WITH DIABETES) (RAD1).
GN RRAD OR RAD.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA RISHI A.K., GULAMHUSSEIN A., STEELE M.P.;
RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- SIMILARITY: BELONGS TO THE RAD/GEN FAMILY OF GTP-BINDING
CC PROTEINS.
KW EMBL: U12187; G595473; -;
DR GTP-BINDING. 59 66 GTP (BY SIMILARITY).
FT NP_BIND 108 112 GTP (BY SIMILARITY).
FT NP_BIND 108 112 GTP (BY SIMILARITY).

FT NP_BIND 163 166 GTP (BY SIMILARITY).
SQ SEQUENCE 268 AA; 29053 MW; CE4C8DC7 CRC32;
Query Match 59.3%; Score 48; DB 1: Length 268;
Best Local Similarity 55.6%; Pred. No. 1.79e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 80 EAEAAGHTY 88
||::||::||
QY 4 EADPTGHSY 12

RESULT 17
ID RAD_HUMAN STANDARD; PRT; 269 AA.
AC P55042;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GTP-BINDING PROTEIN RAD (RAS ASSOCIATED WITH DIABETES) (RAD1).
GN RRAD OR RAD.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RX MEDLINE; 94069319.
RA REYNET C., KAHN C.R.;
RL SCIENCE 262:1441-1444(1993).
CC -!- TISSUE SPECIFICITY: SKELETAL AND CARDIAC MUSCLE, LUNG, LESSER
CC AMOUNTS IN PLACENTA AND KIDNEY. DETECTED IN ADIPOSE TISSUE.
CC OVEREXPRESSED IN MUSCLE OF TYPE II DIABETIC HUMANS.
CC -!- SIMILARITY: BELONGS TO THE RAD/GEN FAMILY OF GTP-BINDING
CC PROTEINS.
CC EMBL: L24564; G439603; -;
DR MIM; 179503; -;
KW GTP-BINDING. 59 66 GTP (BY SIMILARITY).
FT NP_BIND 108 112 GTP (BY SIMILARITY).
FT NP_BIND 164 167 GTP (BY SIMILARITY).
SQ SEQUENCE 269 AA; 29262 MW; 201C9665 CRC32;

Query Match 59.3%; Score 48; DB 1: Length 269;
Best Local Similarity 55.6%; Pred. No. 1.79e+00;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 80 EAEAAGHTY 88
||::||::||
QY 4 EADPTGHSY 12

RESULT 18
ID YCBS_ECOLI STANDARD; PRT; 866 AA.
AC P75857;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN PEPN-PYRD INTERGENIC
DE REGION PRECURSOR.
GN YCBS.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RA BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF A FIMBRIAL
CC SUBUNIT ACROSS THE OUTER MEMBRANE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER FIMBRIAL EXPORT USHER PROTEINS.

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DR EMBL; AE000196; G1787172; -.
DR ECGENE; EG13711; YCBS.
DR PROSITE; PS01151; FIMBRIAL_USHER; 1.
KW HYPOTHETICAL PROTEIN; OUTER MEMBRANE; TRANSMEMBRANE; FIMBRIA;
KW TRANSPORT; SIGNAL.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 866 HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN
FT YCBS.
SQ SEQUENCE 866 AA; 95241 MW; 62A077F2 CRC32;

Query Match 59.3%; Score 48; DB 1; Length 866;
Best Local Similarity 50.0%; Pred. No. 1.79e+00;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 334 EIKADGSVNSY 345
:|||||:|
QY 1 DVKEADPTGHSY 12

RESULT 19
ID PCL_HUMAN STANDARD; PRT; 873 AA.
AC P22413;
DT 01-AUG-1991 (REL. 19, CREATED)
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 (ALKALINE PHOSPHODIESTERASE I
DE (EC 3.1.4.1) / NUCLEOTIDE PYROPHOSPHATASE (EC 3.6.1.9) (NPPASE)).
GN PCL.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91009202.
RA BUCKLEY M.F., LOVELAND K.A., MCKINSTRY W.J., GARSON O.M., GODING J.W.;
RL J. BIOL. CHEM. 265:17506-17511(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92246539.
RA FUNAKOSHI I., KATO H., HORIE K., YANO T., HORI Y., KOBAYASHI H.,
RA INOUE T., SUZUKI H., FUKUI S., TSUKAHARA M., RAJII T.,
RA YAMASHINA I.;
RL ARCH. BIOCHEM. BIOPHYS. 295:180-187(1992).
CC -1- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
CC -1- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
CC OLIGO-NUCLEOTIDES.
CC -1- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER
CC OF NON-LYMPHOID TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE
CC OF THE KIDNEY, CHONDROCYTES, AND EPIDIDYMIS.
CC -1- SIMILARITY: CONTAINS TWO TANDEM COPIES OF A SOMATOMEDIN-B TYPE
CC DOMAIN.
DR EMBL; M57736; G189650; -.
DR EMBL; D12485; G219945; -.
DR EMBL; D12485; G219944; ALT_INIT.
DR PIR; A39216; A39216.
DR MIM; 173335; -.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
KW GLYCOPROTEIN; TRANSMEMBRANE; DUPLICATION; SIGNAL-ANCHOR; HYDROLASE.
FT DOMAIN 1 24 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 25 45 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 46 873 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 52 92 SOMATOMEDIN-B LIKE.
FT DOMAIN 93 136 SOMATOMEDIN-B LIKE.
FT CARBOHYD 127 127 POTENTIAL.
FT CARBOHYD 233 233 POTENTIAL.
FT CARBOHYD 289 289 POTENTIAL.
FT CARBOHYD 425 425 POTENTIAL.
FT CARBOHYD 533 533 POTENTIAL.
FT CARBOHYD 591 591 POTENTIAL.

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FT CARBOHYD 648 648 POTENTIAL.
FT CARBOHYD 679 679 POTENTIAL.
FT CARBOHYD 696 696 POTENTIAL.
SQ SEQUENCE 873 AA; 99929 MW; 580583CD CRC32;

Query Match 59.3%; Score 48; DB 1; Length 873;
Best Local Similarity 66.7%; Pred. No. 1.79e+00;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 322 EPDSSGHSY 330
|:|:|
QY 4 EADPTGHSY 12

RESULT 20
ID KGUA_PIG STANDARD; PRT; 197 AA.
AC P31006;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GUANYLATE KINASE (EC 2.7.4.8) (GMP KINASE).
GN GUKI OR GUK.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE.
RC TISSUE-BRAIN;
RX MEDLINE; 93238695.
RA ZSCHOCKE P.D., SCHILTZ E., SCHULZ G.E.;
RL EUR. J. BIOCHEM. 213:263-269(1993).
CC -1- FUNCTION: ESSENTIAL FOR RECYCLING GMP AND INDIRECTLY, CGMP.
CC -1- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: TO OTHER GUANYLATE KINASES.
DR PIR; S23776; KIPGU.
DR HSP; P15454; 1GKY.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS0052; GUANYLATE_KINASE_2; 1.
KW TRANSFERASE; KINASE; ATP-BINDING; ACETYLATION.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT NP_BIND 10 17 ATP (BY SIMILARITY).
SQ SEQUENCE 197 AA; 21789 MW; 7F9FAF05 CRC32;

Query Match 58.0%; Score 47; DB 1; Length 197;
Best Local Similarity 54.5%; Pred. No. 3.12e+00;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 187 EIKKAQATGHS 197
:|:|:|
QY 1 DVKEADPTGHS 11

RESULT 21
ID GLNA_BACCE STANDARD; PRT; 443 AA.
AC P19064;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
GN GLNA.
OS BACILLUS CEREUS.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
RC STRAIN-IFO 3131.
RX MEDLINE; 90038764.
RA NAKANO Y., KATO C., TANAKA E., KIMURA K., HORIKOSHI K.;
RL J. BIOCHEM. 106:209-215(1989).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
CC ORTHOPHOSPHATE.
CC -1- ENZYME REGULATION: NOT REGULATED BY POST-TRANSLATIONAL

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CC MODIFICATION AND NOT SUBJECT TO FEEDBACK INHIBITION.
 CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 CC HEXAGON
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC EMBL: D00513; G216273; -.
 DR PIR: JU0075; AJBSQU.
 DR HSSP: P06201; ILGR.
 DR PROSITE: PS00180; GLNA_1; 1.
 DR PROSITE: PS00181; GLNA_ATP; 1.
 DR PROSITE: PS00182; GLNA_ADENYLATION; 1.
 KW NITROGEN FIXATION; LIGASE.
 FT INIT_MET 0
 SQ SEQUENCE 443 AA; 50064 MW; 5617AB71 CRC32;

Query Match 58.0%; Score 47; DB 1; Length 443;
 Best Local Similarity 33.3%; Pred. No. 3.12e+00;
 Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 332 EVRSVDPAAAPY 343
 QY 1 DVKEADPTGHSY 12
 :|: ||:::|

RESULT 22
 ID GLNA_BACSU STANDARD; PRT; 443 AA.
 AC P12425;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
 GN GLNA.
 OS BACILLUS SUBTILIS.
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89138001.
 RA STRAUCH M.A., ARONSON A.I., BROWN S.W., SCHREIER H.J.,
 RA SONENSHIN A.L.;
 RL GENE 71:257-265(1988).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
 RC STRAIN=PCI219;
 RX MEDLINE; 89232679.
 RA NAKANO Y., TANAKA E., KATO C., KIMURA K., HORIKOSHI K.;
 RL FEMS MICROBIOL. LETT. 48:81-86(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA BORCHERT S., KLEIN C., PIKSA B., HAMMELMANN M., ENTIAN K.D.;
 RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
 CC ORTHOPHOSPHATE.
 CC -1- ENZYME REGULATION: NOT REGULATED BY POST-TRANSLATIONAL
 CC MODIFICATION AND NOT SUBJECT TO FEEDBACK INHIBITION.
 CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 CC HEXAGON.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC EMBL: M22811; G142986; -.
 DR EMBL: D00854; G216396; -.
 DR EMBL: U66480; G1750111; -.
 DR PIR: JT0392; AJBSOS.
 DR HSSP: A48312; A48312.
 DR HSSP: P06201; ILGR.
 DR SUBTILIST; BG10425; GLNA.
 DR PROSITE: PS00180; GLNA_1; 1.
 DR PROSITE: PS00181; GLNA_ATP; 1.
 DR PROSITE: PS00182; GLNA_ADENYLATION; 1.
 KW NITROGEN FIXATION; LIGASE.
 FT INIT_MET 0
 SQ SEQUENCE 443 AA; 50147 MW; D0084747 CRC32;

Query Match 58.0%; Score 47; DB 1; Length 443;
 Best Local Similarity 33.3%; Pred. No. 3.12e+00;
 Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 332 EVRSVDPAAAPY 343
 QY 1 DVKEADPTGHSY 12
 :|: ||:::|

RESULT 22
 ID GLNA_BACSU STANDARD; PRT; 443 AA.
 AC P12425;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
 GN GLNA.
 OS BACILLUS SUBTILIS.
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89138001.
 RA STRAUCH M.A., ARONSON A.I., BROWN S.W., SCHREIER H.J.,
 RA SONENSHIN A.L.;
 RL GENE 71:257-265(1988).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
 RC STRAIN=PCI219;
 RX MEDLINE; 89232679.
 RA NAKANO Y., TANAKA E., KATO C., KIMURA K., HORIKOSHI K.;
 RL FEMS MICROBIOL. LETT. 48:81-86(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA BORCHERT S., KLEIN C., PIKSA B., HAMMELMANN M., ENTIAN K.D.;
 RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
 CC ORTHOPHOSPHATE.
 CC -1- ENZYME REGULATION: NOT REGULATED BY POST-TRANSLATIONAL
 CC MODIFICATION AND NOT SUBJECT TO FEEDBACK INHIBITION.
 CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 CC HEXAGON.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC EMBL: M22811; G142986; -.
 DR EMBL: D00854; G216396; -.
 DR EMBL: U66480; G1750111; -.
 DR PIR: JT0392; AJBSOS.
 DR HSSP: A48312; A48312.
 DR HSSP: P06201; ILGR.
 DR SUBTILIST; BG10425; GLNA.
 DR PROSITE: PS00180; GLNA_1; 1.
 DR PROSITE: PS00181; GLNA_ATP; 1.
 DR PROSITE: PS00182; GLNA_ADENYLATION; 1.
 KW NITROGEN FIXATION; LIGASE.
 FT INIT_MET 0
 SQ SEQUENCE 443 AA; 50147 MW; D0084747 CRC32;

Query Match 58.0%; Score 47; DB 1; Length 443;
 Best Local Similarity 33.3%; Pred. No. 3.12e+00;
 Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 332 EVRSVDPAAAPY 343
 QY 1 DVKEADPTGHSY 12
 :|: ||:::|

RESULT 23
 ID GLNA_LACDE STANDARD; PRT; 445 AA.
 AC P45627;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
 GN GLNA.
 OS LACTOBACILLUS DELBRUECKII (SUBSP. BULGARICUS).
 OC PROKARYOTA; FIRMICUTES; REGULAR ASPOROGENOUS ROD; LACTOBACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93073924.
 RA ISHINO Y., MORGENTHAUER P., HOTTINGER H., SOELL D.;
 RL APPL. ENVIRON. MICROBIOL. 58:3165-3169(1992).
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
 CC ORTHOPHOSPHATE.
 CC -1- ENZYME REGULATION: DOES NOT SEEM TO BE REGULATED BY ADENYLATION.
 CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 CC HEXAGON (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC EMBL: D10020; G216749; -.
 DR PROSITE; PS00180; GLNA_1; 1.
 DR PROSITE; PS00181; GLNA_ATP; 1.
 KW NITROGEN FIXATION; LIGASE.
 SQ SEQUENCE 445 AA; 50133 MW; F923BB07 CRC32;

Query Match 58.0%; Score 47; DB 1; Length 445;
 Best Local Similarity 33.3%; Pred. No. 3.12e+00;
 Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 335 EMRSTDPANPY 346
 QY 1 DVKEADPTGHSY 12
 :|: ||:::|

RESULT 24
 ID GLNA_STAAU STANDARD; PRT; 446 AA.
 AC Q59812;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE) (GS).
 GN GLNA.
 OS STAPHYLOCOCCUS AUREUS.
 OC PROKARYOTA; FIRMICUTES; COCCI; MICROCOCCACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BB270 / AS63;
 RA STRANDEN A.M., BERGER-BAECHI B.;
 RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) =
 CC ORTHOPHOSPHATE.
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) =
 CC ADP + GLUTAMINE + ORTHOPHOSPHATE.
 CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 CC HEXAGON (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC EMBL: X76490; E214721; -.
 DR PROSITE; PS00180; GLNA_1; 1.
 DR PROSITE; PS00181; GLNA_ATP; 1.
 KW NITROGEN FIXATION; LIGASE.
 SQ SEQUENCE 446 AA; 50840 MW; 830BFD81 CRC32;

Query Match 58.0%; Score 47; DB 1; Length 446;
 Best Local Similarity 33.3%; Pred. No. 3.12e+00;
 Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 335 EVRSVDPANPY 346
 :|: ||:::|
 QY 1 DVKEADPTGHSY 12

RESULT 25
 ID PEN3_ADEL2 STANDARD; PRT; 497 AA.
 AC P36716;
 DT 01-JUN-1994 (REL. 29, CREATED)
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PENTON PROTEIN (VIRION COMPONENT III) (PENTON BASE PROTEIN).
 GN PIII.
 OS HUMAN ADENOVIRUS TYPE 12.
 OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE; MASTADENOVIRUSES.
 CC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94076430.
 RA SPRENGEL J., SCHMITZ B., HEUSS-NEITZEL D., ZOCK C., DOERFLER W.;
 RL J. VIROL. 68:379-389(1994).
 DR EMBL; X73487; G313372; -.
 DR PIR; S33938; S33938.
 KW LATE PROTEIN.
 SQ SEQUENCE 497 AA; 56393 MW; A5BEC571 CRC32;

Query Match 58.0%; Score 47; DB 1; Length 497;
 Best Local Similarity 66.7%; Pred. No. 3.12e+00;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 310 ETDPKGRSY 318
 |::| |::|
 QY 4 EADPTGHSY 12

RESULT 26
 ID XRCC_HUMAN STANDARD; PRT; 633 AA.
 AC P18887;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE DNA-REPAIR PROTEIN XRCC1.
 GN XRCC1.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 CC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91061722.
 RA THOMPSON L.H., BROOKMAN K.W., JONES N.J., ALLEN S.A., CARRANO A.V.;
 RL MOL. CELL. BIOL. 10:6160-6171(1990).
 CC -!- FUNCTION: CORRECTS DEFECTIVE DNA STRAND-BREAK REPAIR AND SISTER
 CHROMATID EXCHANGE FOLLOWING TREATMENT WITH IONIZING RADIATION
 AND ALKYLATING AGENTS.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
 CC -!- SIMILARITY: SOME, TO S.POMBE RAD4/CUT5.
 DR EMBL; M36089; G340397; -.
 DR PIR; A36353; A36353.
 DR MIN; 194360; -.
 KW DNA REPAIR; NUCLEAR PROTEIN.
 SQ SEQUENCE 633 AA; 69525 MW; D382BC2E CRC32;

Query Match 58.0%; Score 47; DB 1; Length 633;
 Best Local Similarity 54.5%; Pred. No. 3.12e+00;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 201 VTASDPAGPSY 211
 |::| |::|
 QY 2 VKADPTGHSY 12

RESULT 27
 ID PA24_BUNMU STANDARD; PRT; 147 AA.
 AC P17934;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
 DE PHOSPHOLIPASE A2, BETA BUNGAROTOXIN A4 CHAIN PRECURSOR (EC 3.1.1.4)
 DE (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE).
 OS BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; REPTILIA;
 OC LEPIDOSAURIA; SERPENTES.
 CC [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM GLAND;
 RA DANSE J.M., GARNIER J.M., KEMP J.;
 RL NUCLEIC ACIDS RES. 18:4610-4610(1990).
 CC -!- FUNCTION: INHIBITS NEUROMUSCULAR TRANSMISSION BY BLOCKING
 ACETYLCHOLINE RELEASE FROM THE NERVE TERMINI. ACT PRESYNAPTICALLY.
 CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
 CC -!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
 PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -!- SUBUNIT: DIMER OF DISSIMILAR CHAINS LINKED BY ONE OR MORE
 DISULFIDE BONDS. THE A CHAINS HAVE PHOSPHOLIPASE A2 ACTIVITY AND
 THE B CHAINS SHOW HOMOMOLOGY WITH THE BASIC PROTEASE INHIBITORS.
 DR EMBL; X53408; G62506; -.
 DR PIR; S10982; PSKFA4.
 DR HSSP; P15445; IPSH.
 DR PROSITE; PS00118; PA2_HIS; 1.
 DR PROSITE; PS00119; PA2_ASP; 1.
 KW HYDROLASE; LIPID DEGRADATION; CALCIUM; MULTIGENE FAMILY; VENOM;
 KW PRESYNAPTIC NEUROTOXIN; SIGNAL.
 FT SIGNAL 1 27
 FT CHAIN 28 147 BETA BUNGAROTOXIN A4 CHAIN.
 FT ACT_SITE 75 75 BY SIMILARITY.
 FT ACT_SITE 119 119 BY SIMILARITY.
 FT DISULFID 42 42 INTERCHAIN (WITH A B CHAIN) (PROBABLE).
 FT DISULFID 54 146 BY SIMILARITY.
 FT DISULFID 56 72 BY SIMILARITY.
 FT DISULFID 71 127 BY SIMILARITY.
 FT DISULFID 78 120 BY SIMILARITY.
 FT DISULFID 88 113 BY SIMILARITY.
 FT DISULFID 106 118 BY SIMILARITY.
 FT CA_BIND 76 76 BY SIMILARITY.
 SQ SEQUENCE 147 AA; 16177 MW; 57165FE9 CRC32;

Query Match 56.8%; Score 46; DB 1; Length 147;
 Best Local Similarity 33.3%; Pred. No. 5.40e+00;
 Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 84 NIRDGDPKTSY 95
 :::: |::|
 QY 1 DVKEADPTGHSY 12

RESULT 28
 ID ARA2_ECOLI STANDARD; PRT; 583 AA.
 AC P52145;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ARSENICAL PUMP-DRIVING ATPASE (EC 3.6.1.-).
 GN ARSA.
 OS ESCHERICHIA COLI.
 OG PLASMID R46.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 CC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96275894.

RA BRUN D.F., LI J., SILVER S., ROBERTO F., ROSEN B.P.;
 RL FEMS MICROBIOL. LETT. 139:149-153(1996).
 CC -!- FUNCTION: ANION-TRANSPORTING ATPASE. CATALYSES THE EXTRUSION
 OF THE OXYANIONS ARSENITE, ANTIMONITE AND ARSENATE. MAINTENANCE
 OF A LOW INTRACELLULAR CONCENTRATION OF OXYANION PRODUCES
 RESISTANCE TO THE TOXIC AGENTS.

DR EMBL; U38947; G1061416; -.
 KW PLASMID; ARSENICAL RESISTANCE; ATP-BINDING.
 FT NP_BIND 15 22 ATP (POTENTIAL).
 FT NP_BIND 334 341 ATP (POTENTIAL).
 SQ SEQUENCE 583 AA; 63521 MW; 1071F37E CRC32;

Query Match 56.8%; Score 46; DB 1; Length 583;
 Best Local Similarity 50.0%; Pred. No. 5.40e+00;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 445 VMDTAPGHT 454
 I::: |||||
 QY 2 VREADPTGHS 11

RESULT 29
 ID ARAL_ECOLI STANDARD; PRT; 583 AA.

AC P08690;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE ARSENICAL PUMP-DRIVING ATPASE (EC 3.6.1.-).
 GN ARSA.

OS ESCHERICHIA COLI.

OG PLASMID R773.

OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 CC ENTEROBACTERIACEAE.

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE; 87033737.

RA CHEN C.-M., MISRA T.K., SILVER S., ROSEN B.P.;

RL J. BIOL. CHEM. 261:15030-15038(1986).

RN [2]

RP REVIEW.

RX MEDLINE; 91126299.

RA ROSEN B.P.;

RL RES. MICROBIOL. 141:336-341(1990).

CC -!- FUNCTION: ANION-TRANSPORTING ATPASE. CATALYSES THE EXTRUSION
 OF THE OXYANIONS ARSENITE, ANTIMONITE AND ARSENATE. MAINTENANCE
 OF A LOW INTRACELLULAR CONCENTRATION OF OXYANION PRODUCES
 RESISTANCE TO THE TOXIC AGENTS.

CC

CC

DR EMBL; J02591; G151857; -.

DR PIR; A25937; A25937.

KW PLASMID; ARSENICAL RESISTANCE; ATP-BINDING.

FT NP_BIND 15 22 ATP (POTENTIAL).

FT NP_BIND 334 341 ATP (POTENTIAL).

SQ SEQUENCE 583 AA; 63188 MW; 79BAEF0A CRC32;

Query Match 56.8%; Score 46; DB 1; Length 583;
 Best Local Similarity 50.0%; Pred. No. 5.40e+00;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 445 VMDTAPGHT 454
 I::: |||||
 QY 2 VREADPTGHS 11

RESULT 30
 ID VP57_BDV STANDARD; PRT; 503 AA.

AC P52638;

DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE 57 KD PROTEIN (P57).

OS BORNA DISEASE VIRUS (BDV).

CC VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; BORNAVIRIDAE.

RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=V;
 RX MEDLINE; 94240137.
 RA BRIESE T., SCHNEEMANN A., LEWIS A.J., PARK Y.-S., KIM S.,
 RA LUDWIG H., LIPKIN W.I.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 91:4362-4366(1994).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

DR EMBL; U04608; G516506; -.

KW GLYCOPROTEIN; TRANSMEMBRANE.

FT TRANSMEM 5 25

FT TRANSMEM 274 294 POTENTIAL.

FT TRANSMEM 468 488 POTENTIAL.

FT CARBOHYD 63 63 POTENTIAL.

FT CARBOHYD 109 109 POTENTIAL.

FT CARBOHYD 139 139 POTENTIAL.

FT CARBOHYD 192 192 POTENTIAL.

FT CARBOHYD 196 196 POTENTIAL.

FT CARBOHYD 202 202 POTENTIAL.

FT CARBOHYD 221 221 POTENTIAL.

FT CARBOHYD 230 230 POTENTIAL.

FT CARBOHYD 235 235 POTENTIAL.

FT CARBOHYD 321 321 POTENTIAL.

FT CARBOHYD 328 328 POTENTIAL.

FT CARBOHYD 388 388 POTENTIAL.

FT CARBOHYD 438 438 POTENTIAL.

SQ SEQUENCE 503 AA; 56652 MW; 5B493E19 CRC32;

Query Match 55.6%; Score 45; DB 1; Length 503;
 Best Local Similarity 55.6%; Pred. No. 9.26e+00;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 416 ETDPINHAY 424
 I::: |||||
 QY 4 EADPTGHSY 12

RESULT 31

ID PBP2_NEIGO STANDARD; PRT; 581 AA.

AC P08149;

DT 01-AUG-1988 (REL. 08, CREATED)

DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)

DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)

DE PENICILLIN-BINDING PROTEIN 2 (PBP-2).

GN PENA.

OS NEISSERIA GONORRHOEA.

OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;

CC NEISSERIACEAE.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 88156937.

RA SPRATT B.G.;

RL NATURE 332:173-176(1988).

CC -!- CATALYTIC ACTIVITY: SYNTHESIS OF CROSS-LINKED PEPTIDOGLYCAN FROM
 THE LIPID INTERMEDIATES. THE ENZYME HAS AN N-TERMINAL PENICILLIN

CC INSENSITIVE TRANSGLYCOSYLASE DOMAIN (FORMATION OF LINEAR GLYCAN
 STRANDS) & A CARBOXY-TERMINAL PENICILLIN-SENSITIVE TRANSEPTIDASE

CC DOMAIN (CROSS-LINKING OF THE PEPTIDE SUBUNITS).

CC -!- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.

CC -!- SUBCELLULAR LOCATION: INNER MEMBRANE.

CC -!- THIS PROTEIN WAS SEQUENCED IN PENICILLIN-SENSITIVE STRAINS LM306,

CC AND FA19, AND IN PENICILLIN-RESISTANT STRAINS CDC84-060384,

CC CDC84-060418 AND CDC77-124615. THE SEQUENCE SHOWN IS THAT OF

CC STRAIN LM306.

DR EMBL; M32091; G150279; -.

DR EMBL; X07468; G44911; -.

DR EMBL; X07469; G44913; -.

DR EMBL; X07470; G44915; -.

DR PIR; S00916; S00916.

KW INNER MEMBRANE; PEPTIDOGLYCAN SYNTHESIS; CELL DIVISION; CELL WALL;

KW ANTIBIOTIC RESISTANCE; MULTIFUNCTIONAL ENZYME.

FT ACT_SITE 310 310 ACYLATED BY PENICILLIN.

FT VARIANT 346 346 D -> DD (IN CDC84-060418, CDC77-124615,

AND CDC84-060384).

FT VARIANT 504 504 F -> L (IN CDC84-060418, CDC77-124615,
 AND CDC84-060384).
 FT VARIANT 510 510 A -> V (IN CDC84-060418, CDC77-124615,
 AND CDC84-060384).
 FT VARIANT 516 516 A -> G (IN CDC84-060418, CDC77-124615,
 AND CDC84-060384).
 FT VARIANT 541 541 H -> N (IN FA19 AND CDC84-060418).
 FT VARIANT 551 551 P -> S (IN CDC77-124615).
 FT VARIANT 551 551 P -> L (IN CDC84-060384).
 FT VARIANT 552 552 P -> V (IN CDC84-060418).
 FT VARIANT 555 555 KI -> QV (IN CDC84-060418).
 FT VARIANT 556 556 I -> V (IN CDC84-060418).
 FT VARIANT 574 574 A -> NV (IN CDC84-060418).
 SQ SEQUENCE 581 AA; 63650 MW; D1275110 CRC32;

Query Match 55.6%; Score 45; DB 1; Length 581;
 Best Local Similarity 45.5%; Pred. No. 9.26e+00;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 533 VTIDEPTAHGY 543
 | :||:|:|
 QY 2 VKADPTGHSY 12

RESULT 32
 ID PBP2_NEIME STANDARD; PRT; 581 AA.
 AC P11882;
 DT 01-OCT-1989 (REL. 12, CREATED)
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE PENICILLIN-BINDING PROTEIN 2 (PBP-2).
 GN PNA.
 OS NEISSERIA MENINGITIDIS.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
 OC NEISSERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SEROGROUP B, STRAIN C311;
 RA MEDLINE; 89345099.
 RX XHANG Q.-Y., SPRATT B.G.;
 RL NUCLEIC ACIDS RES. 17:5383-5383(1989).
 CC -1- CATALYTIC ACTIVITY: SYNTHESIS OF CROSS-LINKED PEPTIDOGLYCAN FROM
 THE LIPID INTERMEDIATES. THE ENZYME HAS AN N-TERMINAL PENICILLIN
 INSENSITIVE TRYGLYCOSYLASE DOMAIN (FORMATION OF LINEAR GLYCAN
 STRANDS) & A CARBOXY-TERMINAL PENICILLIN-SENSITIVE TRANSEPTIDASE
 DOMAIN (CROSS-LINKING OF THE PEPTIDE SUBUNIT).
 CC -1- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: INNER MEMBRANE.
 DR EMBL; X15276; G45178; -.
 DR PIR; S04857; S04857.
 KW INNER MEMBRANE; PEPTIDOGLYCAN SYNTHESIS; CELL DIVISION; CELL WALL;
 KW ANTIBIOTIC RESISTANCE; MULTIFUNCTIONAL ENZYME.
 FT ACT_SITE 310 310 ACYLATED BY PENICILLIN.
 SQ SEQUENCE 581 AA; 63604 MW; 806E7D60 CRC32;

Query Match 55.6%; Score 45; DB 1; Length 581;
 Best Local Similarity 45.5%; Pred. No. 9.26e+00;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 533 VTIDEPTAHGY 543
 | :||:|:|
 QY 2 VKADPTGHSY 12

RESULT 33
 ID MYT1_HUMAN STANDARD; PRT; 725 AA.
 AC Q01538;
 DT 01-JUL-1993 (REL. 26, CREATED)
 DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE MYELIN TRANSCRIPTION FACTOR 1 (MYT1) (MYT1) (PROTEOLIPID PROTEIN
 BINDING PROTEIN) (PLPBI) (FRAGMENT).
 GN PLPBI OR MYT1 OR MYT1.

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA MEDLINE; 93078764.
 RX KIM J.G., HUDSON L.D.;
 RL MOL. CELL. BIOL. 12:5632-5639(1992).
 CC -1- FUNCTION: BINDS TO THE PROMOTER REGIONS OF PROTEOLIPID PROTEINS
 OF THE CENTRAL NERVOUS SYSTEM.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: MOSTLY IN DEVELOPING NERVOUS SYSTEM.
 CC -1- DOMAIN: CONTAINS SIX ZINC FINGERS OF THE C2HC CLASS ARRANGED IN
 TWO WIDELY SEPARATED CLUSTERS. THESE TWO DOMAINS OF DNA BINDING
 CAN FUNCTION INDEPENDENTLY AND RECOGNIZE THE SAME DNA SEQUENCE.
 DR EMBL; M96980; G189042; -.
 DR PIR; A45033; A45033.
 DR PIR; S27964; S27964.
 DR MIM; 600379; -.
 KW TRANSCRIPTION REGULATION; ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN;
 KW REPEAT.
 FT NON_TER 1 1
 FT ZN_FING 17 43 C2HC-TYPE.
 FT ZN_FING 61 87 C2HC-TYPE.
 FT ZN_FING 402 428 C2HC-TYPE.
 FT ZN_FING 451 472 C2HC-TYPE.
 FT ZN_FING 495 521 C2HC-TYPE.
 FT ZN_FING 548 574 C2HC-TYPE.
 SQ SEQUENCE 725 AA; 79149 MW; 6143A6FA CRC32;

Query Match 55.6%; Score 45; DB 1; Length 725;
 Best Local Similarity 33.3%; Pred. No. 9.26e+00;
 Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 348 EPESEPAHSF 359
 | :||:|:|:|
 QY 1 DVKEADPTGHSY 12

RESULT 34
 ID TIR1_ECOLI STANDARD; PRT; 1033 AA.
 AC P10486;
 DT 01-JUL-1989 (REL. 11, CREATED)
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE TYPE I RESTRICTION ENZYME ECOR124II R PROTEIN (EC 3.1.21.3).
 GN HSDR OR HSR.
 OS ESCHERICHIA COLI.
 OG PLASMID R124/3.
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 OC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 89178628.
 RA PRICE C., LINGNER J., BICKLE J., FIRMAN T.A., GLOVER S.W.;
 RL J. MOL. BIOL. 205:115-125(1989).
 CC -1- FUNCTION: THE ECOR124/3 I ENZYME RECOGNIZES 5'GAA(N7)ATCG.
 CC -1- FUNCTION: SUBUNIT R IS REQUIRED FOR BOTH NUCLEASE AND ATPASE
 ACTIVITIES, BUT NOT FOR MODIFICATION.
 CC -1- SUBUNIT: THE TYPE I RESTRICTION & MODIFICATION SYSTEM IS COMPOSED
 OF THREE POLYPEPTIDES R,M AND S.
 CC -1- TYPE I RESTRICTION AND MODIFICATION ENZYMES ARE COMPLEX, MULTI-
 FUNCTIONAL SYSTEMS WHICH REQUIRE ATP, S-ADENOSYL METHIONINE AND
 MG(2+) AS CO-FACTORS AND, IN ADDITION TO THEIR ENDONUCLEOLYTIC
 AND METHYLASE ACTIVITIES, ARE POTENT DNA-DEPENDENT ATPASES.
 CC -1- SIMILARITY: WITH ATPASES.
 DR EMBL; X13145; G41750; -.
 DR PIR; S02168; S02168.
 DR REBASE; RE00748; ECOR124II.
 KW PLASMID; RESTRICTION SYSTEM; DNA-BINDING; ATP-BINDING.
 SQ SEQUENCE 1033 AA; 119656 MW; 9E988CC1 CRC32;

Query Match 55.6%; Score 45; DB 1; Length 1033;
 Best Local Similarity 75.0%; Pred. No. 9.26e+00;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 23 AEPTGDSY 30
 I:|||||
 QY 5 ADPTGHSY 12

RESULT 35
 ID YHV4_LACHE STANDARD; PRT; 22 AA.
 AC P22296;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT 01-AUG-1991 (REL. 19, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL PROTEIN IN HLV 3'REGION (ORF4) (FRAGMENT).
 OS LACTOBACILLUS HELVETICUS.
 OC PROKARYOTA; FIRMICUTES; REGULAR ASPOROGENOUS ROD; LACTOBACILLACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-481;
 RX MEDLINE; 91035244.
 RA JOERGER M.C.; KLAENHAMMER T.R.;
 RL J. BACTERIOL. 172:6339-6347(1990).
 DR EMBL; M59360; G149556; -.
 DR PIR; D37145; D37145.
 KW HYPOTHETICAL PROTEIN.
 FT NON_TER 22
 SQ SEQUENCE 22 AA; 2484 MW; DE81C16E CRC32;

Query Match 54.3%; Score 44; DB 1; Length 22;
 Best Local Similarity 40.0%; Pred. No. 1.57e+01;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 9 KGNSTGQY 18
 I:|||||
 QY 3 KEADPTGHSY 12

Search completed: Tue Apr 7 08:41:45 1998
 Job time : 16 secs.

MAISREH (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:42:35 1998; MasPar time 5.37 Seconds
Tabular output not generated. 95.819 Million cell updates/sec

Title: >US-08-190-411A-4
Description: (1-12) from 5541104.pep
Perfect Score: 81
Sequence: 1 DVKEADPTGHSY 12

Scoring table: PAM 150
Gap 15

Searched: 195121 seqs, 42852602 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: pir55
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 18.565; Variance 47.138; scale 0.394

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	81	100.0	280	2	JC2358 TOIG of: jc2358 check	8.03e-03
2	74	91.4	234	2	I38667 A:Title: Structure, ch 7.31e-02	7.31e-02
3	74	91.4	315	2	I38668 A:Title: Structure, ch 7.31e-02	7.31e-02
4	72	88.9	369	2	I38659 A:Title: Structure, ch 1.36e-01	1.36e-01
5	71	87.7	319	2	I38660 A:Title: Structure, ch 1.85e-01	1.85e-01
6	62	76.5	317	2	JC2359 A:Accession: PH1298.	2.84e+00
7	59	72.8	317	2	I38661 A:Accession: PH1297.	6.86e+00
8	57	70.4	347	2	I38008 TOIG of: i38008 check	1.23e+01
9	53	65.4	314	2	JC2360 A:Title: Structure, ch 3.85e+01	3.85e+01
10	52	64.2	417	2	SL6582 TOIG of: sl6582 check	5.09e+01
11	51	63.0	334	2	E69361 A:Accession: E69361.	6.73e+01
12	50	61.7	314	2	JC2361 A:Title: Human gene MA	8.87e+01
13	50	61.7	381	2	S29560 A:Accession: S29560.	8.87e+01
14	50	61.7	835	2	A49891 TOIG of: a49891 check	8.87e+01
15	49	60.5	417	2	A43929 A:Accession: A39246.	1.17e+02
16	49	60.5	3828	1	MELITNELLY This is a DE line.	1.17e+02
17	48	59.3	90	2	I46953 A:CROSS-references: GB	1.53e+02
18	48	59.3	150	2	S55370 A:CROSS-references: EM	1.53e+02
19	48	59.3	269	2	A49334 TOIG of: a49334 check	1.53e+02
20	48	59.3	866	2	C64834 A:Title: The complete	1.53e+02
21	48	59.3	875	2	G69910 A:Status: preliminary;	1.53e+02
22	48	59.3	925	2	A39216 A:Accession: S51030.	1.53e+02
23	47	58.0	137	1	KIPGGU TOIG of: kippgu check	2.01e+02

A:Contents: L. d. bulg
TOIG of: s3938 check
TOIG of: ajbscu check
A:Experimental source:
A:Accession: A36353.
A:Accession: PH1299.
A:Accession: PH1300.
C:Keywords: calcium; c
A:Accession: S54702.
TOIG of: S25483 check
TOIG of: S65289 check
TOIG of: S66740 check
F:117-121/Region: nucl
F:117-121/Region: nucl
A:Experimental source:
TOIG of: S49923 check
TOIG of: S00916 check
TOIG of: S04857 check
TOIG of: S04857 check
A:CROSS-references: EM
TOIG of: S02168 check
TOIG of: S02168 check
A:Accession: D37145.
A:CROSS-references: EM
A:Title: Bacillus subt
A:Status: preliminary;
TOIG of: S52899 check
A:Accession: S52537.
TOIG of: S55631 check
A:Accession: S75150.
F:25-103/Domain: cytoc
TOIG of: S55874 check
A:Accession: D36904.
A:Accession: E69513.
TOIG of: S54567 check
TOIG of: ajzrq1 check
A:Accession: S46631.
F:17-350/Domain: gelso
A:Accession: I28949.
A:CROSS-references: EM
TOIG of: S64312 check
TOIG of: S44753 check
C:Superfamily: cellula
TOIG of: S44753 check
A:Authors: Geoghagen,
A:Accession: B56556.
A:Accession: D69531.
TOIG of: B36307 check
TOIG of: G00041 check
TOIG of: S37664 check
A:Accession: I38029.
TOIG of: S44842 check
TOIG of: B42161 check
TOIG of: A42161 check
A:Accession: S07103.
F:286-408/Domain: cAMP
A:Accession: A32434.
TOIG of: S44543 check
F:492-773/Domain: lacy
F:492-773/Domain: lacy
F:2123-2198/Domain: ac
A:Title: A giant nucle
A:CROSS-references: GB
C:Date: 30-Sep-1993 #s
TOIG of: gnvqwa check
A:Status: preliminary;
TOIG of: S63404 check
TOIG of: S63404 check
C:Superfamily: dihydro
TOIG of: A42421 check
A:Experimental source:
This is a DE line.
TOIG of: rgaswa check
TOIG of: S49901 check
TOIG of: S38928 check

MEGSVLTIVL

DUCTIVE

S49901

S38928

97 42 51.9 773 2 S46011 A:Accession: S46620. 7.44e+02
98 42 51.9 799 2 A34729 TOIG of: a34729 check 7.44e+02
99 42 51.9 960 2 UCH TOIG of: b47093 check 7.44e+02
100 42 51.9 1132 2 S37932 A:Cross-references: EM 7.44e+02

ALIGNMENTS

RESULT 1
ID JC2358 STANDARD; PRT; 280 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: jc2358 check: 467 from: 1 to: 280.
XX
CC TOIG of: jc2358 check: 467 from: 1 to: 280
CC
CC >P1:JC2358
CC tumor-associated antigen , MAGE-1 - human
CC C:Species: Homo sapiens (man)
CC C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 15-Mar-1996
CC C:Accession: JC2358
CC R: Ding, M.; Beck, R.J.; Keller, C.J.; Panton, R.G.
CC Biochem. Biophys. Res. Commun. 202, 549-555, 1994
CC A:Title: Cloning and analysis of MAGE-1-related genes.
CC A:Reference number: JC2358
CC A:Accession: JC2358
CC A:Molecule type: mRNA
CC A:Residues: 1-280 <DIN>
CC A:Experimental source: melanoma cell line DM150
CC C:Genetics:
CC A:Gene: MAGE
CC F:161-169/Region: HLA-A1 binding #status predicted
SQ SEQUENCE 280 AA; 30932 MW; 426797 CN;

Query Match 100.0%; Score 81; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.03e-03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 158 DVKEADPTGHSY 169
Y 1 DVKEADPTGHSY 12
|||||

RESULT 2
ID I38667 STANDARD; PRT; 234 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A:Title: Structure, chromosomal localization, and expression of 12 genes o
f the MAGE family.
XX

CC A:Title: Structure, chromosomal localization, and expression of 12 genes
of the MAGE family.
CC A:Reference number: I38659; MUID:95012457
CC A:Accession: I38667
CC A:Status: preliminary; translated from GB/EMBL/DDBJ
CC A:Molecule type: DNA
CC A:Residues: 1-234 <RES>
CC A:Cross-references: EMBL:U10693; NID:g533525; PID:g533526
CC C:Genetics:
CC A:Gene: GDB:MAGE8

CC A:Cross-references: GDB:331123
CC A:Map position: Xq28-Xq28
CC A:Introns: #status absent
SQ SEQUENCE 234 AA; 25197 MW; 296950 CN;

Query Match 91.4%; Score 74; DB 2; Length 234;

Best Local Similarity 83.3%; Pred. No. 7.31e-02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 168 DVKEVDPAHGSY 179
Y 1 DVKEADPTGHSY 12
|||||

RESULT 3
ID I38668 STANDARD; PRT; 315 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A:Title: Structure, chromosomal localization, and expression of 12 genes o
f the MAGE family.
XX

CC A:Title: Structure, chromosomal localization, and expression of 12 genes
of the MAGE family.
CC A:Reference number: I38659; MUID:95012457
CC A:Accession: I38668
CC A:Status: preliminary; translated from GB/EMBL/DDBJ
CC A:Molecule type: DNA
CC A:Residues: 1-315 <RES>
CC A:Cross-references: EMBL:U10694; NID:g533527; PID:g533528
CC C:Genetics:
CC A:Gene: GDB:MAGE9
CC A:Cross-references: GDB:331125
CC A:Map position: Xp21.3-Xp21.3
CC A:Introns: #status absent
SQ SEQUENCE 315 AA; 35088 MW; 553046 CN;

Query Match 91.4%; Score 74; DB 2; Length 315;
Best Local Similarity 83.3%; Pred. No. 7.31e-02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 164 DVKEVDPAHGSY 175
Y 1 DVKEADPTGHSY 12
|||||

RESULT 4
ID I38659 STANDARD; PRT; 369 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A:Title: Structure, chromosomal localization, and expression of 12 genes o
f the MAGE family.
XX

CC A:Title: Structure, chromosomal localization, and expression of 12 genes
of the MAGE family.
CC A:Reference number: I38659; MUID:95012457
CC A:Accession: I38659
CC A:Status: preliminary; translated from GB/EMBL/DDBJ
CC A:Molecule type: DNA
CC A:Residues: 1-369 <RES>
CC A:Cross-references: EMBL:U10685; NID:g533510; PID:g533511
CC C:Genetics:
CC A:Gene: GDB:MAGE10

CC A:Cross-references: GDB:331126
CC A:Map position: Xq28-Xq28
CC A:Introns: #status absent
SQ SEQUENCE 369 AA; 40766 MW; 735605 CN;

Query Match 88.9%; Score 72; DB 2; Length 369;
Best Local Similarity 83.3%; Pred. No. 1.36e-01;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 190 DVKEVDPTGHSF 201
Y 1 DVKEADPTGHSY 12
|||||

XX	xxxxxx
XX	01-JAN-1900
XX	A;Accession: PH1297.
XX	A;Accession: PH1297
CC	A:Molecule type: DNA
CC	A:Residues: 169-177 <TRA>
CC	C:Genetics:
CC	A:Gene: GDB:MAGE4
CC	A:Cross-references: GDB:331119
CC	A:Map position: Xq28-Xq28
CC	A:Introns: #status absent
SQ	SEQUENCE 317 AA; 34899 MW; 528124 CN;
Query Match 72.8%; Score 59; DB 2; Length 317;	
Best Local Similarity 58.3%; Pred. NO. 6.86e+00;	
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	
Db	166 DVKEVDPASNTY 177 :::
Qy	1 DVKEADPTGHSY 12
RESULT	8
ID	I38008 STANDARD; PRT; 347 AA.
XX	xxxxxx
XX	01-JAN-1900
XX	TOIG of: i38008 check: 8233 from: 1 to: 347.
XX	TOIG of: i38008 check: 8233 from: 1 to: 347
CC	>P1:I38008
CC	MAGE-xp protein - human
CC	C:Species: Homo sapiens (man)
CC	C>Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 06-Sep-1996
CC	C:Accession: I38008; S52167
CC	R:Muscattelli, F.; Walker, A.P.; De Plaen, E.; Stafford, A.N.; Monaco, A.P.
CC	Proc. Natl. Acad. Sci. U.S.A. 92, 4987-4991, 1995
CC	A>Title: Isolation and characterization of a MAGE gene family in the Xp21.3 region.
CC	A:Reference number: I38008; MUID:95281581
CC	A:Accession: I38008
CC	A>Status: preliminary
CC	A:Molecule type: mRNA
CC	A:Residues: 1-347 <RES>
CC	A:Cross-references: EMBL:X82539; NID:g608992; PID:g608993
CC	C:Genetics:
CC	A:Gene: GDB:MAGELI-LSB
CC	A:Cross-references: GDB:635712
CC	A:Map position: Xp21.3-Xp21.3
SQ	SEQUENCE 347 AA; 39152 MW; 610197 CN;
Query Match 70.4%; Score 57; DB 2; Length 347;	
Best Local Similarity 50.0%; Pred. No. 1.23e+01;	
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;	
Db	164 DLKEDNPFSSHTY 175 : : ::
Qy	1 DVKEADPTGHSY 12
RESULT	9
ID	JC2360 STANDARD; PRT; 314 AA.
XX	xxxxxx

```
XX 01-JAN-1900
DT
DE A:Title: Structure, chromosomal localization, and expression of 12 genes o
f the MAGE family.
XX
CC A:Title: Structure, chromosomal localization, and expression of 12 genes
of the MAGE family.
CC A:Reference number: I38659; MUID:95012457
CC A:Accession: I38665
CC A>Status: preliminary; translated from GB/EMBL/DBDJ
CC A:Molecule type: DNA
CC A:Residues: 1-314 <RES>
CC A:Cross-references: EMBL:U10691; NID:G533522; PID:G533523
CC R:Fenton, R.G.
CC submitted to the EMBL Data Library, June 1994
CC A:Reference number: G07126
CC A:Accession: G01445
CC A>Status: preliminary; translated from GB/EMBL/DBDJ
CC A:Molecule type: mRNA
CC A:Residues: 1-314 <FEN>
CC A:Cross-references: EMBL:U10339; NID:G499121; PID:G499122
CC C:Genetics:
CC A:Gene: GDB:MAGE6
CC A:Cross-references: GDB:331121
CC A:Map position: Xq28-Xq28
CC A:Introns: #status absent
CC F:168-176/Region: HLA-A1 binding #status predicted
SQ SEQUENCE 314 AA; 34891 MW; 534374 CN;

Query Match 65.4%; Score 53; DB 2; Length 314;
Best Local Similarity 50.0%; Pred. No. 3.85e+01;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 165 ELMVEDPIGHVY 176
::: ||| ||
Qy 1 DVKEADPTGHSY 12

RESULT 10
ID S16582 STANDARD; PRT; 417 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: s16582 check: 7441 from: 1 to: 417.
XX
XX TOIG of: s16582 check: 7441 from: 1 to: 417
XX
CC >P1.S16582
CC fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - Arabidopsi
s thaliana
CC C:Species: Arabidopsis thaliana (mouse-ear cress)
CC C:Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 08-Sep-19
97
CC C:Accession: S16582
CC R:Horsnell, P.R.; Raines, C.A.
CC Plant Mol. Biol. 17, 185-186, 1991
CC A:Title: Nucleotide sequence of a cDNA clone encoding chloroplast fructos
e-1,6-bisphosphatase from Arabidopsis thaliana.
CC A:Reference number: S16582; MUID:91329733
CC A:Accession: S16582
CC A:Molecule type: mRNA
CC A:Residues: 1-417 <HOR>
CC A:Cross-references: EMBL:X58148; NID:g11241; PID:g11242
CC A:Experimental source: clone AFBP1
CC C:Genetics:
CC A:Genome: nuclear
CC C:Superfamily: fructose-bisphosphatase
CC C:Keywords: Calvin cycle; chloroplast; gluconeogenesis; phosphoric monoes
ter hydrolase
CC F.1.58/Domain: transit peptide (chloroplast) #status predicted <TNP>
```

```
CC F:59-417/Product: fructose-bisphosphatase #status predicted <MAT>
SQ SEQUENCE 417 AA; 45177 MW; 917183 CN;

Query Match 64.2%; Score 52; DB 2; Length 417;
Best Local Similarity 50.0%; Pred. No. 5.09e+01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 314 DLKDPGPTGKPY 325
I::: ||| :|
Qy 1 DVKEADPTGHSY 12

RESULT 11
ID E69361 STANDARD; PRT; 334 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A:Accession: E69361.
XX
CC A:Accession: E69361
CC A>Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A:Molecule type: DNA
CC A:Residues: 1-334 <KLE>
CC A:Cross-references: GB:AE000782; TIGR:AF0893
SQ SEQUENCE 334 AA; 38033 MW; 575945 CN;

Query Match 63.0%; Score 51; DB 2; Length 334;
Best Local Similarity 41.7%; Pred. No. 6.73e+01;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 314 EVKDNEPTGTGF 325
::: ||| :
Qy 1 DVKEADPTGHSY 12

RESULT 12
ID JC2361 STANDARD; PRT; 314 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A:Title: Human gene MAGE-3 codes for an antigen recognized on a melanoma b
y autologous cytolytic T lymphocytes.
XX
CC A:Title: Human gene MAGE-3 codes for an antigen recognized on a melanoma
by autologous cytolytic T lymphocytes.
CC A:Reference number: I38438; MUID:94157413
CC A:Accession: I38438
CC A>Status: preliminary; translated from GB/EMBL/DBDJ
CC A:Molecule type: DNA
CC A:Residues: 1-314 <RES>
CC A:Cross-references: EMBL:U03735; NID:G468825; PID:G468826
CC C:Genetics:
CC A:Gene: MAGE-3
CC F:168-176/Region: HLA-A1 binding #status predicted
SQ SEQUENCE 314 AA; 34747 MW; 538982 CN;

Query Match 61.7%; Score 50; DB 2; Length 314;
Best Local Similarity 50.0%; Pred. No. 8.87e+01;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 165 ELMVEDPIGHLY 176
::: ||| ||
Qy 1 DVKEADPTGHSY 12

RESULT 13
ID S29560 STANDARD; PRT; 381 AA.
XX
```

```
AC xxxxxx
XX
XX 01-JAN-1900
XX
DE A;Accession: S29560.
XX
XX A;Accession: S29560
CC A:Molecule type: mRNA
CC A;Residues: 1-381 <CAR>
CC A;Cross-references: EMBL:X68826; NID:g20716; PID:g20717
CC C;Superfamily: fructose-bisphosphatase
CC C;Keywords: phosphoric monoester hydrolase
SQ SEQUENCE 381 AA; 41821 MW; 781009 CN;

Query Match 61.7%; Score 50; DB 2; Length 381;
Best Local Similarity 50.0%; Pred. No. 8.87e+01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 278 DLKEPGSGPKY 289
   |||: |||: |
QY 1 DVKEADPTGHSY 12

RESULT 14
ID A49891 STANDARD; PRT; 835 AA.
XX
AC xxxxxx
XX 01-JAN-1900
XX
DE TOIG of: a49891 check: 6404 from: 1 to: 835.
XX
XX TOIG of: a49891 check: 6404 from: 1 to: 835
CC
CC >P1:A49891
CC outer membrane protein Fasd precursor - Escherichia coli
CC C;Species: Escherichia coli
CC C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 14-Nov-1997
CC C;Accession: A49891
CC R;Schifferli, D.M.; Alrutiz, M.A.
CC J. Bacteriol. 176, 1099-1110, 1994
CC A;Title: Permissive linker insertion sites in the outer membrane protein
of 987P fimbriae of Escherichia coli.
CC A;Reference number: A49891
CC A;Accession: A49891
CC A;Status: preliminary
CC A:Molecule type: DNA
CC A;Residues: 1-835 <SCH>
CC A;Cross-references: GB:L22659; NID:g437334; PID:g437336
CC C;Genetics:
CC A;Gene: fasD
CC C;Superfamily: hypothetical protein b0532
CC C;Keywords: membrane protein
SQ SEQUENCE 835 AA; 92353 MW; 3824200 CN;

Query Match 61.7%; Score 50; DB 2; Length 835;
Best Local Similarity 50.0%; Pred. No. 8.87e+01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 324 NIKADGSEHSF 335
   ::|||: ||:
QY 1 DVKEADPTGHSY 12

RESULT 15
ID A43929 STANDARD; PRT; 417 AA.
XX
AC xxxxxx
XX 01-JAN-1900
XX
XX A;Accession: A39246.

XX
CC A;Accession: A39246
CC A:Molecule type: mRNA
CC A;Residues: 1-417 <RE2>
CC A;Cross-references: GB:M27717; NID:g179933; PID:g179934
CC R;Goldstein, S.M.; Kaempfer, C.E.; Kealey, J.T.; Wintroub, B.U.
CC J. Clin. Invest. 83, 1630-1636, 1989
CC A;Title: Human mast cell carboxypeptidase. Purification and characterizat
ion.
CC A;Reference number: A45759
CC A;Accession: A45759
CC A:Molecule type: protein
CC A;Residues: 110-137 <GOL>
CC C;Genetics:
CC A;Gene: GDB:CPA3
CC A;Cross-references: GDB:l25231; OMIM:l14851
CC A;Map position: 3q21.3-3q25
CC A;Introns: 23/2; 48/3; 90/2; 124/3; 158/3; 192/3; 229/3; 260/1; 327/3; 35
6/1
CC C;Superfamily: carboxypeptidase
CC C;Keywords: hydrolase; metallo-carboxypeptidase; metalloprotein; protein
digestion; zinc; zymogen
CC F;1-15/Domain: signal sequence #status predicted <SIG>
CC F;110-109/Domain: activation peptide #status predicted <ACT>
CC F;110-417/Product: carboxypeptidase A, mast cell #status predicted <MAT>
CC F;176-179,304/Binding site: zinc (His, Glu, His) #status predicted
CC F;245-268/Disulfide bonds: #status predicted
CC F;356,378/Active site: Tyr, Glu #status predicted
SQ SEQUENCE 417 AA; 48700 MW; 936226 CN;

Query Match 60.5%; Score 49; DB 2; Length 417;
Best Local Similarity 56.7%; Pred. No. 1.17e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 105 DVKEDIPGRHSY 116
   |||| | |||
QY 1 DVKEADPTGHSY 12

RESULT 16
ID MELITNELLYKTYKQKVGVEPVYDQAGNPLFGERGAHPQSLKLPKRGERNVPTSLASLPKRGDCR
STANDARD; PRT; 3828 AA.
XX
AC xxxxxx
XX 01-JAN-1900
XX
XX This is a DE line.
XX
SQ SEQUENCE 3828 AA; 429949 MW; 77459508 CN;

Query Match 60.5%; Score 49; DB 1; Length 3828;
Best Local Similarity 58.3%; Pred. No. 1.17e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1062 DVVKADPGGGQGY 1073
   || |||| |::|
QY 1 DVKEADPTGHSY 12

RESULT 17
ID I46953 STANDARD; PRT; 90 AA.
XX
AC xxxxxx
XX 01-JAN-1900
XX
XX A;Cross-references: GB:S65218; NID:g410551; PID:g410552.
XX A;Cross-references: GB:S65218; NID:g410551; PID:g410552
CC A;Cross-references: GB:S65218; NID:g410551; PID:g410552
SQ SEQUENCE 90 AA; 10981 MW; 46468 CN;

Query Match 59.3%; Score 48; DB 2; Length 90;
```

```
Best Local Similarity 41.7%; Pred. No. 1.53e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 22 EVMLIDPSGNTY 33
   :|: ||:|:|
Qy 1 DVKEADPTGHSY 12

RESULT 18
ID S55370 STANDARD; PRT; 150 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE A:Cross-references: EMBL:249199; NID:g854176; PID:g854177.
CC
CC A:Cross-references: EMBL:249199; NID:g854176; PID:g854177
SQ SEQUENCE 150 AA; 17143 MW; 115920 CN;

Query Match
Best Local Similarity 59.3%; Score 48; DB 2; Length 150;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 11 DVKDIDPEGRKF 22
   ||: || | :
Qy 1 DVKEADPTGHSY 12

RESULT 19
ID A49334 STANDARD; PRT; 269 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE TOIG of: a49334 check: 9237 from: 1 to: 269.
XX
XX TOIG of: a49334 check: 9237 from: 1 to: 269
CC
CC >P1:A49334
CC Ras homolog Rad - human
CC N:Alternate names: Ras associated with diabetes (Rad)
CC C:Species: Homo sapiens (man)
CC C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-19
94
CC C:Accession: A49334
CC R:Reynet, C.; Kahn, C.R.
CC Science 262, 1441-1444, 1993
CC A:Title: Rad: a member of the Ras family overexpressed in muscle of type
II diabetic humans.
CC A:Reference number: A49334
CC A:Accession: A49334
CC A>Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 1-269 <REV>
CC A:Cross-references: GB:L24564
CC C:Keywords: alternative initiators
SQ SEQUENCE 269 AA; 29262 MW; 334168 CN;

Query Match
Best Local Similarity 59.3%; Score 48; DB 2; Length 269;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 80 EAEAAGHTY 88
   ||:|:|:|
Qy 4 EADPTGHSY 12

RESULT 20
ID C64834 STANDARD; PRT; 866 AA.
XX
AC xxxxxx
```

```
XX 01-JAN-1900
DT
DE A:Title: The complete genome sequence of Escherichia coli K-12.
XX
CC A:Title: The complete genome sequence of Escherichia coli K-12.
CC A:Reference number: A64720; MUID:97426617
CC A:Accession: C64834
CC A>Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A:Molecule type: DNA
CC A:Residues: 1-866 <BLAT>
CC A:Cross-references: GB:AE000196; GB:U00096; NID:g1787169; PID:g1787172; U
WGP:b0940
CC A:Experimental source: strain K-12, substrain MG1655
CC C:Superfamily: hypothetical protein b0532
CC C:Keywords: membrane protein
SQ SEQUENCE 866 AA; 95241 MW; 3791425 CN;

Query Match
Best Local Similarity 59.3%; Score 48; DB 2; Length 866;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 334 EIKADGGSVNSY 345
   :|:|:|:|:|
Qy 1 DVKEADPTGHSY 12

RESULT 21
ID G69910 STANDARD; PRT; 875 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE A>Status: preliminary; nucleic acid sequence not shown; translation not sh
own.
XX
CC A>Status: preliminary; nucleic acid sequence not shown; translation not s
hown
CC A:Molecule type: DNA
CC A:Residues: 1-875 <KUN>
CC A:Experimental source: strain 168
CC C:Genetics:
CC A:Gene: yomG
SQ SEQUENCE 875 AA; 98884 MW; 4045045 CN;

Query Match
Best Local Similarity 45.5%; Score 48; DB 2; Length 875;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 231 INSVNPTGQSY 241
   :|:|:|:|
Qy 2 VKEADPTGHSY 12

RESULT 22
ID A39216 STANDARD; PRT; 925 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE
DE A:Accession: S51030.
XX
CC A:Accession: S51030
CC A>Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 1-80 <BEL>
CC C:Genetics:
CC A:Gene: GDB:PDNP1; M6S1; NPPS
CC A:Cross-references: GDB:132615; OMIM:173335
CC A:Map position: 6q22-6q23
```

CC C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
CC C:Keywords: glycoprotein; phosphoric diester hydrolase; transmembrane pro
tein
CC F:77-97/Domain: transmembrane #status predicted <TM>
CC F:104-144/Domain: somatomedin B homology <SBH1>
CC F:145-188/Domain: somatomedin B homology <SBH2>
CC F:179,285,341,477,578,585,643,700,731,748/Binding site: carbohydrate (Asn
) (covalent) #status predicted
CC F:254/Active site: Thr (covalent substrate-binding) #status predicted
SQ SEQUENCE 925 AA; 104924 MW; 4589090 CN;

Query Match 59.3%; Score 48; DB 2; Length 925;
Best Local Similarity 66.7%; Pred. No. 1.53e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 374 EPDSSGHSY 382
:::|::|::|
QY 4 EADPTGHSY 12

RESULT 23
ID KIPGGU STANDARD; PRT; 197 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
XX
DE TOIG of: kipggg check: 2414 from: 1 to: 197.
XX
XX
XX TOIG of: kipggg check: 2414 from: 1 to: 197
CC
CC
CC >P1.KIPGGU
CC guanylate kinase (EC 2.7.4.8) - pig
CC C:Species: Sus scrofa domestica (domestic pig)
CC C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 23-Aug-19
97
CC C:Accession: S23776; S32545
CC R:Zschocke, P.D.; Schiltz, E.; Schulz, G.E.
CC submitted to the Protein Sequence Database, September 1992
CC A:Reference number: S23776
CC A:Accession: S23776
CC A:Molecule type: protein
CC A:Residues: 1-197 <2SC>
CC R:Zschocke, P.D.; Schiltz, E.; Schulz, G.E.
CC Eur. J. Biochem. 213, 263-269, 1993
CC A:Title: Purification and sequence determination of guanylate kinase from
pig brain.

CC A:Reference number: S32545
CC A:Accession: S32545
CC A:Status: preliminary
CC A:Molecule type: protein
CC A:Residues: 1-197 <2S2>
CC C:Superfamily: guanylate kinase; guanylate kinase homology
CC C:Keywords: acetylated amino end; ATP; magnesium; monomer; P-loop; phospho
transferase
CC F:3-188/Domain: guanylate kinase homology <GKI>
CC F:10-17/Region: nucleotide-binding motif A (P-loop)
CC F:35-82/Region: GMP binding #status predicted
CC F:1/Modified site: acetylated amino end (Gly) #status experimental
CC F:16/Binding site: ATP (Lys) #status predicted
SQ SEQUENCE 197 AA; 21789 MW; 183102 CN;

Query Match 58.0%; Score 47; DB 1; Length 197;
Best Local Similarity 54.5%; Pred. No. 2.01e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 187 EIKQAQATGS 197
:::|::|::|
QY 1 DVKEADPTGHS 11

RESULT 24
ID A48947 STANDARD; PRT; 445 AA.

XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
XX A:Contents: L. d. bulgaricus.
XX
XX A:Contents: L. d. bulgaricus
CC A:Accession: A48947
CC A:Status: preliminary; not compared with conceptual translation
CC A:Molecule type: DNA
CC A:Residues: 1-445 <ISH>
CC A:Experimental source: ATCC 11842
CC A:Note: sequence extracted from NCBI backbone (NCBIP:117804)
CC C:Superfamily: glutamate--ammonia ligase
CC C:Keywords: ligase
SQ SEQUENCE 445 AA; 50133 MW; 1031509 CN;

Query Match 58.0%; Score 47; DB 2; Length 445;
Best Local Similarity 33.3%; Pred. No. 2.01e+02;
Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 335 EMRSTDPANPY 346
:::|::|::|
QY 1 DVKEADPTGHSY 12

RESULT 25
ID S33938 STANDARD; PRT; 497 AA.

XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
XX TOIG of: s33938 check: 2182 from: 1 to: 497.
XX
XX TOIG of: s33938 check: 2182 from: 1 to: 497
CC
CC >P1.S33938
CC penton protein (III) - human adenovirus 12
CC C:Species: Mastadenovirus h12 (human adenovirus 12)
CC C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-19
97
CC C:Accession: S33938
CC R:Sprenkel, J.
CC submitted to the EMBL Data Library, June 1993
CC A:Reference number: S33928
CC A:Accession: S33938
CC A:Status: preliminary
CC A:Molecule type: DNA
CC A:Residues: 1-497 <SPR>
CC A:Cross-references: EMBL:X73487; NID:G313361; PID:G313372
CC C:Superfamily: adenovirus penton protein
SQ SEQUENCE 497 AA; 56393 MW; 1345686 CN;

Query Match 58.0%; Score 47; DB 2; Length 497;
Best Local Similarity 66.7%; Pred. No. 2.01e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 310 ETPDKGRSY 318
|::|::|
QY 4 EADPTGHSY 12

RESULT 26
ID S BOTH MN2+ AND MG2+ IONS FOR HIGH ACTIVITY. STANDARD; PRT; 539
AA.

XX
AC xxxxxx
XX
DT 01-JAN-1900
XX

DE TOIG of: ajbsqu check: 2505 from: 1 to: 444.

CC F:1-27/Domain: signal sequence #status predicted <SIG>
CC F:28-147/Product: phospholipase A2 isoform A4 #status predicted <MAT>
CC F:54-146,56-72,71-127,78-120,88-113,106-118/Disulfide bonds: #status predicted
SQ SEQUENCE 147 AA; 16177 MW; 97291 CN;

Query Match 56.8%; Score 46; DB 1; Length 147;
Best Local Similarity 33.3%; Pred. No. 2.62e+02;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 84 NTRDCDPKTSY 95
XX : : : : :
QY 1 DVKEADPTGHSY 12

RESULT 32
ID S54702 STANDARD; PRT; 382 AA.

XX AC xxxxxx
XX DT 01-JAN-1900
XX

DE A;Accession: S54702.

CC A;Accession: S54702

CC A;Status: preliminary

CC A;Molecule type: DNA

CC A;Residues: 1-382 <WHI>

CC A;Cross-references: EMBL:L27667; NID:g443685; PID:g443686

SQ SEQUENCE 382 AA; 42532 MW; 685630 CN;

Query Match 56.8%; Score 46; DB 2; Length 382;
Best Local Similarity 25.0%; Pred. No. 2.62e+02;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 370 EITDDDPAGRRF 381
XX : : : : :
QY 1 DVKEADPTGHSY 12

RESULT 33
ID S25483 STANDARD; PRT; 439 AA.

XX AC xxxxxx
XX DT 01-JAN-1900

DE TOIG of: s25483 check: 3624 from: 1 to: 439.

XX TOIG of: s25483 check: 3624 from: 1 to: 439

CC >P1:S25483

CC ribulose-bisphosphate carboxylase activase (clone JQ4) - common tobacco
CC N;Alternate names: rubisco activase

CC C;Species: Nicotiana tabacum (common tobacco)

CC C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-19

97

CC C;Accession: S25483

CC R;Rodermel, S.; Qian, J.

CC Submitted to the EMBL Data Library, August 1992

CC A;Description: Characterization of three Rubisco activase cDNAs from tobacco.

CC A;Reference number: S25482

CC A;Accession: S25483

CC A;Molecule type: DNA

CC A;Residues: 1-439 <ROD>

CC A;Cross-references: EMBL:L14980; NID:g19989; PID:g19990

SQ SEQUENCE 439 AA; 48343 MW; 941507 CN;

Query Match 56.8%; Score 46; DB 2; Length 439;
Best Local Similarity 41.7%; Pred. No. 2.62e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 60 EEKDADPKQTY 71
XX : : : : :
QY 1 DVKEADPTGHSY 12

RESULT 34
ID S65289 STANDARD; PRT; 551 AA.

XX AC xxxxxx
XX DT 01-JAN-1900

DE TOIG of: s65289 check: 3373 from: 1 to: 551.

XX TOIG of: s65289 check: 3373 from: 1 to: 551

CC >P1:S65289

CC hypothetical protein YPL258c - yeast (Saccharomyces cerevisiae)

CC N;Alternate names: hypothetical protein P0701

CC C;Species: Saccharomyces cerevisiae

CC C;Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 14-Nov-19

97

CC C;Accession: S65289

CC R;Messenguy, F.; Dubois, E.; Vierendeels, F.; Scherens, B.

CC submitted to the Protein Sequence Database, May 1996

CC A;Reference number: S64935

CC A;Accession: S65289

CC A;Molecule type: DNA

CC A;Residues: 1-551 <MES>

CC A;Cross-references: EMBL:Z73614; NID:g1370531; PID:e246962; PID:g1370532;

MIPS:YPL258c

CC A;Experimental source: strain S288C (AB972)

CC C;Genetics:

CC A;Map position: 16L

SQ SEQUENCE 551 AA; 61334 MW; 1568767 CN;

Query Match 56.8%; Score 46; DB 2; Length 551;
Best Local Similarity 45.5%; Pred. No. 2.62e+02;

Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db 285 VKDNGPINHY 295
XX : : : : :
QY 2 VKEADPTGHSY 12

RESULT 35
ID S66740 STANDARD; PRT; 551 AA.

XX AC xxxxxx
XX DT 01-JAN-1900

DE TOIG of: s66740 check: 1641 from: 1 to: 551.

XX TOIG of: s66740 check: 1641 from: 1 to: 551

CC >P1:S66740

CC probable transcription factor YOL055c - yeast (Saccharomyces cerevisiae)

CC N;Alternate names: protein Ol239

CC C;Species: Saccharomyces cerevisiae

CC C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Nov-19

97

CC C;Accession: S66740; S66747; S59294; S61724

CC R;Ansoorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss,

H.; Wiemann, S.

CC submitted to the Protein Sequence Database, July 1996

CC A;Reference number: S66723

CC A;Accession: S66740

CC A;Molecule type: DNA

CC A;Residues: 1-551 <ANS>

CC A;Cross-references: EMBL:Z74797; NID:g1419864; PID:e251864; PID:g1419865;

MIPS:YOL055c

CC A:Experimental source: strain S288C
CC R:Feldmann, H.; Mannhaupt, G.; Vetter, I.
CC submitted to the Protein Sequence Database, July 1996
CC A:Reference number: S66743
CC A:Accession: S66747
CC A:Molecule type: DNA
CC A:Residues: 1-551 <FEL>
CC A:Cross-references: EMBL:Z74797; NID:gl419864; PID:e251864; PID:gl419865;
CC MIPS:YOL055C
CC A:Experimental source: strain S288C
CC R:Mannhaupt, G.; Vetter, I.; Schwarzlose, C.; Mitzel, S.; Feldmann, H.
CC submitted to the EMBL Data Library, August 1995
CC A:Reference number: S59285
CC A:Accession: S59294
CC A:Molecule type: DNA
CC A:Residues: 1-543 <FEW>
CC A:Cross-references: EMBL:X91067; NID:g984177; PID:g984187
CC R:Mannhaupt, G.; Vetter, I.; Schwarzlose, C.; Mitzel, S.; Feldmann, H.
CC Yeast 12, 67-76, 1996
CC A:Title: Analysis of a 26 kb region on the left arm of yeast chromosome X
V.
CC A:Reference number: S61715
CC A:Accession: S61724
CC A:Status: nucleic acid sequence not shown; translation not shown
CC A:Molecule type: DNA
CC A:Residues: 1-543 <MAN>
CC A:Cross-references: EMBL:X91067; NID:g984177; PID:g984187
CC A:Note: the nucleotide sequence was submitted to the EMBL Data Library, A
CC ugust 1995
CC C:Genetics:
CC A:Map position: 15L
SQ SEQUENCE 551 AA; 61369 MW; 1606714 CN;
Query Match 56.8%; Score 46; DB 2; Length 551;
Best Local Similarity 45.5%; Pred. No. 2.62e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Db 285 VKDNGPINHY 295
||: | | |
QY 2 VKADPTGHSY 12

Search completed: Tue Apr 7 08:42:46 1998
Job time : 11 secs.

MAISEL (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 08:43:04 1998; MasPar time 2.70 Seconds

Tabular output not generated. 75.061 Million cell updates/sec

Title: >US-08-190-411A-4
Description: (1-12) from 5541104.ppe
Perfect Score: 81
Sequence: 1 DVREADTGHSHY 12

Scoring table: PAM 150
Gap 15

Searched: 111725 seqs, 16919825 residues

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database: a-geneseq30
1:a-geneseq1

Statistics: Mean 21.386; Variance 7.814; scale 2.737

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	81	100.0	38	1	R80620 Immunogenic peptide of	2.05e-34
2	81	100.0	335	1	R70909 Human melanoma antigen	2.05e-34
3	61	75.3	35	1	R49224 HLA-A1 MAGE 1 antigen	1.12e-17
4	61	75.3	35	1	R50281 MAGE-1 nonapeptide	1.12e-17
5	61	75.3	35	1	W00897 Human melanoma MAGE1 t	1.12e-17
6	61	75.3	35	1	R78824 MAGE-1 cytotoxic T lymph	1.12e-17
7	61	75.3	35	1	R47330 HLA-A1 MAGE 1 antigen	1.12e-17
8	61	75.3	35	1	R65135 MAGE 1 immunogenic pep	1.12e-17
9	61	75.3	35	1	R99343 MAGE-1 nonapeptide	1.12e-17
10	61	75.3	35	1	R65112 MAGE 1 immunogenic pep	1.12e-17
11	61	75.3	35	1	R83932 MHC class I restricted	1.12e-17
12	61	75.3	35	1	R63875 Synthetic peptide deri	1.12e-17
13	61	75.3	35	1	R75954 Melanoma antigen (MAGE	1.12e-17
14	61	75.3	35	1	R29769 Antigen E peptide	1.12e-17
15	61	75.3	35	1	R82988 P815 antigenic peptide	1.12e-17
16	61	75.3	35	1	R90692 Human leukocyte antigen	1.12e-17
17	59	72.8	35	1	R99342 HLA binding nonapeptid	3.99e-16
18	58	71.6	35	1	R99337 HLA binding nonapeptid	2.33e-15
19	55	67.9	35	1	R99339 HLA binding nonapeptid	4.16e-13
20	55	67.9	35	1	R99340 HLA binding nonapeptid	4.16e-13
21	54	66.7	35	1	R99338 HLA binding nonapeptid	2.26e-12
22	51	63.0	36	1	W13255 MAGE-3 TRAP HLA-B44 mo	3.22e-10
23	50	61.7	117	1	W16333 Baboon MAGE-3 homology	1.61e-09

Baboon MAGE-3 homology	1.61e-09
Baboon MAGE-3 homology	1.61e-09
Human MAGE-3 tumour an	1.61e-09
Baboon MAGE-3 homology	1.61e-09
Baboon MAGE-3 homology	1.61e-09
HLA binding nonapeptid	7.89e-08
Rad protein	3.78e-08
Diabetogene rad: A typ	3.78e-08
Human insulin receptor	3.78e-08
Peptide with glutamine	1.77e-07
MAGE-6 nonapeptide	8.04e-07
MAGE-5/MAGE-51 nonapep	8.04e-07
MAGE-51 nonapeptide	8.04e-07
MAGE-6 nonapeptide	8.04e-07
MAGE-5 nonapeptide	8.04e-07
Human c-met protooncog	8.04e-07
psts variant	3.57e-06
Borna disease virus p5	3.57e-06
Polypeptide with regio	1.54e-05
Human villin	1.54e-05
MAGE-3 nonapeptide	6.47e-05
HLA-A1 MAGE 3 antigen	6.47e-05
MAGE-3 nonapeptide	6.47e-05
MHC class I restricted	6.47e-05
Melanoma antigen (MAGE	6.47e-05
Antigen fragment 167	6.47e-05
Cysteine proteinase fr	6.47e-05
Human matrix metallopr	6.47e-05
abaA gene of Aspergill	6.47e-05
DEN1-S275/90 (ECACC V9	6.47e-05
MAGE-41 nonapeptide	2.64e-04
MAGE-41 nonapeptide	2.64e-04
PLRV viral protein	2.64e-04
Mouse guanylate kinase	2.64e-04
Human hepatoma-derived	2.64e-04
Poliiovirus receptor (4	2.64e-04
H20A receptor	2.64e-04
Poliiovirus receptor	2.64e-04
Poliiovirus receptor (4	2.64e-04
Mature Pseudomonas glu	1.04e-03
PR8 fusion protein	1.04e-03
Parasporium rhizobium	1.04e-03
Hybrid murine IL-7 rec	1.04e-03
Aureobasidin sensiti	1.04e-03
C. albicans caauri gen	1.04e-03
C. albicans caauri gen	1.04e-03
Comamonas acidovorans	1.04e-03
Ri paraneoplastic anti	1.04e-03
Cephalosporin C amidas	1.04e-03
Potassium ion channel	1.04e-03
Porphyromonas gingival	1.04e-03
P. gingivalis haemaggl	1.04e-03
P. gingivalis haag hae	1.04e-03
P. gingivalis haemaggl	1.04e-03
Arg-gingipain-2 prepol	1.04e-03
Prtr antigenic protein	1.04e-03
P. gingivalis porphypa	1.04e-03
PrTK antigenic protein	1.04e-03
Sequence encoded by OR	3.98e-03
Human cadherin-6	3.98e-03
Partial human cadherin	3.98e-03
Murine osteogenic prot	3.98e-03
Mouse osteogenic prote	3.98e-03
MOP-1	3.98e-03
Murine OP-1	3.98e-03
Murine OP-1	3.98e-03
Osteogenic protein MOP	3.98e-03
Murine OP-1	3.98e-03
MOP1	3.98e-03
MOP1-PP prepro form mo	3.98e-03
Mouse osteogenic prote	3.98e-03

97 40 49.4 549 1 R71976 Pertussis A. 3.98e-03
98 40 49.4 1444 1 R71703 Collagen alpha 1 (II) 3.98e-03
99 40 49.4 1444 1 R59751 Type II collagen. 3.98e-03
100 40 49.4 1859 1 R79478 Mouse LTBP-2. 3.98e-03

ALIGNMENTS

RESULT 1
ID R80620 standard; Protein; 12 AA.
AC R80620;
DE 28-FEB-1996 (first entry)
DE Immunogenic peptide of tumour rejection antigen (MAGE-1).
KW Tumour rejection antigen; MAGE-1; monoclonal antibody; Mab;
KW diagnosis; immunoassay; cancer; immunogen; antisera.
OS Homo sapiens.
PN W09520974-AL.
PD 10-AUG-1995.
PF 05-JAN-1995; U000095.
PR 01-FEB-1994; US-190411.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.
PI Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;
PI Stockert E, Van der bruggen P;
DR WPI: 95-283606/37.
PT New monoclonal antibody binding specifically to MAGE-1 - useful for
PT diagnosis and monitoring of cancer, also new hybridomas, recombinant
PT MAGE-1 and immunogenic peptide(s)
PS Claim 12; Page 20; 33pp; English.
CC A monoclonal antibody directed against the tumour rejection antigen
CC (MAGE-1) can be used to detect MAGE-1 in samples by standard
CC immunoassay methods for diagnosis and monitoring of cancer etc. The
CC monoclonal antibody is designated M454 and is produced by the
CC hybridoma deposited as ATCC HB11540. The monoclonal antibody is
CC specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
CC Peptide fragments of MAGE-1 (See R80618-20) may be useful as
CC immunogens for production of the monoclonal antibody and antisera.
SQ Sequence 12 AA;

Query Match 100.0%; Score 81; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.05e-34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 DVKEADPTGHSY 38
Qy 1 DVKEADPTGHSY 12

RESULT 2
ID R70909 standard; Protein; 309 AA.
AC R70909;
DE 09-OCT-1995 (first entry)
DE Human melanoma antigen MAGE-1.
KW Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;
KW HLA-restricted cytotoxic T-lymphocyte activity.
OS Homo sapiens.
PN W09504542-A.
PD 16-FEB-1995.
PF 02-AUG-1994; U08721.
PR 06-AUG-1993; US-103623.
PA (CYTE-) CYTEL CORP.
PI Fikes JD, Livingston BD, Sette AD, Sidney JC;
DR WPI: 95-090881/12.
DR N-PSDB; Q85435.
PT Human melanoma antigen, MAGE-1, peptide(s) - useful for
PT stimulating immune response against melanoma
PS Example 1; Fig 1; 59pp; English.
CC Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used
CC to produce the C-terminal MAGE-1 peptides described in R70915 to
CC R70969. These peptides are useful for defining epitopes that
CC engender a HLA-restricted cytotoxic lymphocyte activity against
CC MAGE-1 antigens. Compns. containing these peptides can be

CC administered, as a vaccine to patients susceptible to MAGE
CC associated tumours, e.g. melanomas.
SQ Sequence 309 AA;

Query Match 100.0%; Score 81; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.05e-34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 184 DVKEADPTGHSY 195
Qy 1 DVKEADPTGHSY 12

RESULT 3
ID R49224 standard; Protein; 9 AA.
AC R49224;
DE 31-AUG-1994 (first entry)
DE HLA-A1 MAGE 1 antigen peptide fragment 958.01.
KW Immunogenic; HLA-A3.2; HLA-A1; binding motif; MHC molecule;
KW immune response; viral infection; cancer; prostate cancer; lymphoma;
KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
OS Synthetic.
PN W09403205-A.
PD 17-FEB-1994.
PF 06-AUG-1993; U07421.
PR 07-AUG-1992; US-926666.
PR 05-MAR-1993; US-027746.
PA (CYTE-) CYTEL CORP.
PI Celis E, Grey HW, Kubo RT, Sette A;
DR WPI: 94-065403/08.
PT Peptide which specifically binds selected MHC allele - used to
PT induce an immune response for treatment or prevention of viral
PT infection or cancer, or for diagnosis
PS Example 16; Page 116; 150pp; English.
CC The sequences given in R47304-33 and R49201-44 are immunogenic
CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A1 binding motif.
CC These peptides may be used in the composition of the invention.
CC These peptides are capable of binding selected MHC molecules and
CC inducing an immune response. They can be used to treat and/or
CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
CC hepatitis or AIDS. They can also be used to produce antibodies for
CC use as diagnostic or therapeutic agents. The peptides can also be
CC used as diagnostic agents.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.12e-17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
Qy 4 EADPTGHSY 12

RESULT 4
ID R50281 standard; Protein; 9 AA.
AC R50281;
DE 26-SEP-1994 (first entry)
DE MAGE-1 nonapeptide.
KW MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA;
KW histocompatibility; human leucocyte antigen; probe; treatment;
KW therapy; vaccine.
OS Synthetic.
PN W09403304-A.
PD 17-MAR-1994.
PF 30-AUG-1993; U08157.
PR 31-AUG-1992; US-938334.
PR 26-MAR-1993; US-037230.
PR 07-JUN-1993; US-073103.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Boon-falleur T, De Plaen E, Lurquin C, Traversari C;
PI Van Derbruggen P;
DR WPI: 94-100844/12.

DR N-PSDB; Q44751.
PT New nona-peptide derived from tumour rejection antigen precursor
PT - presented by HLA-A1 cancer cells, for use in diagnosis or
PT therapy of esp. melanoma and breast cancer.
PT Disclosure; Page 19; 33pp; English.
CC An isolated nonapeptide having the amino acid sequence Glu-Val-Asp-
CC Pro-Ile-Gly-His-Leu-Tyr is derived from the tumour rejection antigen
CC precursor encoded by the MAGE-3 gene and presented by HLA-A1. The
CC nonapeptide can be used in a vaccine to treat a cancerous condition
CC involving HLA-A1 subtype cancerous cells. The nucleic acid encoding
CC the nonapeptide can be used as a probe to identify tumour cells.
CC This sequence is homologous to the peptide described and is encoded
CC by the MAGE-1 gene.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.12e-17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
|||||
QY 4 EADPTGHSY 12

RESULT 5
ID W00897 standard; Peptide; 9 AA.

AC W00897;
DT 23-MAY-1997 (first entry)
DE Human melanoma MAGE1 tumour associated antigen p161-169.
KW Adeno-associated virus; vector; liposome; transfection;
KW dendritic cell; melanoma; MAGE1; adoptive immunotherapy;
KW tumour associated antigen.
OS Homo sapiens.
PN W09703703-Al.
PD 06-FEB-1997.
PF 19-JUL-1996; U12012.
PR 21-JUL-1995; US-001312.
PR 01-NOV-1995; US-007184.
PR 01-DEC-1995; US-566286.
PA (RHON) RHONE POULENC RORER PHARM INC.
PI Lebkowski JS, Philip R;
DR WPI; 97-145208/13.
PT Adeno-associated virus:liposome complexes for transfecting dendritic
PT cells - for inducing immune response, useful for treating e.g.
PT neoplasia or infections
PS Example 5; Page 58; 134pp; English.
CC Tumour associated antigens (W13660-61, W00878-903) can be loaded
CC into dendritic cells and used to induce antitumour immunity.
CC Alternatively, the dendritic cells are transfected with adeno
CC associated virus plasmid DNA (which includes DNA encoding the
CC tumour associated antigen) complexed with cationic liposomes. The
CC antigen loaded or transfected dendritic cells can be used to
CC generate tumour antigen-specific cytotoxic T lymphocytes for use in
CC adoptive immunotherapy in a patient having the corresponding
CC tumour. A suitable antigen comprises amino acids 161-169 (W00897)
CC of human melanoma MAGE1.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.12e-17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
|||||
QY 4 EADPTGHSY 12

RESULT 6

ID R78824 standard; peptide; 9 AA.
AC R78824;
DT 26-MAR-1996 (first entry)
DE MAGE-1 cytotoxic T lymphocyte epitope.
KW MAGE-1; cytotoxic T; CTL; epitope; helper T; HTL; lymphocyte;

KW cell; viruses; parasites; tumours; antigens; disease prevention;
KW treatment.
OS Homo sapiens.
PN W09522317-Al.
PD 24-AUG-1995.
PF 16-FEB-1994; U02121.
PR 16-FEB-1994; US-197484.
PA (CYTE-) CYTEL CORP.
PI Cellis E, Chesnut RW, Grey H, Sette AD, Vitello MA;
DR WPI; 95-302545/39.
PT Compn. inducing cytotoxic T lymphocyte response to pref. viral,
PT bacterial, parasitic or tumour antigens - useful in the treatment
PT and prevention of diseases associated with the antigen e.g.
PT hepatitis B
PS Disclosure; Page 17; 109pp; English.
CC A compn. which induces a cytotoxic T lymphocyte (CTL) response to
CC an antigen (Ag) in a mammal comprises, a CTL Ag response inducing
CC peptide (i.e. R78824-R78853) and a lipid conjugated helper T cell
CC inducing peptide. The compn. induces a CTL response to bacterial,
CC viral or tumour Ags, and is therefore useful in the treatment and
CC prevention of diseases associated with the Ag.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.12e-17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
|||||
QY 4 EADPTGHSY 12

RESULT 7

ID R47330 standard; Protein; 9 AA.
AC R47330;
DT 31-AUG-1994 (first entry)
DE HLA-A1 MAGE 1 antigen peptide fragment 161-169.
KW Immunogenic; HLA-A3.2; HLA-A1; binding motif; MHC molecule;
KW immune response; viral infection; cancer; prostate cancer; lymphoma;
KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
OS Synthetic.
PN W09403205-A.
PD 17-FEB-1994.
PF 06-AUG-1993; U07421.
PR 07-AUG-1992; US-926666.
PR 05-MAR-1993; US-027746.
PA (CYTE-) CYTEL CORP.
PI Cellis E, Grey HM, Kubo RT, Sette A;
DR WPI; 94-065403/08.
PT Peptide which specifically binds selected MHC allele - used to
PT induce an immune response for treatment or prevention of viral
PT infection or cancer, or for diagnosis
PS Example 8; Page 52; 150pp; English.
CC The sequences given in R47304-33 and R49201-44 are immunogenic
CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
CC These peptides may be used in the composition of the invention.
CC These peptides are capable of binding selected MHC molecules and
CC inducing an immune response. They can be used to treat and/or
CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
CC hepatitis or AIDS. They can also be used to produce antibodies for
CC use as diagnostic or therapeutic agents. The peptides can also be
CC used as diagnostic agents.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.12e-17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
|||||
QY 4 EADPTGHSY 12

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RESULT 8
ID R65135 standard; peptide; 9 AA.
AC R65135;
DT 09-OCT-1995 (first entry)
DE MAGE 1 immunogenic peptide A01.
KW MAGE 1; immunogenic peptide A01; cytotoxic C cells;
KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
KW fungal infections; tuberculosis; hepatitis.
OS Homo sapiens.
PN W09504817-A.
PD 16-FEB-1995.
PF 01-AUG-1994; U08672.
PR 06-AUG-1993; US-103401.
PA (CYTE-) CYTEL CORP.
PI Celis E, Kubo R, Serra H, Tsai V, Wentworth P;
DR WPI; 95-090895/12.
PT In vitro activation of cytotoxic T cells for selected killing of
PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
PT incubating them with antigen presenting cells loaded with
PT appropriate immunogenic peptide
PS Example 3: Page 38; 53pp; English.
CC R65109-R65145 are immunogenic peptides, they are used in a new
CC method for the in vitro activation of cytotoxic T cells (CTC).
CC This is achieved by incubating the CTCs with antigen presenting
CC cells loaded with an appropriate immunogenic peptide (e.g. one
CC of the above peptides). By selecting the peptides used the
CC following diseases and infections can be treated: cancer, AIDS,
CC hepatitis, other viral and bacterial infections, malaria and
CC tuberculosis.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.12e-17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
QY 4 EADPTGHSY 12

RESULT 10
ID R65112 standard; peptide; 9 AA.
AC R65112;
DT 06-OCT-1995 (first entry)
DE MAGE 1 immunogenic peptide 161-169.
KW MAGE 1; immunogenic peptide 161-169; cytotoxic C cells;
KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
KW fungal infections; tuberculosis; hepatitis.
OS Homo sapiens.
PN W09504817-A.
PD 16-FEB-1995.
PF 01-AUG-1994; U08672.
PR 06-AUG-1993; US-103401.
PA (CYTE-) CYTEL CORP.
PI Celis E, Kubo R, Serra H, Tsai V, Wentworth P;
DR WPI; 95-090895/12.
PT In vitro activation of cytotoxic T cells for selected killing of
PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
PT incubating them with antigen presenting cells loaded with
PT appropriate immunogenic peptide
PS Example 3: Page 35; 53pp; English.
CC R65109-R65145 are immunogenic peptides, they are used in a new
CC method for the in vitro activation of cytotoxic T cells (CTC).
CC This is achieved by incubating the CTCs with antigen presenting
CC cells loaded with an appropriate immunogenic peptide (e.g. one
CC of the above peptides). By selecting the peptides used the
CC following diseases and infections can be treated: cancer, AIDS,
CC hepatitis, other viral and bacterial infections, malaria and
CC tuberculosis.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.12e-17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
QY 4 EADPTGHSY 12

RESULT 11
ID R83932 standard; peptide; 9 AA.
AC R83932;
DT 05-JUN-1996 (first entry)
DE MHC class I restricted antigenic peptide #2.
KW MHC class I; antigen; MAGE; melanoma; breast cancer; bladder cancer;
KW Titermax; cytotoxic T-lymphocyte; tumour; pathogenic disease; bacteria;
KW parasite; human; animal.
OS Synthetic.
PN W09528958-A1.
PD 02-NOV-1995.
PF 21-APR-1995; U04975.
PR 22-APR-1994; US-233496.
PA (SLOK) SLOAN KETTERING INST CANCER RES.

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RESULT 8
ID R65135 standard; peptide; 9 AA.
AC R65135;
DT 09-OCT-1995 (first entry)
DE MAGE 1 immunogenic peptide A01.
KW MAGE 1; immunogenic peptide A01; cytotoxic C cells;
KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
KW fungal infections; tuberculosis; hepatitis.
OS Homo sapiens.
PN W09504817-A.
PD 16-FEB-1995.
PF 01-AUG-1994; U08672.
PR 06-AUG-1993; US-103401.
PA (CYTE-) CYTEL CORP.
PI Celis E, Kubo R, Serra H, Tsai V, Wentworth P;
DR WPI; 95-090895/12.
PT In vitro activation of cytotoxic T cells for selected killing of
PT target cells - for treating e.g. cancer, AIDS, hepatitis etc.by
PT incubating them with antigen presenting cells loaded with
PT appropriate immunogenic peptide
PS Example 3: Page 38; 53pp; English.
CC R65109-R65145 are immunogenic peptides, they are used in a new
CC method for the in vitro activation of cytotoxic T cells (CTC).
CC This is achieved by incubating the CTCs with antigen presenting
CC cells loaded with an appropriate immunogenic peptide (e.g. one
CC of the above peptides). By selecting the peptides used the
CC following diseases and infections can be treated: cancer, AIDS,
CC hepatitis, other viral and bacterial infections, malaria and
CC tuberculosis.
SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.12e-17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
QY 4 EADPTGHSY 12

RESULT 9
ID R99343 standard; Protein; 9 AA.
AC R99343;
DT 22-APR-1997 (first entry)
DE MAGE-1 nonapeptide.
KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;
KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
KW therapy.
OS Homo sapiens.
PN W09626214-A1.
PD 29-AUG-1996.
PF 01-FEB-1996; U01489.
PR 23-FEB-1995; US-393273.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Boon-Falleur T, De Plaen E, Gaugler B, Lurquin C;
PI Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;
DR WPI; 96-402317/40.
DR N-PSDB; T35408.
PT New nona-peptide(s) that bind to HLA molecule(s) and induce lysis -
PT by specific cytolytic T cells, for diagnosis and treatment of
PT tumours and to expand T cells in vitro.
PS Example 4; Fig 4; 41pp; English.
CC R99343-R99350 represent MAGE nonapeptides, based on the tumour rejection
CC antigen region of the full length MAGE sequences. These peptides were
CC used to design the nonapeptides of the invention (see R99337-R99342),
CC which bind to a HLA molecule on a cell, and provoke lysis by cytolytic T
CC cells (CTLs) specific for a complex of the HLA molecule and nonapeptide.
CC The nonapeptides can be used diagnostically to identify tumours
CC expressing a particular HLA molecule, or to identify cancer cells. The
CC peptides can also be used therapeutically, to induce a CTL response to
CC tumours (where the peptides are optionally coupled to tumour-specific
CC antibodies), or to induce a response by CTLs that are otherwise inactive.

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PI Dyall R, Nikolic-Zugic J;
 DR WPI; 95-382848/49.
 PT Cytotoxic T-cell induction by MHC class I-restricted peptide in
 PT adjuvant - useful for treating tumours and bacterial or parasitic
 PT pathogenic diseases
 PS Claim 11; Page 38; 50pp; English.
 CC The sequences given in R83931-49 are MHC class I restricted 8-12
 CC amino acid antigenic peptides. This peptide is derived from MAGE
 CC and is present in melanoma, breast and bladder cancer. These
 CC peptides may be administered to a subject in combination with a
 CC suitable adjuvant, pref. Titermax (RTM), to induce cytotoxic T-
 CC lymphocytes. This method may be used in the treatment of a tumour
 CC or a pathogenic disease, esp. diseases of bacterial or parasitic
 CC origin, in humans and animals, e.g monkeys, dogs cows, horses, etc.
 SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.12e-17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
 |||||
 QY 4 EADPTGHSY 12

RESULT 12

ID R63675 standard; Protein; 9 AA.
 AC R63675;
 DT 22-JUN-1995 (first entry)
 DE Synthetic peptide derived from exon 3.1 of MAGE 1.
 KW Melanoma antigen-1; MAGE-1; cytolytic T cells; antigen E; exon 3.1.
 OS Synthetic.
 PN WO9423031-A.
 PD 13-OCT-1994.
 PF 17-MAR-1994; U02877.
 PR 26-MAR-1993; US-037230.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boon-falleur T, Gaugler B, Van Den Eynde B, Van Der Bruggen P;
 DR WPI; 94-333192/41.
 PT New tumour rejection antigen precursor MAGE3 - useful in
 PT treatment and diagnosis of cancer
 PS Example 34; Page 36; 105pp; English.
 CC R63675 is a synthetic peptide derived from exon 3.1 of melanoma
 CC antigen-1 (MAGE-1), it was used to transfer antigen-E cytolytic T
 CC lymphocyte sensitivity to normally non-sensitive cells.
 SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.12e-17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
 |||||
 QY 4 EADPTGHSY 12

RESULT 13

ID R75954 standard; Peptide; 9 AA.
 AC R75954;
 DT 06-MAR-1996 (first entry)
 DE Melanoma antigen (MAGE-1) epitope.
 KW MAGE-3; melanoma antigen; vaccine; immune response; immunogenic peptide;
 KW cytotoxic T lymphocyte response; CTL; melanoma; breast cancer; antibody.
 OS Homo sapiens.
 PN WO9519783-A1.
 PD 27-JUL-1995.
 PF 25-JAN-1995; U01000.
 PR 25-JAN-1994; US-186266.
 PA (CYTE-) CYTEL CORP.
 PI Cellis E, Grey HM, Kubo RT, Sette A;
 DR WPI; 95-269270/35.
 PT Immunogenic peptide(s) that induce immune response to cancer cells
 PT - that express a MAGE-3 protein peptide epitope used in vaccines or

PT adoptive immuno:therapy to induce cytotoxic T lymphocytes
 PS Example; Page 33; 44pp; English.
 CC R75954 is derived from MAGE-1 protein. It was used to show the
 CC specificity of CTL response to MAGE-3 peptides shown in R75942-53.
 CC R75942 is derived from the sequence of the melanoma antigen (MAGE-3)
 CC protein and can be used to elicit a primary cytotoxic T lymphocyte
 CC response against cells expressing MAGE-3. Synthetic peptides R75945-53
 CC can be used therapeutically to elicit CTL responses to melanoma, breast,
 CC colon, prostate, or other cells which express proteins with this epitope.
 CC The peptides have specific HLA-A1 binding capacity.
 SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.12e-17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
 |||||
 QY 4 EADPTGHSY 12

RESULT 14

ID R29769 standard; Peptide; 9 AA.
 AC R29769;
 DT 22-APR-1993 (first entry)
 DE Antigen E peptide.
 KW Antigen; tumorigenic cell; A+ B+; T-cell; response; syngeneic;
 KW animal; mouse; tumour rejection antigen precursor; TRAP; PIA.
 OS Homo sapiens.
 PN WO9220356-A.
 PD 26-NOV-1992.
 PF 22-MAY-1992; U04354.
 PR 23-MAY-1991; US-705702.
 PR 09-JUL-1991; US-728838.
 PR 23-SEP-1991; US-764364.
 PR 12-DEC-1991; US-807043.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
 PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;
 DR WPI; 92-415460/50.
 PT Nucleic acid mol. encoding a human tumour rejection antigen
 PT precursor - useful as an immunostimulant in a vaccine for
 PT treating and preventing cancers, also useful in diagnosis
 PT disclosure; Page 97; 142pp; English.
 PS This sequence represents the sequence of the antigen E. Antigens such
 CC as this one cause a T-cell response to be elicited which transplanted
 CC into a syngeneic animal, usually a mouse. This antigen is derived from
 CC the cell line MEL3.1. See also Q32351.
 SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.12e-17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
 |||||
 QY 4 EADPTGHSY 12

RESULT 15

ID R82988 standard; Peptide; 9 AA.
 AC R82988;
 DT 26-FEB-1996 (first entry)
 DE P815 antigenic peptide.
 DE P815 antigen; p1A antigen; cancer; vaccine.
 KW Synthetic.
 OS Homo sapiens.
 PN WO9523874-A1.
 PD 08-SEP-1995.
 PF 23-FEB-1995; U02203.
 PR 01-MAR-1994; US-204727.
 PR 10-MAR-1994; US-209172.
 PR 01-SEP-1994; US-299849.
 PR 30-NOV-1994; US-346774.

PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
 PI De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
 PI Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;
 DR WPI; 95-320586/41.
 PT Determn. of cancerous condition(s) - using a nucleic acid as a
 PT primer to determine expression of a MAGE tumour rejection antigen
 PT precursor
 PS Example 13; Page 22; 121pp; English.
 CC Using the sequence of the P815A antigen precursor gene p1A
 CC (F01176), an antigenic peptide (R82988) which was A+B+ (i.e.
 CC characteristic of cells which express both A and B antigens) was
 CC produced. The peptide lysed PO.HTR cells in the presence of
 CC cytolytic T lymphocyte cell lines, and may be useful as a vaccine
 CC component.
 SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.12e-17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
 |||||
 QY 4 EADPTGHSY 12

RESULT 16

ID R90692 standard; peptide; 9 AA.
 AC R90692;
 DE 31-JUL-1996 (first entry)
 DE Human leukocyte antigen (HLA-A1) presented peptide M22-E.
 KW Human leukocyte antigen; HLA-A1; MAGE-1 derived;
 KW blood mononuclear cell; BMC; CD8-beta+ cell; cytolytic T cell;
 KW CTL cell; treatment; tumour cell; diagnosis; assay;
 KW presented peptide.
 OS Synthetic.
 PN WO9535500-A1.
 PD 28-DEC-1995.
 PF 14-JUN-1995; U07559.
 PR 17-JUN-1994; US-261541.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boon-Falleur T, Coulie P, Van Der Bruggen P;
 DR WPI; 96-058510/06.
 PT Prodn. of specific cytolytic T cell sub-populations - by contacting
 PT blood mononuclear cells with specific peptide(s) and a population of
 PT CD8-beta(+) cells
 PS Claim 5; Page 19; 25pp; English.
 CC The present peptide is the human leukocyte antigen (HLA-A1), MAGE-1
 CC derived presented peptide, M22-E. By contacting a sample of blood
 CC mononuclear cells (BMC) with the peptide (which binds directly to
 CC HLA-A1 mols. on the surface of the BMC) and CD8-beta+ cells (which
 CC stimulate peptide/HLA-A1 complex specific CD8-beta+ cells), a
 CC peptide/HLA-A1 complex specific cytolytic T (CTL) cell
 CC subpopulation can be obt'd. The CTL cells obt'd. can be
 CC administered to a patient to treat tumour cell related conditions,
 CC and can be used in diagnostic methods, e.g. in assays for the
 CC peptide/HLA-A1 complex.
 SQ Sequence 9 AA;

Query Match 75.3%; Score 61; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.12e-17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
 |||||
 QY 4 EADPTGHSY 12

RESULT 17

ID R99342 standard; peptide; 9 AA.
 AC R99342;
 DT 22-APR-1997 (first entry)
 *DE HLA binding nonapeptide #6.

KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;
 KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
 KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
 KW therapy.
 OS Synthetic.
 PN WO9626214-A1.
 PD 29-AUG-1996.
 PF 01-FEB-1996; U01489.
 PR 23-FEB-1995; US-393273.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boon-Falleur T, De Plaen E, Gaugler B, Lurquin C;
 PI Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;
 DR WPI; 96-402317/40.
 PT New nona-peptide(s) that bind to HLA molecule(s) and induce lysis -
 PT by specific cytolytic T cells, for diagnosis and treatment of
 PT tumours and to expand T cells in vitro.
 PS Claim 9; Page 30; 41pp; English.
 CC R99337-R99342 represent nonapeptides of the invention. These sequences
 CC bind to a HLA molecule on a cell, and provoke lysis by cytolytic T cells
 CC (CTLs) specific for a complex of the HLA molecule and nonapeptide. These
 CC sequences are based on regions of proteins in the MAGE family of human
 CC tumour rejection antigen precursors. They are specifically based on
 CC fragments of the tumour rejection antigen (TRA) of MAGE-1. The
 CC nonapeptides can be used diagnostically to identify tumours expressing a
 CC particular HLA molecule, or to identify cancer cells. The peptides can
 CC also be used therapeutically, to induce a CTL response to tumours (where
 CC the peptides are optionally coupled to tumour-specific antibodies), or to
 CC induce a response by CTLs that are otherwise inactive. These sequences
 CC may also be used to expand specific CTLs in vitro for later return to the
 CC patient, such as for treating melanoma. Tumour cells can be identified
 CC by using DNA encoding these sequences as probes. Non-human cells
 CC transformed with the HLA-A1 gene and a DNA sequence encoding one of these
 CC peptides, can be used to generate CTLs, or to detect the presence of CTLs
 CC in human samples. The non-human transformed cells, when polytransformed,
 CC are universal effector cells, and can be used in vaccines, or for
 CC treating melanoma or breast cancer.
 SQ Sequence 9 AA;

Query Match 72.8%; Score 59; DB 1; Length 35;
 Best Local Similarity 88.9%; Pred. No. 3.99e-16;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
 |||||
 QY 4 EADPTGHSY 12

RESULT 18

ID R99339 standard; peptide; 9 AA.
 AC R99339;
 DT 22-APR-1997 (first entry)
 DE HLA binding nonapeptide #3.
 KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;
 KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
 KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
 KW therapy.
 OS Synthetic.
 PN WO9626214-A1.
 PD 29-AUG-1996.
 PF 01-FEB-1996; U01489.
 PR 23-FEB-1995; US-393273.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boon-Falleur T, De Plaen E, Gaugler B, Lurquin C;
 PI Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;
 DR WPI; 96-402317/40.
 PT New nona-peptide(s) that bind to HLA molecule(s) and induce lysis -
 PT by specific cytolytic T cells, for diagnosis and treatment of
 PT tumours and to expand T cells in vitro.
 PS Claim 9; Page 30; 41pp; English.
 CC R99337-R99342 represent nonapeptides of the invention. These sequences
 CC bind to a HLA molecule on a cell, and provoke lysis by cytolytic T cells
 CC (CTLs) specific for a complex of the HLA molecule and nonapeptide. These
 CC sequences are based on regions of proteins in the MAGE family of human

CC tumour rejection antigen precursors. They are specifically based on
 CC fragments of the tumour rejection antigen (TRA) of MAGE-1. The
 CC nonpeptides can be used diagnostically to identify tumours expressing a
 CC particular HLA molecule, or to identify cancer cells. The peptides can
 CC also be used therapeutically, to induce a CTL response to tumours (where
 CC the peptides are optionally coupled to tumour-specific antibodies), or to
 CC induce a response by CTLs that are otherwise inactive. These sequences
 CC may also be used to expand specific CTLs in vitro for later return to the
 CC patient, such as for treating melanoma. Tumour cells can be identified
 CC by using DNA encoding these sequences as probes. Non-human cells
 CC transformed with the HLA-A1 gene and a DNA sequence encoding one of these
 CC peptides, can be used to generate CTLs, or to detect the presence of CTLs
 CC in human samples. The non-human transformed cells, when polytransformed,
 CC are universal effector cells, and can be used in vaccines, or for
 CC treating melanoma or breast cancer.
 SQ Sequence 9 AA;

Query Match 71.6%; Score 58; DB 1; Length 35;
 Best Local Similarity 88.9%; Pred. No. 2.33e-15;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
 ||||:||||
 QY 4 EADPTGHSY 12

RESULT 19

ID R99337 standard; peptide; 9 AA.
 AC R99337;
 DT 22-APR-1997 (first entry)
 DE HLA binding nonapeptide #1.
 KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
 KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
 KW therapy.
 OS Synthetic.
 PN WO9626214-A1.
 PD 29-AUG-1996.
 PF 01-FEB-1996; U01489.
 PR 23-FEB-1995; US-393273.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boon-Falleur T, De Plaen E, Gaugler B, Lurquin C;
 PI Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;
 DR WPI: 96-402317/40.
 PT New nona:peptide(s) that bind to HLA molecule(s) and induce lysis -
 PT by specific cytolytic T cells, for diagnosis and treatment of
 PT tumours and to expand T cells in vitro.
 PS Claim 9; Page 30; 41pp; English.

CC R99337-R99342 represent nonapeptides of the invention. These sequences
 CC bind to a HLA molecule on a cell, and provoke lysis by cytolytic T cells
 CC (CTLs) specific for a complex of the HLA molecule and nonapeptide. These
 CC sequences are based on regions of proteins in the MAGE family of human
 CC tumour rejection antigen precursors. They are specifically based on
 CC fragments of the tumour rejection antigen (TRA) of MAGE-1. The
 CC nonapeptides can be used diagnostically to identify tumours expressing a
 CC particular HLA molecule, or to identify cancer cells. The peptides can
 CC also be used therapeutically, to induce a CTL response to tumours (where
 CC the peptides are optionally coupled to tumour-specific antibodies), or to
 CC induce a response by CTLs that are otherwise inactive. These sequences
 CC may also be used to expand specific CTLs in vitro for later return to the
 CC patient, such as for treating melanoma. Tumour cells can be identified
 CC by using DNA encoding these sequences as probes. Non-human cells
 CC transformed with the HLA-A1 gene and a DNA sequence encoding one of these
 CC peptides, can be used to generate CTLs, or to detect the presence of CTLs
 CC in human samples. The non-human transformed cells, when polytransformed,
 CC are universal effector cells, and can be used in vaccines, or for
 CC treating melanoma or breast cancer.
 SQ Sequence 9 AA;

Query Match 67.9%; Score 55; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 4.16e-13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 ADPTGHSY 35
 |||||
 QY 5 ADPTGHSY 12

RESULT 20

ID R99340 standard; peptide; 9 AA.
 AC R99340;
 DT 22-APR-1997 (first entry)
 DE HLA binding nonapeptide #4.
 KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;
 KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
 KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
 KW therapy.
 OS Synthetic.
 PN WO9626214-A1.
 PD 29-AUG-1996.
 PF 01-FEB-1996; U01489.
 PR 23-FEB-1995; US-393273.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boon-Falleur T, De Plaen E, Gaugler B, Lurquin C;
 PI Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;
 DR WPI: 96-402317/40.
 PT New nona:peptide(s) that bind to HLA molecule(s) and induce lysis -
 PT by specific cytolytic T cells, for diagnosis and treatment of
 PT tumours and to expand T cells in vitro.
 PS Claim 9; Page 30; 41pp; English.

CC R99337-R99342 represent nonapeptides of the invention. These sequences
 CC bind to a HLA molecule on a cell, and provoke lysis by cytolytic T cells
 CC (CTLs) specific for a complex of the HLA molecule and nonapeptide. These
 CC sequences are based on regions of proteins in the MAGE family of human
 CC tumour rejection antigen precursors. They are specifically based on
 CC fragments of the tumour rejection antigen (TRA) of MAGE-1. The
 CC nonapeptides can be used diagnostically to identify tumours expressing a
 CC particular HLA molecule, or to identify cancer cells. The peptides can
 CC also be used therapeutically, to induce a CTL response to tumours (where
 CC the peptides are optionally coupled to tumour-specific antibodies), or to
 CC induce a response by CTLs that are otherwise inactive. These sequences
 CC may also be used to expand specific CTLs in vitro for later return to the
 CC patient, such as for treating melanoma. Tumour cells can be identified
 CC by using DNA encoding these sequences as probes. Non-human cells
 CC transformed with the HLA-A1 gene and a DNA sequence encoding one of these
 CC peptides, can be used to generate CTLs, or to detect the presence of CTLs
 CC in human samples. The non-human transformed cells, when polytransformed,
 CC are universal effector cells, and can be used in vaccines, or for
 CC treating melanoma or breast cancer.
 SQ Sequence 9 AA;

Query Match 67.9%; Score 55; DB 1; Length 35;
 Best Local Similarity 88.9%; Pred. No. 4.16e-13;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADPTGHSY 35
 |||||:||||
 QY 4 EADPTGHSY 12

RESULT 21

ID R99338 standard; peptide; 9 AA.
 AC R99338;
 DT 22-APR-1997 (first entry)
 DE HLA binding nonapeptide #2.
 KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;
 KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
 KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
 KW therapy.
 OS Synthetic.
 PN WO9626214-A1.
 PD 29-AUG-1996.
 PF 01-FEB-1996; U01489.
 PR 23-FEB-1995; US-393273.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boon-Falleur T, De Plaen E, Gaugler B, Lurquin C;

PI Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;
DR WPI; 96-402317/40
PT New nona-peptide(s) that bind to HLA molecule(s) and induce lysis -
PT by specific cytolytic T cells, for diagnosis and treatment of
PT tumours and to expand T cells in vitro.
PS Claim 9; Page 30; 41pp; English.
CC R99337-R99342 represent nonapeptides of the invention. These sequences
CC bind to a HLA molecule on a cell, and provoke lysis by cytolytic T cells
CC (CTLs) specific for a complex of the HLA molecule and nonapeptide. These
CC sequences are based on regions of proteins in the MAGE family of human
CC tumour rejection antigen precursors. They are specifically based on
CC fragments of the tumour rejection antigen (TRA) of MAGE-1. The
CC nonapeptides can be used diagnostically to identify tumours expressing a
CC particular HLA molecule, or to identify cancer cells. The peptides can
CC also be used therapeutically, to induce a CTL response to tumours (where
CC the peptides are optionally coupled to tumour-specific antibodies), or to
CC induce a response by CTLs that are otherwise inactive. These sequences
CC may also be used to expand specific CTLs in vitro for later return to the
CC patient, such as for treating melanoma. Tumour cells can be identified
CC by using DNA encoding these sequences as probes. Non-human cells
CC transformed with the HLA-A1 gene and a DNA sequence encoding one of these
CC peptides, can be used to generate CTLs, or to detect the presence of CTLs
CC in human samples. The non-human transformed cells, when polytransformed,
CC are universal effector cells, and can be used in vaccines, or for
CC treating melanoma or breast cancer.
SQ Sequence 9 AA;

Query Match 66.7%; Score 54; DB 1; Length 35;
Best Local Similarity 88.9%; Pred. No. 2.26e-12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 27 EADATGHSY 35
|||:|||||
Qy 4 EADPTGHSY 12

RESULT 22
ID W13255 standard; Peptide; 10 AA.
AC W13255; 1997 (first entry)
DE MAGE-3 TRAP HLA-B44 motif.
KW HLA-B44; tumour rejection antigen; TRAP; cancer; melanoma;
KW MAGE-3; human; diagnosis; therapy.
OS Homo sapiens.
PN W09710837-A1.
PD 27-MAR-1997.
PF 19-SEP-1996; U15078.
PR 21-SEP-1995; US-531864.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Boon-Falleur T, Coullie P, Herman J, Van der Bruggen P;
DR WPI; 97-202614/18.
PT HLA-B44 molecule binding peptide(s) - useful to identify HLA-B44
PT positive cells, and develop products for diagnosis and therapy of,
PT e.g. cancer
PS Claim 2; Page 36; 55pp; English.
CC A peptide (W13255) corresponds to amino acids 167-176 of MAGE-3
CC tumour rejection antigen precursor (TRAP). It binds to HLA-B44
CC positive cells and provokes lysis by cytotoxic T lymphocytes. It
CC can be used in competition assays to identify similarly active
CC peptides. HLA-B44 binding peptides (see also W13251-54 and W13256)
CC can be used to identify HLA-B44 positive cells, and to develop
CC products for the diagnosis and therapy (e.g. antibodies) of
CC disorders in which the TRAP is expressed, e.g. cancer
CC (particularly melanoma).
SQ Sequence 10 AA;

Query Match 63.0%; Score 51; DB 1; Length 36;
Best Local Similarity 63.6%; Pred. No. 3.22e-10;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 26 VMEVDPTGHL 36
|:|:|:|:|:|
"Qy" '2 VKEADPTGHSY 12

RESULT 23
ID W16333 standard; Protein; 91 AA.
AC W16333;
DT 05-SEP-1997 (first entry)
DE Baboon MAGE-3 homologue D.
KW MAGE-3; tumour antigen; vaccine; cancer; immunotherapy; therapy.
OS Papio sp.
PN W09713858-A2.
PD 17-APR-1997.
PF 10-OCT-1996; U16319.
PR 12-OCT-1995; US-005117.
PA (CHIR) CHIRON CORP.
PI Ralston RO, Ring DB;
DR WPI; 97-235894/21.
DR N-PSDB; T63348.
PT New isolated baboon MAGE-3 homologues - used for stimulating the
PT immune system of humans to generate an immune response against
PT MAGE-3 tumour antigen
PS Example; Page 29; 36pp; English.
CC Baboon MAGE-3 polypeptides A, C, D, B and F (W16331-35) are
CC homologues of the human MAGE-3 tumour antigen (see also W16330),
CC and are encoded by gene fragments (T63346-50) derived from baboon
CC testis RNA. The baboon polypeptides, expressed in host cells or
CC in vivo, can be used to stimulate the immune system of humans.
CC They can also be used to generate an immune response against cells
CC expressing MAGE-3. They are different enough to be recognised as
CC foreign antigens more readily than human MAGE-3, but similar enough
CC to enable the immune system to mount a response that will also
CC recognise human MAGE-3.
SQ Sequence 91 AA;

Query Match 61.7%; Score 50; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 1.61e-09;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 30 ELMEVDVPVGHLY 41
:::|:|:|:|:|
Qy 1 DVKEADPTGHSY 12

RESULT 24
ID W16332 standard; Protein; 88 AA.
AC W16332;
DT 05-SEP-1997 (first entry)
DE Baboon MAGE-3 homologue C.
KW MAGE-3; tumour antigen; vaccine; cancer; immunotherapy; therapy.
OS Papio sp.
PN Key Location/Qualifiers
FT /label= Val, Asp
FT W09713858-A2.
PD 17-APR-1997.
PF 10-OCT-1996; U16319.
PR 12-OCT-1995; US-005117.
PA (CHIR) CHIRON CORP.
PI Ralston RO, Ring DB;
DR WPI; 97-235894/21.
DR N-PSDB; T63347.
PT New isolated baboon MAGE-3 homologues - used for stimulating the
PT immune system of humans to generate an immune response against
PT MAGE-3 tumour antigen
PS Example; Page 29; 36pp; English.
CC Baboon MAGE-3 polypeptides A, C, D, B and F (W16331-35) are
CC homologues of the human MAGE-3 tumour antigen (see also W16330),
CC and are encoded by gene fragments (T63346-50) derived from baboon
CC testis RNA. The baboon polypeptides, expressed in host cells or
CC in vivo, can be used to stimulate the immune system of humans.
CC They can also be used to generate an immune response against cells
CC expressing MAGE-3. They are different enough to be recognised as
CC foreign antigens more readily than human MAGE-3, but similar enough
CC to enable the immune system to mount a response that will also

CC recognise human MAGE-3.
SQ Sequence 88 AA;

Query Match 61.7%; Score 50; DB 1; Length 122;

Best Local Similarity 50.0%; Pred. No. 1.61e-09;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 38 ELMEVDVPVGHLY 49
:::| || || |
QY 1 DVKEADPTGHSY 12

RESULT 25

ID W16335 standard; Protein; 91 AA.

AC W16335;

DT 05-SEP-1997 (first entry)

DE Baboon MAGE-3 homologue F.

KW MAGE-3; tumour antigen; vaccine; cancer; immunotherapy; therapy.

OS Papio sp.

FH Key Location/Qualifiers

FT Misc_difference 77

FT /label= Val, Phe

PN WO9713858-A2.

PD 17-APR-1997.

PF 10-OCT-1996; U16319.

PR 12-OCT-1995; US-005117.

PA (CHIR) CHIRON CORP.

PI Ralston RO, Ring DB;

DR WPI: 97-235894/21.

DR N-PSDB; T63350.

PT New isolated baboon MAGE-3 homologues - used for stimulating the

PT immune system of humans to generate an immune response against

PT MAGE-3 tumour antigen

PS Example; Page 29; 36pp; English.

CC Baboon MAGE-3 polypeptides A, C, D, B and F (W16331-35) are

CC homologues of the human MAGE-3 tumour antigen (see also W16330),

CC and are encoded by gene fragments (T63346-50) derived from baboon

CC testis RNA. The baboon polypeptides, expressed in host cells or

CC in vivo, can be used to stimulate the immune system of humans.

CC They can also be used to generate an immune response against cells

CC expressing MAGE-3. They are different enough to be recognised as

CC foreign antigens more readily than human MAGE-3, but similar enough

CC to enable the immune system to mount a response that will also

CC recognise human MAGE-3.

SQ Sequence 91 AA;

Query Match 61.7%; Score 50; DB 1; Length 125;

Best Local Similarity 50.0%; Pred. No. 1.61e-09;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 38 ELMEVDVPVGHLY 49
:::| || || |
QY 1 DVKEADPTGHSY 12

RESULT 26

ID W16330 standard; Protein; 126 AA.

AC W16330;

DT 05-SEP-1997 (first entry)

DE Human MAGE-3 tumour antigen.

KW MAGE-3; tumour antigen; vaccine; cancer; immunotherapy; therapy.

OS Homo sapiens.

PN WO9713858-A2.

PD 17-APR-1997.

PF 10-OCT-1996; U16319.

PR 12-OCT-1995; US-005117.

PA (CHIR) CHIRON CORP.

PI Ralston RO, Ring DB;

DR WPI: 97-235894/21.

DR N-PSDB; T63345.

PT New isolated baboon MAGE-3 homologues - used for stimulating the

PT immune system of humans to generate an immune response against

PT MAGE-3 tumour antigen

PS Example; Page 29; 36pp; English.

CC A polypeptide (W16330) comprises a partial sequence of human

CC MAGE-3, a tumour antigen recognised on melanoma cells by

CC autologous cytolytic T lymphocytes. It shows homology to baboon

CC polypeptides (W16311-35) encoded by gene fragments (T63346-50)

CC that were derived from baboon testis RNA using primers (see also

CC T63351-53) based on human MAGE-3 sequences. The baboon MAGE-3

CC homologues can be used to stimulate the immune system of humans

CC to generate an immune response against MAGE-3.

SQ Sequence 126 AA;

Query Match

Best Local Similarity 50.0%; Score 50; DB 1; Length 152;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 30 ELMEVDPIGHLY 41
:::| || || |
QY 1 DVKEADPTGHSY 12

RESULT 27

ID W16331 standard; Protein; 125 AA.

AC W16331;

DT 05-SEP-1997 (first entry)

DE Baboon MAGE-3 homologue A.

KW MAGE-3; tumour antigen; vaccine; cancer; immunotherapy; therapy.

OS Papio sp.

FH Key Location/Qualifiers

FT Misc_difference 18

FT /label= Val, Asp

FT Misc_difference 116

FT /note= "residue 116 could not be determined due to

FT DNA sequence ambiguity"

FT Misc_difference 124

FT /note= "residue 124 could not be determined due to

FT DNA sequence ambiguity"

PN WO9713858-A2.

PD 17-APR-1997.

PF 10-OCT-1996; U16319.

PR 12-OCT-1995; US-005117.

PA (CHIR) CHIRON CORP.

PI Ralston RO, Ring DB;

DR WPI: 97-235894/21.

DR N-PSDB; T63346.

PT New isolated baboon MAGE-3 homologues - used for stimulating the

PT immune system of humans to generate an immune response against

PT MAGE-3 tumour antigen

PS Example; Page 29; 36pp; English.

CC Baboon MAGE-3 polypeptides A, C, D, B and F (W16331-35) are

CC homologues of the human MAGE-3 tumour antigen (see also W16330),

CC and are encoded by gene fragments (T63346-50) derived from baboon

CC testis RNA. The baboon polypeptides, expressed in host cells or

CC in vivo, can be used to stimulate the immune system of humans.

CC They can also be used to generate an immune response against cells

CC expressing MAGE-3. They are different enough to be recognised as

CC foreign antigens more readily than human MAGE-3, but similar enough

CC to enable the immune system to mount a response that will also

CC recognise human MAGE-3.

SQ Sequence 125 AA;

Query Match

Best Local Similarity 50.0%; Score 50; DB 1; Length 150;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 38 ELMEVDPIGHLY 49
:::| || || |
QY 1 DVKEADPTGHSY 12

RESULT 28

ID W16334 standard; Protein; 126 AA.

AC W16334;

DT 05-SEP-1997 (first entry)

DE Baboon MAGE-3 homologue B.
KW MAGE-3; tumour antigen; vaccine; cancer; immunotherapy; therapy.
OS Papio sp. Location/Qualifiers
FH Key difference 77
FT /label= Val, Phe
FT MISC_difference 110
FT /note= "residue 110 could not be determined due to
FT DNA sequence ambiguity"
FT MISC_difference 117
FT /note= "residue 117 could not be determined due to
FT DNA sequence ambiguity"
FT MISC_difference 125
FT /note= "residue 125 could not be determined due to
FT DNA sequence ambiguity"
PN W09713858-A2.
PD 17-APR-1997.
PF 10-OCT-1996; U16319.
PR 12-OCT-1995; US-005117.
PA (CHIR) CHIRON CORP.
PI Ralston RO. Ring DB;
DR WPI; 97-235894/21.
DR N-PSDB; T63349.
PT New isolated baboon MAGE-3 homologues - used for stimulating the
PT immune system of humans to generate an immune response against
PT MAGE-3 tumour antigen
PS Example: Page 29; 36pp; English.
CC Baboon MAGE-3 polypeptides A, C, D, B and F (W16331-35) are
CC homologues of the human MAGE-3 tumour antigen (see also W16330),
CC and are encoded by gene fragments (T63346-50) derived from baboon
CC testis RNA. The baboon polypeptides, expressed in host cells or
CC in vivo, can be used to stimulate the immune system of humans.
CC They can also be used to generate an immune response against cells
CC expressing MAGE-3. They are different enough to be recognised as
CC foreign antigens more readily than human MAGE-3, but similar enough
CC to enable the immune system to mount a response that will also
CC recognise human MAGE-3.
SQ Sequence 126 AA;

Query Match 61.7%; Score 50; DB 1; Length 160;
Best Local Similarity 50.0%; Pred. No. 1.61e-09;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 38 ELMEVDVPVGHLY 49
Qy 1 DVKEADPTGHSY 12

RESULT 29
ID R99341 standard; peptide; 9 AA.
AC R99341; 1997 (first entry)
DE HLA binding nonapeptide #5.
KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;
KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
KW therapy.
OS Synthetic.
PN W09626214-A1.
PD 29-AUG-1996.
PF 01-FEB-1996; U01489.
PR 23-FEB-1995; US-393273.
PA (JUDW-) LUDWIG INST CANCER RES.
PI Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;
PI Boon-Falleur T, De Plaen E, Gaugler B, Lurquin C;
DR WPI; 96-402317/40.
PT New nona-peptide(s) that bind to HLA molecule(s) and induce lysis
PT tumours and to expand T cells in vitro.
PS Claim 9; Page 30; 41pp; English.
CC R99337-R99342 represent nonapeptides of the invention. These sequences
CC bind to a HLA molecule on a cell, and provoke lysis by cytolytic T cells
CC (CTLs) specific for a complex of the HLA molecule and nonapeptide. These

CC sequences are based on regions of proteins in the MAGE family of human
CC tumour rejection antigen precursors. They are specifically based on
CC fragments of the tumour rejection antigen (TRA) of MAGE-1. The
CC nonapeptides can be used diagnostically to identify tumours expressing a
CC particular HLA molecule, or to identify cancer cells. The peptides can
CC also be used therapeutically, to induce a CTL response to tumours (where
CC the peptides are optionally coupled to tumour-specific antibodies), or to
CC induce a response by CTLs that are otherwise inactive. These sequences
CC may also be used to expand specific CTLs in vitro for later return to the
CC patient, such as for treating melanoma. Tumour cells can be identified
CC by using DNA encoding these sequences as probes. Non-human cells
CC transformed with the HLA-A1 gene and a DNA sequence encoding one of these
CC peptides, can be used to generate CTLs, or to detect the presence of CTLs
CC in human samples. The non-human transformed cells, when polytransformed,
CC are universal effector cells, and can be used in vaccines, or for
CC treating melanoma or breast cancer.
SQ Sequence 9 AA;

Query Match 60.5%; Score 49; DB 1; Length 35;
Best Local Similarity 88.9%; Pred. No. 7.89e-09;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 27 EADPTGASY 35
Qy 4 EADPTGHSY 12

RESULT 30
ID W13869 standard; Protein; 308 AA.
AC W13869;
DT 12-MAY-1997 (first entry)
DE Rad protein.
KW Human; rad; C9D6; diabetogene; diabetes; obesity; ras/GTPase; antibody;
KW glucose metabolism; Type II diabetes; transgenic animal.
OS Homo sapiens.
PN US5589374-A.
PD 31-DEC-1996.
PF 19-JUN-1992; 901710.
PR 19-JUN-1992; US-901710.
PR 11-JUN-1993; US-076089.
PA (JOSL-) JOSLIN DIABETES CENT INC.
PI Kahn CR, Reynet C;
DR WPI; 97-107140/10.
DR N-PSDB; T60034.
PT DNA encoding human rad protein - for prodn. of recombinant protein,
PT useful to prepare antibodies and in therapeutic compns.
PS Claim 8; Column 17-20; 17pp; English.
CC This sequence represents the human rad protein. Rad (formerly referred
CC to as C9D6) is a diabetogene. A diabetogene is a gene whose expression,
CC at the mRNA level, is altered in an individual with diabetes and/or
CC obesity. Rad encodes a member of the ras/GTPase related gene family, and
CC shares 45-55% homology (at the nucleotide level) with other members of
CC this family. This sequence can be used for the production of recombinant
CC rad, which can then be used to produce anti-rad antibodies, and in
CC therapeutic compositions. The rad protein can also be used for
CC investigating the basis of glucose metabolism in normal and disease
CC states at the level of gene structure and gene expression. The protein
CC can also be used to determine if a subject is at risk for a glucose
CC metabolism related disorder (such as Type II diabetes), evaluating the
CC effect of a treatment on the level of expression of a diabetogene,
CC evaluating animal models for resemblance to a human disorder involving a
CC diabetogene, and for making transgenic animals, and genetically altered
CC cell lines for use in research.
SQ Sequence 308 AA;

Query Match 59.3%; Score 48; DB 1; Length 334;
Best Local Similarity 55.6%; Pred. No. 3.78e-08;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 145 EAAAGHTY 153
Qy 4 EADPTGHSY 12

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RESULT 31
ID R45431 standard; Protein; 308 AA.
AC R45431.
DE 13-JUN-1994 (first entry)
DI Diabetogene rad: A type II.
KW Diabetogene rad; rad gene; diabetogene rad protein; diabetes;
  obesity.
OS Homo sapiens.
PN WO9400558-A.
PD 06-JAN-1994.
PR 11-JUN-1993; U05643.
PI 19-JUN-1992; US-901710.
PA (JOSL-) JOSLIN DIABETES CENT INC.
PI Kahn CR, Reynet C;
DR WPI: 94-026198/03.
DR P-PSDB; Q55175.
PT Purified DNA - includes type II diabetes-specific gene.
PT Diabetogenic rad
PS Disclosure: Page 37-38; 57pp; English.
CC A gene encoding diabetogene rad protein R45431 is given in sequence
CC Q55175. The gene is used to determine the risk of diabetes or
CC obesity. And the protein is used to treat deficiency of diabetogene
CC product.
SQ Sequence 308 AA;

Query Match 59.3%; Score 48; DB 1: Length 334;
Best Local Similarity 55.6%; Pred. No. 3.78e-08;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 145 EAEAGTCHSY 153
QY 4 EADPTGHSY 12
II:::II:::

RESULT 32
ID R79148 standard; protein; 925 AA.
AC R79148;
DE 28-DEC-1995 (first entry)
DI Human insulin receptor tyrosine kinase inhibitor PC-1.
KW Insulin receptor tyrosine kinase inhibitor; PC-1; insulin resistance;
  plasma cell membrane glycoprotein; insulin-dependent diabetes;
  diabetes mellitus.
OS Homo sapiens.
PN WO9519570-A.
PD 20-JUL-1995.
PF 28-DEC-1994; U14893.
PR 14-JAN-1994; US-182241.
PA (GETH ) GENENTECH INC.
PA (REGC ) UNIV CALIFORNIA.
PI Goldfine ID, Grupe A, Maddux BA, Spencer S, Stewart TA;
DR WPI: 95-263954/34.
DI Diagnosis and treatment of insulin resistance - using antagonists,
  partic. antibodies to insulin receptor tyrosine kinase inhibitor
  proteins.
PS Disclosure: Fig 1; 63pp; English.
CC PC-1 is a class II (cytoplasmic N terminus) membrane glycoprotein.
CC It is the same protein as liver nucleoside pyrophosphatase/alkaline
CC phosphodiesterase I. Rebbe et al., Mol. Immuno., 30: 87-93 (1993).
CC The size of PC-1 is 115-135 kDa, depending on the tissue studies. PC-
CC 1 also exists as a 230-260 kDa dimer. Human PC-1 has been deduced to
CC have 873 AAs and is mapped to the chromosome location 6q22-6q23,
CC Funakoshi et al., Arch. Biochem. Biophys., 295:180-187 (1992). The
CC full length AA sequence of PC-1 is provided in R79148. PC-1 was
CC purified from fibroblasts from an individual showing marked
CC inhibition of insulin receptor autophosphorylation in vivo. A method
CC for detecting or measuring the amount of PC-1 is claimed. This
CC method can be used in the diagnosis and treatment of diseases
CC involving inappropriate insulin receptor tyrosine kinase inhibitor
CC expression e.g. non-insulin dependent diabetes mellitus.
SQ Sequence 925 AA;

Query Match 59.3%; Score 48; DB 1: Length 951;

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Best Local Similarity 66.7%; Pred. No. 3.78e-08;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 400 EPDSSGHSY 408
QY 4 EADPTGHSY 12
II:::II:::

RESULT 33
ID P93191 standard; protein; 443 AA.
AC P93191;
DE 26-MAR-1990 (first entry)
DI Peptide with glutamine synthetase activity.
KW Glutamine synthetase; Bacillus sp. EH113 (FERM BP-2281);
  E.coli DH1 pGS2 (FERM BP-2265); plasmid pGS2.
OS Bacillus sp. EH113 (FERM BP-2281).
PN DE3909249-A.
PD 02-NOV-1989.
PR 21-MAR-1988; JP-P68671.
PA (TOXN) Toyo Jozo Co. Ltd.
PI Sagai H, Ohta H;
DR WPI: 89-32536/45.
DR N-PSDB; N92017.
PT New DNA encoding new glutamine synthetase peptide - useful as reagent for
  ammonium ion assay, and transformed microorganisms providing efficient
  prodn. of high purity enzyme.
PS Claim 2; page 11; 17pp; german.
CC The peptide has glutamine synthetase activity. It is useful as a reagent
CC for assaying ammonium ions, or cpds. such as urea which generate them.
CC DNA encoding the peptide is obtd. from Bacillus sp. EH113 (FERM BP-2281).
CC and is expressed in host cell E.coli DH1 pGS2 (FERM BP-2265) using pGS2.
CC This plasmid comprises a HindIII fragment from FERM BP-2281 inserted into
CC HindIII-linearised pBR322. Culturing the transformant gives efficient
CC prodn. of high purity peptide at reduced costs.
SQ Sequence 443 AA;

Query Match 58.0%; Score 47; DB 1: Length 471;
Best Local Similarity 33.3%; Pred. No. 1.77e-07;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 360 EVRSVDPAAAPY 371
QY 1 DVKEADPTGHSY 12
II:::II:::

RESULT 34
ID R99350 standard; Protein; 9 AA.
AC R99350;
DE 22-APR-1997 (first entry)
DI MAGE-6 nonapeptide.
KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;
  tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
  antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
  therapy.
OS Homo sapiens.
PN WO9626214-A1.
PD 29-AUG-1996.
PF 01-FEB-1996; U01489.
PR 23-FEB-1995; US-393273.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Boon-Faller T, De Plaen E, Gaugler B, Lurquin C;
DR Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;
DR WPI: 96-402317/40.
DR N-PSDB; T35415.
PT New nona-peptide(s) that bind to HLA molecule(s) and induce lysis
  by specific cytolytic T cells, for diagnosis and treatment of
  tumours and to expand T cells in vitro.
PS Example 4; Fig 4; 41pp; English.
CC R99343-R99350 represent MAGE nonapeptides, based on the tumour rejection
CC antigen region of the full length MAGE sequences. These peptides were
CC used to design the nonapeptides of the invention (see R99337-R99342),
CC which bind to a HLA molecule on a cell, and provoke lysis by cytolytic T

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CC cells (CTLs) specific for a complex of the HLA molecule and nonapeptide.
 CC The nonapeptides can be used diagnostically to identify tumours
 CC expressing a particular HLA molecule, or to identify cancer cells. The
 CC peptides can also be used therapeutically, to induce a CTL response to
 CC tumours (where the peptides are optionally coupled to tumour-specific
 CC antibodies), or to induce a response by CTLs that are otherwise inactive.
 CC The peptide sequences may also be used to expand specific CTLs in vitro
 CC for later return to the patient, such as for treating melanoma. Tumour
 CC cells can be identified by using DNA encoding the nonapeptides as probes.
 CC Non-human cells transformed with the HLA-A1 gene and a DNA sequence
 CC encoding one of the peptides, can be used to generate CTLs, or to detect
 CC the presence of CTLs in human samples. The non-human transformed cells,
 CC when polytransformed, are universal effector cells, and can be used in
 CC vaccines, or for treating melanoma or breast cancer.
 SQ Sequence 9 AA;

Query Match 56.8%; Score 46; DB 1; Length 35;
 Best Local Similarity 66.7%; Pred. No. 8.04e-07;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 27 EVDPIGHVY 35
 QY 4 EADPTGHSY 12

RESULT 35
 ID R99349 standard; Protein; 9 AA.
 AC R99349;
 DT 22-APR-1997 (first entry)
 DE MAGE-5/MAGE-51 nonapeptide.
 KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;
 KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
 KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
 KW therapy.
 OS Homo sapiens.
 PN W09626214-A1.
 PD 29-AUG-1996.
 PF 01-FEB-1996; U01489.
 PR 23-FEB-1995; US-393273.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Boon-Falleur T, De Plaen E, Gaugler B, Lurquin C;
 PI Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;
 DR WPI; 96-402317/40.
 DR N-PSDB: T35414.
 PT New nona-peptide(s) that bind to HLA molecule(s) and induce lysis
 PT by specific cytolytic T cells, for diagnosis and treatment of
 PT tumours and to expand T cells in vitro.
 PS Example 4; Fig 4; 41pp; English.
 CC R99343-R99350 represent MAGE nonapeptides, based on the tumour rejection
 CC antigen region of the full length MAGE sequences. These peptides were
 CC used to design the nonapeptides of the invention (see R99337-R99342),
 CC which bind to a HLA molecule on a cell, and provoke lysis by cytolytic T
 CC cells (CTLs) specific for a complex of the HLA molecule and nonapeptide.
 CC The nonapeptides can be used diagnostically to identify tumours
 CC expressing a particular HLA molecule, or to identify cancer cells. The
 CC peptides can also be used therapeutically, to induce a CTL response to
 CC tumours (where the peptides are optionally coupled to tumour-specific
 CC antibodies), or to induce a response by CTLs that are otherwise inactive.
 CC The peptide sequences may also be used to expand specific CTLs in vitro
 CC for later return to the patient, such as for treating melanoma. Tumour
 CC cells can be identified by using DNA encoding the nonapeptides as probes.
 CC Non-human cells transformed with the HLA-A1 gene and a DNA sequence
 CC encoding one of the peptides, can be used to generate CTLs, or to detect
 CC the presence of CTLs in human samples. The non-human transformed cells,
 CC when polytransformed, are universal effector cells, and can be used in
 CC vaccines, or for treating melanoma or breast cancer.
 SQ Sequence 9 AA;

Query Match 56.8%; Score 46; DB 1; Length 35;
 Best Local Similarity 66.7%; Pred. No. 8.04e-07;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db... 27 EADPTGHSY 35

QY 4 EADPTGHSY 12

Search completed: Tue Apr 7 08:43:12 1998
 Job time : 8 secs.

MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Apr 7 08:46:06 1998; MasPar time 1.50 Seconds
Tabular output not generated.
Title: >US-08-190-411A-4
Description: (1-12) from 5541104.pep
Perfect Score: 81
Sequence: 1 DVKEADPTGHSY 12
Scoring table: PAM 150
Gap 15
Searched: 60183 seqs, 5492030 residues
Post-processing: Minimum Match 0%
Listing first 100 summaries
Database: a-issued
1-back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9: PCT90
10: PCT91 11: PCT92 12: PCT93 13: PCT94 14: PCT95 15: PCT96
Statistics: Mean 15.516; Variance 38.247; scale 0.406
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
Result No. Score Query Match Length DB ID Description Pred. No.

1 81 100.0 12 6 US-08-190- Sequence 4, Applicatio 2.03e-04
2 61 75.3 9 14 PCT-US95-0 Sequence 1, Applicatio 1.60e-01
3 61 75.3 9 7 US-08-299- Sequence 26, Applicati 1.60e-01
4 61 75.3 9 14 PCT-US95-0 Sequence 2, Applicatio 1.60e-01
5 61 75.3 9 7 US-08-186- Sequence 1, Applicatio 1.60e-01
6 61 75.3 9 5 US-07-938- Sequence 1, Applicatio 1.60e-01
7 61 75.3 9 7 US-08-473- Sequence 12, Applicati 1.60e-01
8 61 75.3 9 5 US-08-073- Sequence 14, Applicati 1.09e+00
9 55 67.9 8 7 US-08-443- Sequence 13, Applicati 6.95e+00
10 55 67.9 8 5 US-08-073- Sequence 13, Applicati 6.95e+00
11 49 60.5 8 5 US-08-443- Sequence 21, Applicati 6.95e+00
12 49 60.5 8 7 US-07-938- Sequence 21, Applicati 6.95e+00
13 49 60.5 417 6 US-08-430- Sequence 6, Applicatio 6.95e+00
14 49 60.5 417 3 US-07-649- Sequence 6, Applicatio 6.95e+00
15 49 60.5 417 3 PCT-US94-1 Sequence 1, Applicatio 9.41e+00
16 49 60.5 925 13 PCT-US94-1 Sequence 1, Applicatio 9.41e+00
17 48 59.3 9 5 US-08-073- Sequence 20, Applicati 1.72e+01
18 46 56.8 9 5 US-07-938- Sequence 9, Applicati 1.72e+01
19 46 56.8 9 5 US-08-073- Sequence 21, Applicati 1.72e+01
20 46 56.8 9 5 US-08-073- Sequence 8, Applicatio 1.72e+01
21 46 56.8 9 5 US-07-938- Sequence 21, Applicati 1.72e+01
22 46 56.8 9 7 US-08-443- Sequence 21, Applicati 1.72e+01

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Apr 7 08:46:06 1998; MasPar time 1.50 Seconds
Tabular output not generated.
Title: >US-08-190-411A-4
Description: (1-12) from 5541104.pep
Perfect Score: 81
Sequence: 1 DVKEADPTGHSY 12
Scoring table: PAM 150
Gap 15
Searched: 60183 seqs, 5492030 residues
Post-processing: Minimum Match 0%
Listing first 100 summaries
Database: a-issued
1-back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9: PCT90
10: PCT91 11: PCT92 12: PCT93 13: PCT94 14: PCT95 15: PCT96
Statistics: Mean 15.516; Variance 38.247; scale 0.406
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
Result No. Score Query Match Length DB ID Description Pred. No.

1 81 100.0 12 6 US-08-190- Sequence 4, Applicatio 2.03e-04
2 61 75.3 9 14 PCT-US95-0 Sequence 1, Applicatio 1.60e-01
3 61 75.3 9 7 US-08-299- Sequence 26, Applicati 1.60e-01
4 61 75.3 9 14 PCT-US95-0 Sequence 2, Applicatio 1.60e-01
5 61 75.3 9 7 US-08-186- Sequence 1, Applicatio 1.60e-01
6 61 75.3 9 5 US-07-938- Sequence 1, Applicatio 1.60e-01
7 61 75.3 9 7 US-08-473- Sequence 12, Applicati 1.60e-01
8 61 75.3 9 5 US-08-073- Sequence 14, Applicati 1.09e+00
9 55 67.9 8 7 US-08-443- Sequence 13, Applicati 6.95e+00
10 55 67.9 8 5 US-08-073- Sequence 13, Applicati 6.95e+00
11 49 60.5 8 5 US-08-443- Sequence 21, Applicati 6.95e+00
12 49 60.5 8 7 US-07-938- Sequence 21, Applicati 6.95e+00
13 49 60.5 417 6 US-08-430- Sequence 6, Applicatio 6.95e+00
14 49 60.5 417 3 US-07-649- Sequence 6, Applicatio 6.95e+00
15 49 60.5 417 3 PCT-US94-1 Sequence 1, Applicatio 9.41e+00
16 49 60.5 925 13 PCT-US94-1 Sequence 1, Applicatio 9.41e+00
17 48 59.3 9 5 US-08-073- Sequence 20, Applicati 1.72e+01
18 46 56.8 9 5 US-07-938- Sequence 9, Applicati 1.72e+01
19 46 56.8 9 5 US-08-073- Sequence 21, Applicati 1.72e+01
20 46 56.8 9 5 US-08-073- Sequence 8, Applicatio 1.72e+01
21 46 56.8 9 5 US-07-938- Sequence 21, Applicati 1.72e+01
22 46 56.8 9 7 US-08-443- Sequence 21, Applicati 1.72e+01

23	46	56.8	9	7	US-08-443-	Sequence 22, Applicati	1.72e+01
24	46	56.8	9	5	US-07-938-	Sequence 7, Applicati	1.72e+01
25	46	56.8	9	5	US-08-073-	Sequence 22, Applicati	1.72e+01
26	46	56.8	9	7	US-08-443-	Sequence 20, Applicati	1.72e+01
27	46	56.8	999	6	US-08-252-	Sequence 2, Applicati	1.72e+01
28	43	53.1	9	14	PCT-US95-0	Sequence 1, Applicatio	4.15e+01
29	43	53.1	9	7	US-08-443-	Sequence 17, Applicati	4.15e+01
30	43	53.1	9	7	US-08-186-	Sequence 2, Applicati	4.15e+01
31	43	53.1	9	5	US-07-938-	Sequence 4, Applicatio	4.15e+01
32	43	53.1	9	5	US-08-073-	Sequence 17, Applicati	4.15e+01
33	43	53.1	32	7	US-08-186-	Sequence 9, Applicatio	4.15e+01
34	43	53.1	559	12	PCT-US93-0	Sequence 12, Applicati	4.15e+01
35	43	53.1	559	8	US-08-368-	Sequence 12, Applicati	4.15e+01
36	43	53.1	2509	7	US-08-469-	Sequence 10, Applicati	4.15e+01
37	42	51.9	8	5	US-07-938-	Sequence 22, Applicati	5.54e+01
38	42	51.9	9	5	US-07-938-	Sequence 6, Applicatio	5.54e+01
39	42	51.9	9	5	US-08-073-	Sequence 19, Applicati	5.54e+01
40	42	51.9	9	7	US-08-443-	Sequence 19, Applicati	5.54e+01
41	42	51.9	375	12	PCT-US93-0	Sequence 8, Applicatio	5.54e+01
42	42	51.9	375	5	US-08-121-	Sequence 8, Applicatio	5.54e+01
43	41	50.6	36	7	US-08-050-	Sequence 30, Applicati	7.39e+01
44	41	50.6	91	6	US-08-225-	Sequence 16, Applicati	7.39e+01
45	41	50.6	343	7	US-08-187-	Sequence 2, Applicatio	7.39e+01
46	41	50.6	417	6	US-08-430-	Sequence 7, Applicatio	7.39e+01
47	41	50.6	417	5	US-08-277-	Sequence 7, Applicatio	7.39e+01
48	41	50.6	417	3	US-07-649-	Sequence 7, Applicatio	7.39e+01
49	41	50.6	459	1	5194375-6	Patent No. 5194375,	7.39e+01
50	41	50.6	530	7	US-08-187-	Sequence 4, Applicatio	7.39e+01
51	41	50.6	889	7	US-08-118-	Sequence 4, Applicatio	7.39e+01
52	41	50.6	942	5	US-08-141-	Sequence 14, Applicati	7.39e+01
53	41	50.6	942	8	US-08-541-	Sequence 14, Applicati	7.39e+01
54	40	49.4	414	7	US-08-332-	Sequence 46, Applicati	9.82e+01
55	40	49.4	414	7	US-08-332-	Sequence 52, Applicati	9.82e+01
56	40	49.4	414	6	US-08-188-	Sequence 52, Applicati	9.82e+01
57	40	49.4	430	5	US-08-147-	Sequence 25, Applicati	9.82e+01
58	40	49.4	430	11	PCT-US92-0	Sequence 19, Applicati	9.82e+01
59	40	49.4	430	12	PCT-US93-0	Sequence 9, Applicatio	9.82e+01
60	40	49.4	430	12	PCT-US93-0	Sequence 19, Applicati	9.82e+01
61	40	49.4	430	12	PCT-US93-1	Sequence 6, Applicatio	9.82e+01
62	40	49.4	430	12	PCT-US93-0	Sequence 4, Applicatio	9.82e+01
63	40	49.4	430	12	PCT-US93-0	Sequence 19, Applicati	9.82e+01
64	40	49.4	430	12	PCT-US93-0	Sequence 19, Applicati	9.82e+01
65	40	49.4	430	12	PCT-US93-0	Sequence 19, Applicati	9.82e+01
66	40	49.4	430	12	PCT-US93-0	Sequence 19, Applicati	9.82e+01
67	40	49.4	430	4	US-07-901-	Sequence 9, Applicatio	9.82e+01
68	40	49.4	430	8	US-08-447-	Sequence 25, Applicati	9.82e+01
69	40	49.4	430	7	US-08-155-	Sequence 19, Applicati	9.82e+01
70	40	49.4	430	7	US-08-406-	Sequence 6, Applicatio	9.82e+01
71	40	49.4	430	7	US-08-479-	Sequence 19, Applicati	9.82e+01
72	40	49.4	430	8	US-08-643-	Sequence 19, Applicati	9.82e+01
73	40	49.4	430	3	US-07-841-	Sequence 25, Applicati	9.82e+01
74	40	49.4	430	7	US-08-480-	Sequence 6, Applicatio	9.82e+01
75	40	49.4	430	9	PCT-US90-0	Sequence 2, Applicatio	9.82e+01
76	40	49.4	430	7	US-08-278-	Sequence 19, Applicati	9.82e+01
77	40	49.4	440	4	US-07-637-	Sequence 4, Applicatio	9.82e+01
78	40	49.4	440	4	US-08-112-	Sequence 4, Applicatio	9.82e+01
79	40	49.4	440	4	US-07-637-	Sequence 7, Applicatio	9.82e+01
80	40	49.4	824	7	US-08-221-	Sequence 3, Applicatio	9.82e+01
81	40	49.4	1833	14	PCT-US95-0	Sequence 18, Applicati	9.82e+01
82	39	48.1	9	5	US-07-938-	Sequence 5, Applicatio	1.30e+02
83	39	48.1	131	7	US-08-468-	Sequence 4, Applicatio	1.30e+02
84	39	48.1	181	7	US-07-949-	Sequence 2, Applicatio	1.30e+02
85	39	48.1	306	14	PCT-US95-0	Sequence 2, Applicatio	1.30e+02
86	39	48.1	350	15	PCT-US96-0	Sequence 2, Applicatio	1.30e+02
87	39	48.1	350	15	PCT-US96-0	Sequence 2, Applicatio	1.30e+02
88	39	48.1	440	4	US-08-112-	Sequence 5, Applicatio	1.30e+02
89	39	48.1	440	4	US-07-637-	Sequence 13, Applicati	1.30e+02
90	39	48.1	528	12	PCT-US93-0	Sequence 6, Applicatio	1.30e+02
91	39	48.1	628	14	PCT-US95-0	Sequence 2, Applicatio	1.30e+02
92	39	48.1	635	5	US-07-832-	Sequence 2, Applicatio	1.30e+02
93	39	48.1	878	14	PCT-US95-0	Sequence 2, Applicatio	1.30e+02
94	39	48.1	878	7	US-08-237-	Sequence 2, Applicatio	1.30e+02
95	39	48.1	1026	12	PCT-US93-1	Sequence 95, Applicati	1.30e+02

96 39 48.1 1026 14 PCT-US95-0 Sequence 95, Applicati 1.30e+02
97 39 48.1 1155 5 US-08-286- Sequence 46, Applicati 1.30e+02
98 39 48.1 1203 14 PCT-US95-0 Sequence 103, Applicat 1.30e+02
99 39 48.1 1203 12 PCT-US93-1 Sequence 103, Applicat 1.30e+02
100 39 48.1 1513 12 PCT-US93-0 Sequence 2, Applicatio 1.30e+02

ALIGNMENTS

RESULT 1
ID US-08-190-411A-4 STANDARD; PRT; 12 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 4, Application US/08190411A.
XX CC Sequence 4, Application US/08190411A
XX CC Patent No. 5541104
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Chen, Yao-Tsung; Stockert, Elisabeth;
XX CC APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
XX CC APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
XX CC APPLICANT: Old, Lloyd J.
XX CC TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
XX CC NANT MAGE-1, TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBI
XX CC TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
XX CC NUMBER OF SEQUENCES: 4
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: Felfe & Lynch
XX CC STREET: 805 Third Avenue
XX CC CITY: New York City
XX CC STATE: New York
XX CC ZIP: 10022
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
XX CC COMPUTER: IBM
XX CC OPERATING SYSTEM: PC-DOS
XX CC SOFTWARE: Wordperfect
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/190,411A
XX CC FILING DATE: 01-FEBRUARY-1994
XX CC CLASSIFICATION: 436
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: 037,230
XX CC FILING DATE: 26-MARCH-1993
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: PCT/US92/04354
XX CC FILING DATE: 22-MAY-1992
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: 07/807,043
XX CC FILING DATE: 12-DECEMBER-1991
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: 07/764,364
XX CC FILING DATE: 23-SEPTEMBER-1991
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: 07/728,838
XX CC APPLICATION NUMBER: 9-JULY-1991
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: 07/705,702
XX CC FILING DATE: 23-MAY-1991
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Hadson, No. 5541104man D.
XX CC REGISTRATION NUMBER: 30,946
XX CC REFERENCE/DOCKET NUMBER: LUD 5354
XX CC TELEPHONE: (212) 688-9200
XX CC TELEFAX: (212) 838-3884
XX CC INFORMATION FOR SEQ ID NO: 4:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 12 amino acid residues

CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 12 AA; 1318 MW; 944 CN;
Query Match 100.0%; Score 81; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.03e-04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 DVKEADPTGHSY 12
| | | | | | | | | |
Qy 1 DVKEADPTGHSY 12
RESULT 2
ID PCT-US95-02121-1 STANDARD; PRT; 9 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 1, Application PC/TUS9502121.
XX CC Sequence 1, Application PC/TUS9502121
XX CC GENERAL INFORMATION:
XX CC APPLICANT:
XX CC TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
XX CC TITLE OF INVENTION: CTL IMMUNITY
XX CC NUMBER OF SEQUENCES: 153
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: PatentIn Release #1.0, Version #1.25
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: PCT/US95/02121
XX CC FILING DATE: 16-FEB-1995
XX CC CLASSIFICATION:
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/197,484
XX CC FILING DATE: 16-FEB-1994
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/935,811
XX CC FILING DATE: 26-AUG-1992
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/874,491
XX CC FILING DATE: 27-APR-1992
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/827,682
XX CC FILING DATE: 29-JAN-1992
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/749,568
XX CC FILING DATE: 26-AUG-1991
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Parmelee, Steven W.
XX CC REGISTRATION NUMBER: 31,990
XX CC REFERENCE/DOCKET NUMBER: 14137-26-4PC
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: (206) 467-9600
XX CC TELEFAX: (415) 543-5043
XX CC INFORMATION FOR SEQ ID NO: 1:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 9 amino acids
XX CC TYPE: amino acid
XX CC STRANDEDNESS: unknown
XX CC TOPOLOGY: unknown
XX CC MOLECULE TYPE: peptide
SQ SEQUENCE 9 AA; 976 MW; 576 CN;
Query Match 75.3%; Score 61; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.60e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EADPTGHSY 9
|||||
QY 4 EADPTGHSY 12

RESULT 3
US-08-299-849B-26 STANDARD; PRT; 9 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 26, Application US/08299849B.
XX
CC Sequence 26, Application US/08299849B
CC Patent No. 5612201
CC GENERAL INFORMATION:
CC APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC APPLICANT: Chomez, Patrick
CC TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurs
or
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felife & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/299,849B
CC FILING DATE: 1-SEPTEMBER-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/037,230
CC FILING DATE: 26-MARCH-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/04354
CC FILING DATE: 22-MAY-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/807,043
CC FILING DATE: 12-DECEMBER-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/764,364
CC FILING DATE: 23-SEPTEMBER-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/728,838
CC FILING DATE: 9-JULY-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/705,702
CC FILING DATE: 23-MAY-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5612201man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5355
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 26:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acids
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 9 AA; 976 MW; 576 CN;
Query Match 75.3%; Score 61; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.60e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EADPTGHSY 9
|||||
QY 4 EADPTGHSY 12

RESULT 4
ID PCT-US95-04975-2 STANDARD; PRT; 9 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application PC/TUS9504975.
XX
CC Sequence 2, Application PC/TUS9504975
CC GENERAL INFORMATION:
CC APPLICANT: Nikolic-Zugic, Janko
CC APPLICANT: Dyall, Rubendra
CC TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T LYMPHOCYTES (CTL)/USING
CC TITLE OF INVENTION: ANTIGENIC PEPTIDES AND A SUITABLE ADJUVANT
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Cooper & Dunham LLP
CC STREET: 1185 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.24
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/04975
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/233,496
CC FILING DATE: April 22, 1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: White Esq., John P.
CC REGISTRATION NUMBER: 28,678
CC REFERENCE/DOCKET NUMBER: 45059/JPW/MSC/AMB
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212-278-0400
CC TELEFAX: 212-391-0525
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acids
CC TOPOLOGY: Linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: N
CC ANTI-SENSE: N
CC SEQUENCE 9 AA; 976 MW; 576 CN;
Query Match 75.3%; Score 61; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.60e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EADPTGHSY 9
|||||
QY 4 EADPTGHSY 12

RESULT 5
ID US-08-186-266-1 STANDARD; PRT; 9 AA.
XX
AC xxxxxx

XX 01-JAN-1900
DT Sequence 1, Application US/08186266.
DE
XX
CC Sequence 1, Application US/08186266.
CC Patent No. 5662907
CC GENERAL INFORMATION:
CC APPLICANT: KUBO, Ralph T.
CC APPLICANT: GREY, Howard M.
CC APPLICANT: SETTE, Alessandro
CC APPLICANT: CELIS, Esteban
CC TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
CC TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING
CC TITLE OF INVENTION: SYNTHETIC PEPTIDE EPIPTOPES
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: Stewart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/186,266
CC FILING DATE: 25-JAN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/159,339
CC FILING DATE: 29-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/103,396
CC FILING DATE: 06-AUG-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/027,746
CC FILING DATE: 05-MAR-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/926,666
CC FILING DATE: 07-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bastian, Kevin L.
CC REGISTRATION NUMBER: 34,774
CC REFERENCE/DOCKET NUMBER: 14137-50-4
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 9 AA; 976 MW; 576 CN;
Query Match 75.3%; Score 61; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.60e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 EADPTGHSY 9
QY 4 EADPTGHSY 12
RESULT 6
ID US-07-938-334C-1 STANDARD; PRT; 9 AA.
XX
AC xxxxxx
XX

DT 01-JAN-1900
XX Sequence 1, Application US/07938334C.
DE
XX
CC Sequence 1, Application US/07938334C
CC Patent No. 5405940
CC GENERAL INFORMATION:
CC APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
CC APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE GENES AND USES THEREOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/938,334C
CC FILING DATE: 31-AUG-1992
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5405940man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 293
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acid residues
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: MAGE-1 derived nonapeptide
CC SEQUENCE 9 AA; 976 MW; 576 CN;
Query Match 75.3%; Score 61; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.60e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 EADPTGHSY 9
QY 4 EADPTGHSY 12
RESULT 7
ID US-08-443-341-12 STANDARD; PRT; 9 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 12, Application US/08443341.
XX
CC Sequence 12, Application US/08443341
CC Patent No. 5695994
CC GENERAL INFORMATION:
CC APPLICANT: Boon-Falleur, Thierry
CC APPLICANT: van der Bruggen, Pierre
CC APPLICANT: De Plaen, Etienne
CC APPLICANT: Lurquin, Christophe
CC APPLICANT: Traversari, Catia
CC APPLICANT: Gaugler, Beatrice
CC APPLICANT: Van den Eynde, Benoit

CC CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC CC TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THER
CC EOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/443,341
CC FILING DATE: 17-MAY-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/073,103
CC FILING DATE: 7-JUNE-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/938,334
CC FILING DATE: 31-AUG-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/037,230
CC FILING DATE: 26-MARCH-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5695994man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5293.5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 9 AA; 976 MW; 576 CN;
SQ
Query Match 75.3%; Score 61; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.60e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 EADPTGHSY 9
QY 4 EADPTGHSY 12
RESULT 8
ID US-08-073-103A-12 STANDARD; PRT; 9 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE Sequence 12, Application US/08073103A.
XX
CC Sequence 12, Application US/08073103A
CC Patent No. 5462871
CC GENERAL INFORMATION:
CC APPLICANT: Boon-Falleur, Thierry
CC APPLICANT: van der Bruggen, Pierre
CC APPLICANT: De Plaen, Etienne
CC APPLICANT: Lurquin, Christophe
CC APPLICANT: Traversari, Catia
CC APPLICANT: Gaugler, Beatrice
CC APPLICANT: Van den Eynde, Benoit

CC CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC CC TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THER
CC EOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/073,103A
CC FILING DATE: 7-JUNE-1993
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/938,334
CC FILING DATE: 31-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5462871man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5293.1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 9 AA; 976 MW; 576 CN;
SQ
Query Match 75.3%; Score 61; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.60e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 EADPTGHSY 9
QY 4 EADPTGHSY 12
RESULT 9
ID US-08-073-103A-14 STANDARD; PRT; 8 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
DE Sequence 14, Application US/08073103A.
XX
CC Sequence 14, Application US/08073103A
CC Patent No. 5462871
CC GENERAL INFORMATION:
CC APPLICANT: Boon-Falleur, Thierry
CC APPLICANT: van der Bruggen, Pierre
CC APPLICANT: De Plaen, Etienne
CC APPLICANT: Lurquin, Christophe
CC APPLICANT: Traversari, Catia
CC APPLICANT: Gaugler, Beatrice
CC APPLICANT: Van den Eynde, Benoit
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC CC TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THER
CC EOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch

CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/073.103A
CC FILING DATE: 7-JUNE-1993
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/938,334
CC FILING DATE: 31-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5462871man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5293.1
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 8 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 8 AA; 847 MW; 480 CN;

Query Match 67.9%; Score 55; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.09e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ADPTGHSY 8
| | | | | | | |
QY 5 ADPTGHSY 12

RESULT 10
ID US-08-443-341-14 STANDARD; PRT; 8 AA.

XX xxxxxx
AC
XX
DT 01-JAN-1900
XX
DE Sequence 14, Application US/08443341.
XX
Sequence 14, Application US/08443341
Patent No. 5695994
GENERAL INFORMATION:
CC APPLICANT: Boon-Falleur, Thierry
CC APPLICANT: van der Bruggen, Pierre
CC APPLICANT: De Plaen, Etienne
CC APPLICANT: Lurquin, Christophe
CC APPLICANT: Traversari, Catia
CC APPLICANT: Gaugler, Beatrice
CC APPLICANT: Van den Eynde, Benoit
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF

CC EOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC .ZIP: 10022
CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/443,341
CC FILING DATE: 17-MAY-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/073,103
CC FILING DATE: 7-JUNE-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/938,334
CC FILING DATE: 31-AUG-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/037,230
CC FILING DATE: 26-MARCH-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5695994man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5293.5
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 8 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 8 AA; 847 MW; 480 CN;

Query Match 67.9%; Score 55; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.09e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ADPTGHSY 8
| | | | | | | |
QY 5 ADPTGHSY 12

RESULT 11
ID US-08-073-103A-13 STANDARD; PRT; 8 AA.

XX xxxxxx
AC
XX
DT 01-JAN-1900
XX
DE Sequence 13, Application US/08073103A.
XX
Sequence 13, Application US/08073103A
Patent No. 5462871
GENERAL INFORMATION:
CC APPLICANT: Boon-Falleur, Thierry
CC APPLICANT: van der Bruggen, Pierre
CC APPLICANT: De Plaen, Etienne
CC APPLICANT: Lurquin, Christophe
CC APPLICANT: Traversari, Catia
CC APPLICANT: Gaugler, Beatrice
CC APPLICANT: Van den Eynde, Benoit
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF

CC EOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC .ZIP: 10022
CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/073,103A
CC FILING DATE: 7-JUNE-1993
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/938,334
CC FILING DATE: 31-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5462871man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5293.1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 8 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 8 AA; 813 MW; 405 CN;

Query Match 60.5%; Score 49; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.95e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EADPTGHS 8
|||||
QY 4 EADPTGHS 11

RESULT 12
ID US-08-443-341-13 STANDARD; PRT; 8 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 13, Application US/08443341.

XX Sequence 13, Application US/08443341
CC Patent No. 5695994

CC GENERAL INFORMATION:

CC APPLICANT: Boon-Falleur, Thierry
CC APPLICANT: van der Bruggen, Pierre
CC APPLICANT: De Plaen, Etienne
CC APPLICANT: Lurquin, Christophe
CC APPLICANT: Traversari, Catia
CC APPLICANT: Gaugler, Beatrice
CC APPLICANT: Van den Eynde, Benoit
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF

EOF

CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/443,341

CC FILING DATE: 17-MAY-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/073,103
CC FILING DATE: 7-JUNE-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/938,334
CC FILING DATE: 31-AUG-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/037,230
CC FILING DATE: 26-MARCH-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5695994man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5293.5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 8 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 8 AA; 813 MW; 405 CN;

Query Match 60.5%; Score 49; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.95e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EADPTGHS 8
|||||
QY 4 EADPTGHS 11

RESULT 13
ID US-07-938-334C-21 STANDARD; PRT; 8 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 21, Application US/07938334C.

XX Sequence 21, Application US/07938334C
CC Patent No. 5405940

CC GENERAL INFORMATION:

CC APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
CC APPLICANT: De Plaen, Etienne; Lurquin, Christophe; Traversari, Catia
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE GENES AND USES THEREOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/938,334C
CC FILING DATE: 31-AUG-1992
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5405940man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 293

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 8 amino acid residues
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 8 AA; 813 MW; 405 CN;

Query Match 60.5%; Score 49; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.95e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 EADPTGHS 8
QY 4 EADPTGHS 11

RESULT 14
ID US-08-430-787A-6 STANDARD; PRT; 417 AA.

XX
AC xxxxxx
DT 01-JAN-1900
XX Sequence 6, Application US/08430787A.

CC Sequence 6, Application US/08430787A.
CC Patent No. 5593674
CC GENERAL INFORMATION:
CC APPLICANT: Drayna, Dennis T.; Eaton, Dan L.
CC TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/430,787A
CC FILING DATE: 27-APR-1995
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/277,540
CC FILING DATE: 19-JUL-1994
CC APPLICATION NUMBER: 08/167727
CC FILING DATE: 15-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/959944
CC FILING DATE: 14-OCT-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/649591
CC FILING DATE: 01-FEB-91
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hasak, Janet E.
CC REGISTRATION NUMBER: 28,616
CC REFERENCE/DOCKET NUMBER: 689D1C1D1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-1896
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 417 amino acids

CC TYPE: amino acid
CC TOPOLOGY: linear
SQ SEQUENCE 417 AA; 48700 MW; 936226 CN;

Query Match 60.5%; Score 49; DB 6; Length 417;
Best Local Similarity 66.7%; Pred. No. 6.95e+00;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 105 DVKEDIPGRHSY 116
QY 1 DVKEDPTGHSY 12

RESULT 15
ID US-08-277-540-6 STANDARD; PRT; 417 AA.

XX
AC xxxxxx
DT 01-JAN-1900
XX

DE Sequence 6, Application US/08277540.

XX Sequence 6, Application US/08277540
CC Patent No. 5474901
CC GENERAL INFORMATION:
CC APPLICANT: Drayna, Dennis T.; Eaton, Dan L.
CC TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/277,540
CC FILING DATE: 19-JUL-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/167727
CC FILING DATE: 15-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/959944
CC FILING DATE: 14-OCT-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/649591
CC FILING DATE: 01-FEB-91
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hasak, Janet E.
CC REGISTRATION NUMBER: 28,616
CC REFERENCE/DOCKET NUMBER: 689D1C1D1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-1896
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 417 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
SQ SEQUENCE 417 AA; 48700 MW; 936226 CN;

Query Match 60.5%; Score 49; DB 5; Length 417;
Best Local Similarity 66.7%; Pred. No. 6.95e+00;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 105 DVKEDIPGRHSY 116

||||| I |||
QY 1 DVKEADPTGHSY 12

RESULT 16
ID US-07-649-591B-6 STANDARD; PRT; 417 AA.
XX AC xxxxxx
DT 01-JAN-1900
XX Sequence 6, Application US/07649591B.
XX Patent No. 5206161
CC GENERAL INFORMATION:
CC APPLICANT: Dennis Drayna and Daniel Eaton
CC TITLE OF INVENTION: NO. 5206161el Plasma Carboxypeptidase
CC NUMBER OF SEQUENCES: 8
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/649,591B
CC FILING DATE: 19910201
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hasak, Janet E.
CC REGISTRATION NUMBER: 28,616
CC REFERENCE/DOCKET NUMBER: 689
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/266-1896
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 6:
CC LENGTH: 417 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
SQ SEQUENCE 417 AA; 48700 MW; 936226 CN;

Query Match 60.5%; Score 49; DB 3; Length 417;
Best Local Similarity 66.7%; Pred. No. 6.95e+00;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 105 DVKEDIPGRHSY 116
||||| I |||
QY 1 DVKEADPTGHSY 12

RESULT 17
ID PCT-US94-14893-1 STANDARD; PRT; 925 AA.
XX AC xxxxxx
DT 01-JAN-1900
XX Sequence 1, Application PC/TUS9414893.
XX Sequence 1, Application PC/TUS9414893
CC GENERAL INFORMATION:

CC APPLICANT: Genentech, Inc.
CC APPLICANT: The Regents of the University of California
CC APPLICANT: Goldfine, Ira D.
CC APPLICANT: Grupe, Andrew
CC APPLICANT: Maddux, Betty A.
CC APPLICANT: Spencer, Steven
CC APPLICANT: Stewart, Timothy A.
CC TITLE OF INVENTION: Antagonists to Insulin Receptor Tyrosine Kinase I
nhibitor

CC NUMBER OF SEQUENCES: 1
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/14893
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/182241
CC FILING DATE: 14-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kubinec, Jeffrey S.
CC REGISTRATION NUMBER: 36,575
CC REFERENCE/DOCKET NUMBER: 875P1PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE:
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 925 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
SQ SEQUENCE 925 AA; 104924 MW; 4589090 CN;

Query Match 59.3%; Score 48; DB 13; Length 925;
Best Local Similarity 66.7%; Pred. No. 9.41e+00;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 374 EPDSSGHSY 382
|:|:|:|:|:|
QY 4 EADPTGHSY 12

RESULT 18
ID US-08-073-103A-20 STANDARD; PRT; 9 AA.
XX AC xxxxxx
DT 01-JAN-1900
XX Sequence 20, Application US/08073103A.
XX

Sequence 20, Application US/08073103A
Patent No. 5462871
CC GENERAL INFORMATION:
CC APPLICANT: Boon-Falleur, Thierry
CC APPLICANT: van der Bruggen, Pierre
CC APPLICANT: De Plaen, Etienne
CC APPLICANT: Lurquin, Christophe
CC APPLICANT: Traversari, Catia
CC APPLICANT: Gaugler, Beatrice
CC APPLICANT: van den Eynde, Benoit
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM

TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF

CC
EOF

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/073,103A

FILING DATE: 7-JUNE-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/938,334

FILING DATE: 31-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5462871man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5293.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 9 AA; 997 MW; 590 CN;

Query Match 56.8%; Score 46; DB 5; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.72e+01;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 EADPTSNTY 9

|||||:|

QY 4 EADPTGHSY 12

RESULT 19

ID US-07-938-334C-9

STANDARD; PRT; 9 AA.

XX

AC

XX

DT 01-JAN-1900

XX

DE Sequence 9, Application US/07938334C.

XX

Sequence 9, Application US/07938334C

Patent No. 5405940

GENERAL INFORMATION:

APPLICANT: Boon, Thierry; van der Bruggen, Pierre;

ADDRESSEE: Felfe & Lynch

TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM

TITLE OF INVENTION: MAGE GENES AND USES THEREOF

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/938,334C

FILING DATE: 31-AUG-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5405940man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 293

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acid residues

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: MAGE-6 derived nonapeptide

SEQUENCE 9 AA; 1028 MW; 611 CN;

Query Match 56.8%; Score 46; DB 5; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.72e+01;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 EVDPIGHVY 9

|||||

QY 4 EADPTGHSY 12

RESULT 20

ID US-08-073-103A-21

STANDARD; PRT; 9 AA.

XX

AC

XX

DT 01-JAN-1900

XX

DE Sequence 21, Application US/08073103A.

Sequence 21, Application US/08073103A

Patent No. 5462871

GENERAL INFORMATION:

APPLICANT: Boon-Falleur, Thierry

APPLICANT: van der Bruggen, Pierre

APPLICANT: De Plaen, Etienne

APPLICANT: Lurquin, Christophe

APPLICANT: Traversari, Catia

APPLICANT: Gaugler, Beatrice

APPLICANT: Van den Eynde, Benoit

TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM

TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF

EOF

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/073,103A

FILING DATE: 7-JUNE-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 07/938,334
CC FILING DATE: 31-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5452871man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5293.1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 9 AA; 997 MW; 590 CN;

Query Match 56.8%; Score 46; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.72e+01;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 EADPTSNTY 9
QY 4 EADPTGHSY 12
|||||:::|

RESULT 21
ID US-07-938-334C-8 STANDARD; PRT; 9 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 8, Application US/07938334C.
XX Sequence 8, Application US/07938334C
Patent No. 5405940
GENERAL INFORMATION:
CC APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
CC APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE GENES AND USES THEREOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/938,334C
CC FILING DATE: 31-AUG-1992
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5405940man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 293
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acid residues
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein

CC FEATURE:
CC NAME/KEY: MAGE-5 derived nonapeptide
SQ SEQUENCE 9 AA; 997 MW; 590 CN;

Query Match 56.8%; Score 46; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.72e+01;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 EADPTSNTY 9
QY 4 EADPTGHSY 12
|||||:::|

RESULT 22
ID US-08-443-341-21 STANDARD; PRT; 9 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 21, Application US/08443341.
XX Sequence 21, Application US/08443341
Patent No. 5695994
GENERAL INFORMATION:
CC APPLICANT: Boon-Falleur, Thierry
CC APPLICANT: van der Bruggen, Pierre
CC APPLICANT: De Plaen, Etienne
CC APPLICANT: Lurquin, Christophe
CC APPLICANT: Traversari, Catia
CC APPLICANT: Gaugler, Beatrice
CC APPLICANT: Van den Eynde, Benoit
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/443,341
CC FILING DATE: 17-MAY-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/073,103
CC FILING DATE: 7-JUNE-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/938,334
CC FILING DATE: 31-AUG-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/037,230
CC FILING DATE: 26-MARCH-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5695994man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5293.5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single

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CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 9 AA; 1028 MW; 611 CN;

Query Match 56.8%; Score 46; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.72e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db      1 EVDPIGHVY 9
      | | | | |
QY      4 EADPTGHSY 12

RESULT 24
US-07-938-334C-7 STANDARD; PRT: 9 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
Sequence 7, Application US/07938334C.
DE
XX
Sequence 7, Application US/07938334C
Patent No. 5405940
CC GENERAL INFORMATION:
CC APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
CC APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE GENES AND USES THEREOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/938,334C
CC FILING DATE: 31-AUG-1992
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5405940man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 293
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acid residues
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: MAGE-5 derived nonapeptide
SQ      SEQUENCE 9 AA; 997 MW; 590 CN;

Query Match 56.8%; Score 46; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.72e+01;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db      1 EADPTSNTY 9
      | | | | |
QY      4 EADPTGHSY 12

RESULT 25

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DE Sequence 2, Application US/08252626A.
XX Sequence 2, Application US/08252626A
CC Patent No. 5585269
CC GENERAL INFORMATION:
CC APPLICANT: Earp, Henry S.
CC APPLICANT: Graham, Douglas K.
CC APPLICANT: Dawson, Thomas L.
CC APPLICANT: Mullaney, David L.
CC APPLICANT: Snodgrass, Hiram R.
CC TITLE OF INVENTION: Isolated DNA Encoding C-MER
CC TITLE OF INVENTION: Protooncogene
CC NUMBER OF SEQUENCES: 9
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kenneth D. Sibley
CC STREET: P.O. Drawer 34009
CC CITY: Charlotte
CC STATE: No. 5585269th Carolina
CC COUNTRY: USA
CC ZIP: 28234
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/252,626A
CC FILING DATE: 02-JUN-1994
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Sibley, Kenneth D.
CC REGISTRATION NUMBER: 31,665
CC REFERENCE/DOCKET NUMBER: 5470-81
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (919) 881-3140
CC TELEFAX: (919) 881-3175
CC TELEX: 575102
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 999 amino acids s
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 999 AA: 110390 MW; 5284465 CN;
SQ
Query Match 56.8%; Score 46; DB 6; Length 999;
Best Local Similarity 63.6%; Pred. No. 1.72e+01;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 320 OVKEADPLGNG 330
Qy :|||||:::
1 DVKEADPTGHS 11
RESULT 28
ID PCT-US95-04975-1 STANDARD; PRT; 9 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 1, Application PC/TUS9504975.
XX
Sequence 1, Application PC/TUS9504975
CC GENERAL INFORMATION:
CC APPLICANT: Nikolic-Zugic, Janko
CC APPLICANT: Dyall, Rubendra
CC TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T LYMPHOCYTES (CTL) USING
CC TITLE OF INVENTION: ANTIGENIC PEPTIDES AND A SUITABLE ADJUVANT
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Cooper & Dunham LLP
CC STREET: 1185 Avenue of the Americas

CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.24
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/04975
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/233,496
CC FILING DATE: April 22, 1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: White Esq., John P.
CC REGISTRATION NUMBER: 28,678
CC REFERENCE/DOCKET NUMBER: 45059/JPW/MSC/AMB
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212-278-0400
CC TELEFAX: 212-391-0525
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acid
CC TOPOLOGY: Linear
CC MOLECULE TYPE: peptide
CC HYPOTHETICAL: N
CC ANTI-SENSE: N
CC SEQUENCE 9 AA: 1042 MW; 539 CN;
SQ
Query Match 53.1%; Score 43; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.15e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 1 EVDPIGHLY 9
Qy :|||||
4 EADPTGHSY 12
RESULT 29
ID US-08-443-341-17 STANDARD; PRT; 9 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 17, Application US/08443341.
XX
Sequence 17, Application US/08443341
CC Patent No. 5695994
CC GENERAL INFORMATION:
CC APPLICANT: Boon-Falleur, Thierry
CC APPLICANT: van der Bruggen, Pierre
CC APPLICANT: De Plaen, Etienne
CC APPLICANT: Lurquin, Christophe
CC APPLICANT: Traversari, Catia
CC APPLICANT: Gaugler, Beatrice
CC APPLICANT: Van den Eynde, Benoit
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
CC
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022
CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/443,341
CC FILING DATE: 17-MAY-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/073,103
CC FILING DATE: 7-JUNE-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/938,334
CC FILING DATE: 31-AUG-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/037,230
CC FILING DATE: 26-MARCH-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5695994man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LUD 5293.5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 9 AA; 1042 MW; 539 CN;

Query Match 53.1%; Score 43; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.15e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 EVDPIGHL 9
| | | | |
Qy 4 EADPTGHSY 12

RESULT 30
ID US-08-186-266-2 STANDARD; PRT; 9 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application US/08186266.
XX
XX Sequence 2, Application US/08186266
CC Patent No. 5662907
CC GENERAL INFORMATION:
CC APPLICANT: KUBO, Ralph T.
CC APPLICANT: GREY, Howard M.
CC APPLICANT: SETTE, Alessandro
CC APPLICANT: CELIS, Esteban
CC TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
CC TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING
CC TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/186,266
CC FILING DATE: 25-JAN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/159,339
CC FILING DATE: 29-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/103,396
CC FILING DATE: 06-AUG-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/027,746
CC FILING DATE: 05-MAR-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/926,666
CC FILING DATE: 07-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bastian, Kevin L.
CC REGISTRATION NUMBER: 34,774
CC REFERENCE/DOCKET NUMBER: 14137-50-4
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 9 AA; 1042 MW; 539 CN;

Query Match 53.1%; Score 43; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.15e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 EVDPIGHL 9
| | | | |
Qy 4 EADPTGHSY 12

RESULT 31
ID US-07-938-334C-4 STANDARD; PRT; 9 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 4, Application US/07938334C.
XX
XX Sequence 4, Application US/07938334C
CC Patent No. 5405940
CC GENERAL INFORMATION:
CC APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
CC APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE GENES AND USES THEREOF
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/938,334C
CC FILING DATE: 31-AUG-1992

CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5405940man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LOD 293
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acid residues
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: MAGE-3 derived nonapeptide
CC SEQUENCE 9 AA; 1042 MW; 539 CN;
SQ
Query Match 53.1%; Score 43; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.15e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 1 EVDPIGHLY 9
QY 4 EADPTGHSY 12
RESULT 32
ID US-08-073-103A-17 STANDARD; PRT; 9 AA.
XX
AC xxxxxx
DT 01-JAN-1900
XX
DE Sequence 17, Application US/08073103A.
CC
CC Sequence 17, Application US/08073103A
CC Patent No. 5462871
CC GENERAL INFORMATION:
CC APPLICANT: Boon-Falleur, Thierry
CC APPLICANT: van der Bruggen, Pierre
CC APPLICANT: De Plaen, Etienne
CC APPLICANT: Lurquin, Christophe
CC APPLICANT: Traversari, Catia
CC APPLICANT: Gaugler, Beatrice
CC APPLICANT: Van den Eynde, Benoit
CC TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
CC TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
CC
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Felfe & Lynch
CC STREET: 805 Third Avenue
CC CITY: New York City
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10022
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: PC-DOS
CC SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/073,103A
CC FILING DATE: 7-JUNE-1993
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION NUMBER: 07/938,334
CC FILING DATE: 31-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hanson, No. 5462871man D.
CC REGISTRATION NUMBER: 30,946
CC REFERENCE/DOCKET NUMBER: LOD 5293.1

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 688-9200
CC TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 9 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 9 AA; 1042 MW; 539 CN;
SQ
Query Match 53.1%; Score 43; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.15e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 1 EVDPIGHLY 9
QY 4 EADPTGHSY 12
RESULT 33
ID US-08-186-266-9 STANDARD; PRT; 32 AA.
XX
AC xxxxxx
DT 01-JAN-1900
XX
DE Sequence 9, Application US/08186266.
CC
CC Sequence 9, Application US/08186266
CC Patent No. 5662907
CC GENERAL INFORMATION:
CC APPLICANT: KUBO, Ralph T.
CC APPLICANT: GREY, Howard M.
CC APPLICANT: SETTE, Alessandro
CC APPLICANT: CELIS, Esteban
CC TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
CC TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: Stewart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/186,266
CC FILING DATE: 25-JAN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/159,339
CC FILING DATE: 29-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/103,396
CC FILING DATE: 06-AUG-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/027,746
CC FILING DATE: 05-MAR-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/926,666
CC FILING DATE: 07-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bastian, Kevin L.
CC REGISTRATION NUMBER: 34,774
CC REFERENCE/DOCKET NUMBER: 14137-50-4

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 32 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FEATURE:
CC NAME/KEY: Modified-site
CC LOCATION: 1
CC OTHER INFORMATION: /note= "The Lys at the N-terminus
CC OTHER INFORMATION: is lipdated using two palmitic acid residues."
SQ SEQUENCE 32 AA; 3365 MW; 5057 CN;

Query Match 53.1%; Score 43; DB 7; Length 32;
Best Local Similarity 66.7%; Pred. No. 4.15e+01;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 24 EVDPTGHSY 32
QY 4 EADPTGHSY 12

RESULT 34
ID PCR-US93-02172-12 STANDARD; PRT; 559 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 12, Application PC/TUS9302172.
XX
CC Sequence 12, Application PC/TUS9302172
CC GENERAL INFORMATION:
CC APPLICANT: La Jolla Cancer Research Foundation
CC TITLE OF INVENTION: RECOMBINANT CALF INTESTINAL ALKALINE
CC TITLE OF INVENTION: PHOSPHATASE
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: La Jolla Cancer Research Foundation
CC STREET: 10901 North Torrey Pines Road
CC CITY: La Jolla
CC STATE: California
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PatentIn Release #1.0, Version 1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/02172
CC FILING DATE: 19930310
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/07/849,219
CC FILING DATE: 10-MAR-1992
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-6480
CC TELEFAX: (619) 455-0181
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 559 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC SEQUENCE 559 AA; 60255 MW; 1639274 CN;

Query Match 53.1%; Score 43; DB 12; Length 559;
Best Local Similarity 41.7%; Pred. No. 4.15e+01;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 427 NVTAAESSGSSY 438
QY 1 DVREADPTGHSY 12

RESULT 35
ID US-08-368-071-12 STANDARD; PRT; 559 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 12, Application US/08368071.
XX
CC Sequence 12, Application US/08368071
CC Patent No. 5707853
CC GENERAL INFORMATION:
CC APPLICANT: MILLAN, JOSE L.
CC TITLE OF INVENTION: RECOMBINANT CALF INTESTINAL ALKALINE
CC TITLE OF INVENTION: PHOSPHATASE
CC NUMBER OF SEQUENCES: 13
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CAMPBELL AND FLORES
CC STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CC CITY: SAN DIEGO
CC STATE: CALIFORNIA
CC COUNTRY: UNITED STATES
CC ZIP: 92122
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/368,071
CC FILING DATE: 03-JAN-1995
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: CAMPBELL, CATHRYN
CC REGISTRATION NUMBER: 31,815
CC REFERENCE/DOCKET NUMBER: P-LJ 1275
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-535-9001
CC TELEFAX: 619-535-8949
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 559 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 559 AA; 60255 MW; 1639274 CN;

Query Match 53.1%; Score 43; DB 8; Length 559;
Best Local Similarity 41.7%; Pred. No. 4.15e+01;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 427 NVTAAESSGSSY 438
QY 1 DVREADPTGHSY 12

Search completed: Tue Apr 7 08:46:21 1998
Job time : 15 secs.